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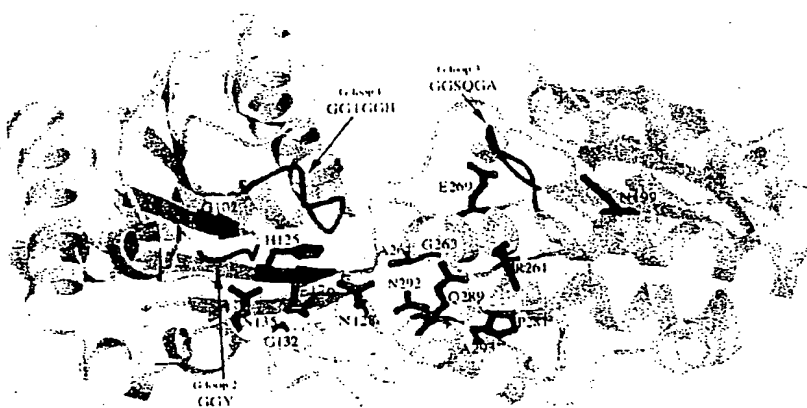
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(54) Title: METHODS OF MAKING MODELS. METHODS OF USING MODELS OF MURG, COMPOUNDS THAT BIND, INHIBIT OR STIMULATE MURET PROTEINS, AND THERAPEUTIC COMPOSITIONS THEREOF



(57) Abstract: The present invention relates to crystals of the *Escherichia coli* MurG, a membrane-associated UDP-glycosyltransferase involved in peptidoglycan biosynthesis. The present invention also relates to three-dimensional atomic coordinates of the MurG protein, three-dimensional structures of the protein, and images thereof. The present invention also relates to the atomic coordinates and three-dimensional structures of the α -carbon backbone and the α -carbon backbone and conserved amino acid residue sidechains of the MurG protein and images thereof. The present invention further relates to three-dimensional atomic

coordinates of the donor nucleotide binding site, the acceptor binding site, and the membrane association site of the MurG protein, three-dimensional structures of the binding domains, and images thereof. The present invention also relates to computer readable media encoded with sets of the three dimensional coordinates described herein. The present invention relates to methods of crystallizing MurG proteins. The present invention relates to models of three dimensional structures of UDP-glycosyltransferases and, in particular, MurG proteins, based on the three dimensional structure dimensional structure of crystals of the *Escherichia coli* MurG. The present invention also relates to models of the three dimensional structures of the α -carbon backbone and the α -carbon backbone and conserved amino acid residue sidechains of UDP-glycosyltransferases and MurG proteins and of the binding sites thereof. The present invention also relates to methods of drug design using models of this invention, the compounds identified using models of the present invention that bind, inhibit or stimulate UDP-glycosyltransferases or MurG proteins, and compositions comprising compounds identified using the models of this invention for therapeutic or diagnostic uses. Also, the present invention relates to methods of making models of the present invention.

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METHODS OF MAKING MODELS, METHODS OF USING MODELS OF MURG, COMPOUNDS THAT BIND, INHIBIT OR STIMULATE MURG PROTEINS, AND THERAPEUTIC COMPOSITIONS THEREOF

FIELD OF THE INVENTION

The present invention relates to crystals of the *Escherichia coli* MurG, a membrane-associated UDP-glycosyltransferase involved in peptidoglycan biosynthesis. The present invention also relates to three-dimensional atomic coordinates of the MurG protein, three-dimensional structures of the protein, and images thereof. The present invention also relates to the atomic coordinates and three-dimensional structures of the α -carbon backbone of the MurG protein and images thereof. The present invention further relates to the atomic coordinates and three-dimensional structures of the α -carbon backbone and conserved amino acid residue sidechains of the MurG protein and images thereof. The present invention further relates to three-dimensional atomic coordinates of the donor nucleotide binding site, the acceptor binding site, and the membrane association site of the MurG protein, three-dimensional structures of the binding domains, and images thereof. The present invention also relates to computer readable media encoded with sets of the three dimensional coordinates of the *E. coli* MurG protein, the α -carbon backbone of the MurG protein, the α -carbon backbone and the conserved amino acid residue sidechains of the MurG protein, the donor nucleotide binding site, the acceptor binding site, and the membrane association site. The present invention relates to methods of crystallizing MurG proteins.

The present invention relates to models of three dimensional structures of UDP-glycosyltransferases and, in particular, MurG proteins, based on the three dimensional structure of crystals of the *Escherichia coli* MurG. The present invention also relates to models of the three dimensional structures of the α -carbon backbone of UDP-glycosyltransferases and MurG proteins. The present invention further relates to models of the three dimensional structure of the α -carbon backbone and conserved amino acid residue sidechains of gUDP-glycosyltransferases, in particular, MurG proteins. The present invention further relates to models of the three-dimensional structures of donor nucleotide binding sites, acceptor binding sites, and membrane association sites of UDP-glycosyltransferases, in particular, MurG proteins. The present invention also relates to methods of drug design using models of this invention. The present invention further relates to compounds identified using models of the present invention that bind, inhibit or stimulate UDP-glycosyltransferases or MurG proteins. The present invention relates to compositions comprising compounds identified using the models of this invention for therapeutic or diagnostic uses. Also, the present invention relates to methods of making models of the present invention.

BACKGROUND OF THE INVENTION

The increasing frequency of resistance to existing antibiotics represents a serious public health threat. Structural and mechanistic information on essential bacterial enzymes could lead to the development of antibiotics that are active against resistant microorganisms. Both gram positive and gram negative bacterial cells are surrounded by a cross-linked carbohydrate polymer, peptidoglycan, which protects them from rupturing under high osmotic pressures. Many of the best antibiotics function by inhibiting peptidoglycan synthesis, which ultimately causes cell lysis. In recent years, intense effort has been focused on determining the structures of the enzymes that synthesize peptidoglycan. Structures of several of the early enzymes in the biosynthetic pathway have been reported (Benson *et al.*, 1995; Bertrand *et al.*, 1997; Fan *et al.*, 1994; Skarzynski *et al.*, 1996); however, the later enzymes have proven more difficult to study because both they and their substrates are membrane-associated.

MurG is the last enzyme involved in the intracellular phase of peptidoglycan synthesis (Bugg & Walsh, 1993). It catalyzes the transfer of N-acetyl glucosamine

(NAG) from UDP to the C4 hydroxyl of a lipid-linked N-acetylmuramoyl pentapeptide (NAM) to form a β -linked NAG-NAM disaccharide that is transported across the cell membrane where it is polymerized and cross-linked (Fig. 1). In bacterial cells MurG associates with the cytoplasmic surface of the membrane (Bupp & van Heijenoort, 1993). However, we have found that *E. coli* MurG can be solubilized at high concentrations in active form (Ha *et al.*, 1999).

The elucidation of the protein structure of a MurG protein is of importance in the identification and formulation of anti-bacterial agents. Until the discovery of the present invention, the structure and resulting mechanism by which MurG functions was not known. Thus, despite the important role of MurG in peptidoglycan synthesis, development of useful agents for treatment or diagnosis of disease was hindered by lack of structural information of the protein.

In order to obtain structural information on a MurG protein, it is important to have purified, active enzyme. The demonstration of activity requires a suitable assay, which in turn requires access to the natural substrates or analogues thereof. The study of MurG was hampered by difficulties obtaining and handling the lipid-linked NAM substrate (commonly known as Lipid I). This problem was overcome by Walker and coworkers, who developed a synthetic route to a set of substrate analogues of Lipid I that were shown to function as glycosyl acceptors in a glycosyl transfer reaction catalyzed by MurG. Some of these substrate analogues are freely water soluble, making it possible to monitor the activity of purified *E. coli* MurG in buffer in the absence of natural or artificial membranes or detergents.

The linear nucleic acid and amino acid sequences of *E. coli* MurG were reported in 1992. Subsequently, the nucleic acid and amino acid sequence of *B. subtilis* MurG was reported. Since then, many bacterial genomes have been sequenced and the information has been deposited in databases. Information based only on linear sequences, however, cannot accurately predict the three-dimensional structure of the protein and its functional domains.

Therefore, there is a need in the art to elucidate the three-dimensional structure of a MurG protein. One three dimensional structure of a MurG-protein can be used to construct models of other MurG proteins and to facilitate the structure determination of crystalline forms of other MurG proteins. Structures and models of MurG proteins can

also be used to design proteins containing only the donor binding site or the acceptor binding site. These proteins can be used in assays, including NMR-based assays, to identify -- or characterize the mode of binding of -- ligands that bind in or near the vicinity of the substrates. These ligands or compounds can then be used as leads for the design of inhibitors that have therapeutic activity. Structures and models of MurG proteins can also be used in computer-based drug design.

SUMMARY OF THE INVENTION

The present invention relates to crystalline *Escherichia coli* MurG protein. Obtaining such crystals is an unexpected result. It is well known in the protein crystallographic art that obtaining crystals of quality sufficient for determining the structure of a protein is unpredictable. In particular, obtaining crystals of quality sufficient for determining the three-dimensional (3-D) structure of MurG has not been achievable until the crystallization of MurG as disclosed in the present application. As such, determination of the three-dimensional structure of MurG has not been possible until the discovery of the present invention. Additionally, until the discovery of the present invention, derivation of the three-dimensional structure and models of other MurG proteins has not been possible. The present inventors are also the first to define the three-dimensional structure and provide three-dimensional models for drug design for MurG proteins.

Accordingly, one object of the present invention is to provide crystals of sufficient quality to obtain a determination of the three-dimensional atomic coordinates and structures of MurG to high resolution, preferably to the resolution of less than 2.0 angstroms (Å). The present invention also provides methods for producing crystalline MurG protein.

The value of the crystals of *E. coli* MurG protein extends beyond merely being able to obtain such crystals. The knowledge obtained concerning the MurG crystal structure, for example, has been used by the present inventors to define the heretofore unknown tertiary structure of the MurG protein and to identify the location of the glycosyl donor and glycosyl acceptor binding domains, as well as the location of the amino acid residues that are invariant in all MurG proteins. This information can be used to design inhibitors of MurG that have therapeutic utility. The atomic coordinates of *E.*

coli MurG also are used to model the heretofore unknown tertiary structures of other MurG proteins having substantially related linear amino acid sequences, such as for MurG proteins from other microorganisms. It is anticipated that homology models can be constructed even from amino acid sequences with relatively low homology because the present inventors have identified the location of the invariant amino acid residues in MurG. The relative spatial orientations of such residues is expected to be conserved in all MurG proteins.

Comparison of nucleic acid and amino acid sequences of MurG proteins indicates that the linear amino acid sequences can vary significantly. Homology between MurG proteins from different microorganisms varies from less than 30% to greater than 90%, reflecting the evolutionary relationship between the organisms. The low homology between distantly related MurG homologues is not believed to reflect significantly different folded structures. It is well known that many amino acid sequences are capable of adopting the same general fold. *E. coli* MurG contains an alpha/beta folding pattern, one of the most common folds known in proteins. It is likely that all MurG homologues contain a similar alpha/beta fold despite the differences in the linear amino acid sequences. What gives these proteins their identity is not the general fold, but the specific details – *i.e.*, the presentation of certain amino acids on the folded structure. The present inventors have identified the location in *E. coli* MurG of a set of residues that are invariant in all MurG homologues. It is to be expected that these residues would adopt a similar spatial location with respect to the folded structure in all MurG homologues. Therefore, these invariant residues, which have been selected by evolution as the critical residues for the binding and catalytic function of the protein, provide essential information on the location of the active site and on critical contacts to the substrates/products. They also serve as constraints that make it possible to predict the three-dimensional structures even of distantly related MurG homologues. Thus, knowledge of the three-dimensional structure of the *E. coli* MurG protein has provided a starting point for investigation into the structure of all MurG proteins.

Accordingly, a object of the present invention is to provide information regarding the atomic coordinates and three-dimensional structures of (1) the MurG protein, (2) the α -carbon backbone of the MurG protein, (3) the α -carbon backbone and conserved

amino acid residues of the MurG protein, (4) the donor nucleotide binding site, (5) the acceptor binding site, and (6) the membrane association site MurG proteins.

It is also an object of this invention to solve the three-dimensional structure of UDP-glycosyltransferases, in particular target MURG proteins, and to determine their structure and/or atomic coordinates. Further, it is an object of this invention to use the structure or atomic coordinates of the *E. coli* MurG crystal to solve the structure of different MURG protein crystals, or a crystal of a mutant protein, homolog or co-complex of MurG.

The present invention relates to models of three dimensional structures of UDP-glycosyltransferases, in particular MurG proteins, based on the atomic coordinates of crystalline *E. coli* MurG protein.

It is a further object of this invention to provide UDP-glycosyltransferase enzyme mutants characterized by one or more different properties as compared with wild-type MURG. These properties include altered surface charge, increased stability to subunit dissociation, altered substrate specificity or higher specific activity. MURG mutants are useful to identify those amino acids that are most important for the enzymatic activity of MURG. This information, in turn, allows the design of improved inhibitors of MURG as compared with peptidic MURG inhibitors.

Another object of the present invention is to provide computer readable mediums encoded with a set of three-dimensional coordinates of the *E. coli* MurG protein, the α -carbon backbone of the MurG protein, the α -carbon backbone and conserved amino acid residues of the MurG protein, and the nucleotide donor binding site, the acceptor binding site, the membrane association site of the MurG protein.

Another embodiment of the present invention provides three-dimensional and two-dimensional computer images of the three dimensional structure of MurG protein, the α -carbon backbone of the MurG protein, the α -carbon backbone and conserved amino acid residues of the MurG protein, and the nucleotide donor binding site, the acceptor binding site, the membrane association site of the MurG protein.

The knowledge of the three dimensional structure of MurG also provides a means for designing proteins that have altered beneficial functions by analyzing the structure and interactions between individual amino acids of the protein. For example, the present inventors have shown that *E. coli* MurG consists of two domains separated by a cleft.

Noncovalent interactions between the two domains are not extensive. The present inventors have shown that the domains fold independently and can, therefore, be expressed independently either alone or as part of a recombinant protein containing the acceptor binding site from one MurG homologue and the donor binding site from another MurG homologue. It would be expected that the domains of other MurG proteins could also be expressed independently, either alone or as chimaeras with other MurG domains. Independently expressed domains of the protein are useful for discovering ligands that bind to the individual domains.

The knowledge of the three-dimensional structure of *E. coli* MurG protein and models of other MurG proteins also provides a means for designing and producing compounds that regulate, inhibit or antagonize functions of the MurG protein (i.e., structure based drug design). For example, chemical compounds can be designed to block binding of UDP-GlcNAc to a MurG protein using various computer programs and models.

It is also an object of this invention to use the structure coordinates and atomic details of MURG, or its mutants or homologues or co-complexes, to design, evaluate computationally, synthesize and use inhibitors of MURG that avoid the undesirable physical and pharmacologic properties of peptidic MURG inhibitors. Another embodiment of the present invention is a composition comprising MurG protein in a crystalline form.

Yet another embodiment of the present invention is a method for producing crystals of MurG, comprising combining MurG protein in a suitable buffer with a suitable amount of a reservoir buffer containing a detergent, and inducing crystal formation to produce said MurG crystals.

BRIEF DESCRIPTION OF THE DRAWINGS

Fig. 1. Pathway for peptidoglycan biosynthesis.

Fig. 2. Overall architecture of MurG. A. Stereo view of the MurG structure. The N domain is shown in purple; the C domain is shown in green. The figure was generated with the programs MOLSCRIPT (Klailis, 1991) and RASTER3D (Merrit & Murphy, 1994). B. Topology diagram of MurG.

Fig. 3. Identification of critical residues in MurG and related glycosyltransferases. **A.** Sequence alignment of *E. coli* MurG with homologs from seven other bacterial strains, deliberately chosen to represent a disparate group of organisms. The secondary structure of *E. coli* MurG is shown above the sequences. Gaps mapping to the loop regions of *E. coli* MurG suggest that some sequences include other structural elements. Residues highlighted in blue are invariant among the eighteen MurG sequences available. Residues highlighted in yellow are identical in 85% of the eighteen homologs, while in the remaining 15%, only closely related amino acid substitutions are found. Highly conserved residues that do not meet the stringent criteria established for highlighting are shown in the consensus sequence. A consensus motif for UDP-glucuronosyltransferases is also shown. Numbering is with respect to the overexpressed *E. coli* MurG construct, which contains an additional N-terminal methionine. **B.** Mapping of the G loops and other highlighted residues from Fig. 3a in red on the MurG structure. Side chains for highly conserved residues are also shown. **C.** Model for the proposed UDP-binding subdomain found in many UDP-glycosyltransferases based on the *E. coli* MurG structure. Conserved residues in UDP-glucuronosyltransferases are highlighted in red. Side chains are shown for residues that are located near the cleft and may be involved in substrate binding. The glutamate residue is proposed to interact with the ribose sugar. The dotted loop varies in length within the MurG family and in other UDP-sugar transferases, but the N and Q on the following helix are invariant. Note that the UDP-glucuronosyltransferases contain a conserved D preceding the Q, which is not shown on this model.

Fig 4. Structural analysis of the substrate binding pockets in MurG. **A.** Structural comparison between the C-terminal domain of phage T4 β -glucosyltransferase (left) and the C-terminal domain of *E. coli* MurG (right). The aligned six β -strands are magenta, the aligned β -helices are orange, and the other structural elements are blue. In β -glucosyltransferase, key residues involved in UDP binding are highlighted in yellow. The analogous residues in MurG are also highlighted in yellow. **B.** A close-up view of the proposed donor binding pocket in the MurG C domain with the docked UDP-GlcNAc. Conserved residues in MurG are colored magenta. The carbonyl oxygen of

residue I245 is shown in red, and its backbone nitrogen is shown in blue. C. The surface of *E. coli* MurG. The G loops and other conserved residues in MurG are colored magenta. The proposed membrane binding interface is also highlighted with hydrophobic residues in yellow and positively charged residues in blue.

DEFINITIONS

It is to be noted that the term "a" or "an" entity refers to one or more of that entity; for example, a compound refers to one or more compounds or at least one compound. As such, the terms "a" (or "an"), "one or more", and "at least one" can be used interchangeably herein.

It is also to be noted that the terms "comprising", "including" and "having" can be used interchangeably. Furthermore, a compound "selected from the group consisting of" refers to one or more of the compounds in the list that follows, including mixtures (i.e., combinations) of two or more of the compounds.

According to the present invention, an isolated, or pure, protein, is a protein that has been removed from its natural milieu. As such, "isolated" and "biologically pure" do not necessarily reflect the extent to which the protein has been purified. An isolated protein of the present invention can be obtained from its natural source, can be produced using recombinant DNA technology or can be produced by chemical synthesis.

It is also to be noted that the terms "tertiary" and "three dimensional" can be used interchangeably.

It is also to be noted that reference to a "MurG protein" can also be recited as "MurG" and such terms can be used to refer to the complete MurG protein, a portion of the MurG protein, such as a polypeptide.

The following terms are also used herein:

The term "naturally occurring amino acids" means the L-isomers of the naturally occurring amino acids. The naturally occurring amino acids are glycine, alanine, valine, leucine, isoleucine, serine, methionine, threonine, phenylalanine, tyrosine, tryptophan, cysteine, proline, histidine, aspartic acid, asparagine, glutamic acid, glutamine, gamma-carboxyglutamic acid, arginine, ornithine and lysine. Unless specifically indicated, all amino acids referred to in this application are in the L-form.

The term "unnatural amino acids" means amino acids that are not naturally found in proteins. Examples of unnatural amino acids used herein, include racemic mixtures of selenocysteine and selenomethionine. In addition, unnatural amino acids include the D or L forms of nor-leucine, para-nitrophenylalanine, homophenylalanine, para-fluorophenylalanine, 3-amino-p2-benzylpropionic acid, homoarginine, and D-phenylalanine.

The term "positively charged amino acid" includes any naturally occurring or unnatural amino acid having a positively charged side chain under normal physiological conditions. Examples of positively charged naturally occurring amino acids are arginine, lysine and histidine.

The term "negatively charged amino acid" includes any naturally occurring or unnatural amino acid having a negatively charged side chain under normal physiological conditions. Examples of negatively charged naturally occurring amino acids are aspartic acid and glutamic acid.

The term "hydrophobic amino acid" means any amino acid having an uncharged, nonpolar side chain that is relatively insoluble in water. Examples of naturally occurring hydrophobic amino acids are alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan and methionine.

The term "hydrophilic amino acid" means any amino acid having an uncharged, polar side chain that is relatively soluble in water. Examples of naturally occurring hydrophilic amino acids are serine, threonine, tyrosine, asparagine, glutamine, and cysteine.

The term "MurG" refers to a UDP-glycosyltransferase that has a two domain structure, where each domain contains a set of invariant residues as shown in Figure 3a, including any mutant, homologue or co-complex or any similar enzyme that catalyzes the transfer of N-acetylglucosamine (GlcNAc) from UDP to the C4 hydroxyl of the lipid-linked MurNAc pentapeptide.

The term "mutant" refers to a MurG polypeptide, *i.e.*, a polypeptide displaying the biological activity of a wild-type MurG, characterized by the replacement of at least one amino acid from the wild-type, *E. coli* MURG sequence according to Ikeda, et al., Nucleic Acids Res. 1990, and Mengin-LeCreuix et al., Nucleic Acids Res. 1990. Such a

mutant may be prepared, for example, by expression of MURG cDNA previously altered in its coding sequence by PCR-based mutagenesis method.

MurG mutants may also be generated by site-specific incorporation of unnatural amino acids into MURG proteins using the general biosynthetic method of Noren, C. J., et al., *Science*, 244, pp. 182-188 (1989). In this method, the codon encoding the amino acid of interest in wild-type MURG is replaced by a "blank" nonsense codon, TAG, using oligonucleotide-directed mutagenesis (described in detail, *infra*). A suppressor tRNA directed against this codon is then chemically aminoacylated in vitro with the desired unnatural amino acid. The aminoacylated tRNA is then added to an in vitro translation system to yield a mutant MURG enzyme with the site-specific incorporated unnatural amino acid.

Selenocysteine or selenomethionine may be incorporated into wild-type or mutant MURG by expression of MURG-encoding cDNAs in auxotrophic *E. coli* strains. Hendrickson, W. A. et al., *EMBO J.*, 9(5), pp. 1665-1672 (1990). In this method, the wild-type or mutagenized MURG CDNA may be expressed in a host organism on a growth medium depleted of either natural cysteine or methionine (or both) but enriched in selenocysteine or selenomethionine (or both).

The term "altered surface charge" means a change in one or more of the charge units of a mutant polypeptide, at physiological pH, as compared to wild-type MURG. This is preferably achieved by mutation of at least one amino acid of wild-type MURG to an amino acid comprising a side chain with a different charge at physiological pH than the original wild-type side chain.

The change in surface charge is determined by measuring the isoelectric point (pI) of the polypeptide molecule containing the substituted amino acid and comparing it to the isoelectric point of the wild-type MURG molecule.

The term "altered substrate specificity" refers to a change in the ability of a mutant MURG to cleave a substrate as compared to wild-type MURG.

The "kinetic form" of MURG refers to the condition of the enzyme in its free or unbound form or bound to a chemical entity at either its active site or accessory binding site.

A "competitive" inhibitor is one that inhibits MURG activity by binding to the same kinetic form, of MURG, as its substrate binds—thus directly competing with the

substrate for the active site of MURG. Competitive inhibition can be reversed completely by increasing the substrate concentration.

An "uncompetitive" inhibitor is one that inhibits MURG by binding to a different kinetic form of the enzyme than does the substrate. Such inhibitors bind to MURG already bound with the substrate and not to the free enzyme. Uncompetitive inhibition cannot be reversed completely by increasing the substrate concentration.

A "non-competitive" inhibitor is one that can bind to either the free or substrate bound form of MURG.

Those of skill in the art may identify inhibitors as competitive, uncompetitive or non-competitive, by computer fitting enzyme kinetic data using standard equations according to Segel, I. H., *Enzyme Kinetics*, J. Wiley & Sons, (1975). It should also be understood that uncompetitive or non-competitive inhibitors according to this invention may bind to the accessory binding site.

The term "homolog" means a protein having at least 25% amino acid sequence identity with MURG or any functional part of MURG, and including certain invariant amino acid residues corresponding to G14, G15, G18, H19, G104, H124, E125, G190, G191, S192, G194, A195, R261, G263, A264, E269, P281, Q289, N292 and A293 (as numbered in the *E.coli* MurG sequence set forth in Figure 3a) and also including three glycine rich loops. A homolog may contain some or all of the invariant residues.

The term "co-complex" means MURG or a mutant or homologue of MURG in covalent or non-covalent association with a chemical entity or compound.

The term "associating with" refers to a condition of proximity between a chemical entity or compound, or portions thereof, and a MurG molecule or portions thereof. The association may be non-covalent--wherein the juxtaposition is energetically favored by hydrogen bonding or van der Waals or electrostatic interactions--or it may be covalent.

The term ".beta.-sheet" refers to the conformation of a polypeptide chain stretched into an extended zig-zig conformation. Portions of polypeptide chains that run "parallel" all run in the same direction. Polypeptide chains that are "antiparallel" run in the opposite direction from the parallel chains.

The terms "atomic coordinates" or "structure coordinates" refer to mathematical coordinates derived from mathematical equations related to the patterns obtained on diffraction of a monochromatic beam of X-rays by the atoms (scattering centers) of a

MurG molecule in crystal form. The diffraction data are used to calculate an electron density map of the repeating unit of the crystal. The electron density maps are used to establish the positions of the individual atoms within the unit cell of the crystal.

The term "heavy atom derivatization" refers to the method of producing a chemically modified form of a crystal of MURG. In practice, a MurG crystal is soaked in a solution containing heavy metal atom salts, or organometallic compounds, e.g., lead chloride, gold thiomalate, thimerosal, uranyl acetate or mercuric chloride, which can diffuse through the crystal and bind to the surface of the protein. The location(s) of the bound heavy metal atom(s) can be determined by X-ray diffraction analysis of the soaked crystal. This information, in turn, is used to generate the phase information used to construct three-dimensional structure of the enzyme. Blundel, T. L. and N. L. Johnson, Protein Crystallography, Academic Press (1976).

Those of skill in the art understand that a set of structure coordinates determined by X-ray crystallography is not without standard error. For the purpose of this invention, any set of structure coordinates for MURG or MURG homologues or MURG mutants that have a root mean square deviation of protein backbone atoms (N, C.alpha., C and O) of less than 0.75 Å when superimposed--using backbone atoms--on the structure coordinates listed in Table 1, Table 2 or Table 3 shall be considered identical.

The term "unit cell" refers to a basic parallelepiped shaped block. The entire volume of a crystal may be constructed by regular assembly of such blocks. Each unit cell comprises a complete representation of the unit of pattern, the repetition of which builds up the crystal.

The term "space group" refers to the arrangement of symmetry elements of a crystal.

The term "molecular replacement" refers to a method that involves generating a preliminary model of a MurG crystal whose structure coordinates are unknown, by orienting and positioning a molecule whose structure coordinates are known (e.g., MURG coordinates from Table 1, 2, or 3) within the unit cell of the unknown crystal so as best to account for the observed diffraction pattern of the unknown crystal. Phases can then be calculated from this model and combined with the observed amplitudes to give an approximate Fourier synthesis of the structure whose coordinates are unknown. This, in turn, can be subject to any of the several forms of refinement to provide a final,

accurate structure of the unknown crystal. Lattman, E., "Use of the Rotation and Translation Functions", in Methods in Enzymology, 115, pp. 55-77 (1985); M. G. Rossmann, ed., "The Molecular Replacement Method", Int. Sci. Rev. Ser., No. 13, Gordon & Breach, New York, (1972). Using the structure coordinates of MURG provided by this invention, molecular replacement may be used to determine the structure coordinates of a crystalline mutant or homologue of MURG or of a different crystal form of MURG.

DETAILED DESCRIPTION OF THE INVENTION

The present invention relates to the discovery of the three-dimensional structure of the crystalline form of the *E. coli* MurG protein, models of such three-dimensional structures, a method of structure based drug design using such structures, methods to identify ligands or compounds that interact or bind with such structures, the compounds identified by such methods, and the use of such compounds in therapeutic compositions.

More particularly, the present invention relates to novel crystals of *E. coli* MurG protein, methods of production of such crystals, three dimensional coordinates of MurG protein, MurG structures and models derived from the *E. coli* MurG structure, and uses of such structures and models to derive other MurG structures and in ligand discovery and drug design strategies.

The present invention also relates to three-dimensional structures and coordinates of the donor nucleotide binding site, the acceptor binding site, and the membrane association site of the MurG protein, structures and models of the binding sites, and uses of such structures and models to derive the binding sites of other MurG proteins and in drug design strategies.

Solely for ease of explanation, the description of the invention is divided into the following sections: (1) crystals of MurG protein; (2) methods of crystallization; (3) three-dimensional crystal coordinates and structure of *E. coli* MurG; (4) three-dimensional coordinates and structure of the donor nucleotide binding site of MurG; (5) coordinates and structure of the acceptor binding site of MurG; (5) three dimensional coordinates and structure of the membrane association site; (6) two dimensional and three dimensional images of the protein, α -carbon backbone, α -carbon backbone with conserved amino

acid residues, and binding sites; and (7) computer readable mediums comprising the three dimensional coordinates of the MurG protein, α -carbon backbone, α -carbon backbone with conserved amino acid residues, and binding sites; (8) images of structures of MurG proteins and binding sites; (9) models of MurG proteins and binding sites thereof and methods of using the structure of MurG to determine the structures of other MurG proteins and binding sites; (10) structure based drug design using models of MurG protein and binding site structures; (11) compounds derived from structure based drug design; and (12) therapeutic compositions using drugs designed from structure based drug design.

CRYSTALS

One embodiment of the present invention includes a composition comprising a MurG protein in a crystalline form (i.e., MurG crystals). As used herein, the terms "crystalline MurG" and "MurG crystal" both refer to crystallized MurG protein and are intended to be used interchangeably. More particularly, an embodiment of the present invention includes a composition comprising an *E. coli* MurG protein in a crystalline form. Preferably, a crystalline MurG is produced using the crystal formation method described herein; in particular according to the method disclosed in Example 1. A MurG crystal of the present invention comprises any crystal structure and preferably precipitates as a triclinic crystal. Preferably, a composition of the present invention includes MurG crystal molecules arranged in a crystalline manner in a P1 space group with two molecules per asymmetric unit so as to form a unit cell of dimensions $a=60.613 \text{ \AA}$, $b=66.356 \text{ \AA}$, $c=67.902 \text{ \AA}$, $\alpha=64.294^\circ$, $\beta=83.520^\circ$, $\gamma=65.448^\circ$. A preferred crystal of the present invention provides X-ray diffraction data for determination of atomic coordinates to a resolution of about 3.0 \AA , preferably to about 2.4 \AA , and more preferably to about 1.8 \AA .

Another embodiment of the present invention includes crystalline MurG protein co-crystallized with a donor nucleotide or substrate or substrate analog. Preferably, a donor nucleotide is UDP or UDP-GlcNAc (UDP-N-acetylglucosamine) or an analog thereof. The substrate or substrate analog is preferably Lipid I or Lipid II, or analogs of Lipid I or Lipid II. More specifically, Lipid I and II analogs are as described in PCT/US99/02187, published as WO99/38958 and US Provisional Application Nos.

60/122,966 filed March 3, 1999 and 60/137,696 filed June 4, 1999, and International Application No. PCT/US00/05554 entitled "Bacterial transglycosylases: Assays for monitoring the activity using lipid II substrate analogs and methods for discovering antibiotics," all incorporated herein by reference in their entirety.

Included in the present invention, a variety of MurG proteins from numerous organisms can be used to prepare MurG crystals, including but not limited to, microorganisms such as bacteria, higher-order bacteria, thermal stable bacteria, spirochetes, small pathogenic organisms, fungi, protozoa, cyanobacteria, and trypanosomes. More particularly, bacteria such as but not limited to, *Escherichia coli*, *Bacillus subtilis*, *Aquifex aeolicus*, *Borrelia burgdorferi*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Enterococcus faecalis*, *Enterococcus hirae*, *Haemophilus influenzae*, *Helicobacter pylori* J99, *Helicobacter pylori*, *Mycobacterium tuberculosis*, *Porphyromonas gingivalis*, *Rickettsia prowazekii*, *Streptomyces coelicolor*, *Streptomyces collinus*, *Streptococcus pneumoniae*, *Synechocystis* sp. (strain PCC6803), *Thermotoga maritima*, and *Treponema pallidum*.

In another embodiment of the present invention, the MurG proteins or fragments thereof, mutants or homologs are expressed in, for example, an *E. coli* host cell for use expressing sufficient quantities of sufficiently purified protein to form crystals. The present inventors have demonstrated that it is possible to express *Enterococcus faecalis* MurG in *E. coli* cells – so the MurG proteins from many organisms can be cloned into expression vectors suitable for expression in *E. coli* cells. This would facilitate obtaining sufficient quantities of isolated or purified MurG proteins. The expression of *E. faecalis* MurG protein in *E. coli* host cells is performed, for example, by expressing the *E. faecalis* MurG gene cloned into a pET21b expression vector and transformed into an *E. coli* host cell. The MurG protein is over-expressed with a C-terminal his tag (LEHHHHHH) which allows the protein to be purified using a His-tag affinity column. The protein is then crystallized and the atomic coordinates are determined using X-ray diffraction and methods known to those skilled in the art.

It is another embodiment of the present invention to provide for the construction and expression of chimeric MurG proteins to enable the crystallization and determination of the three dimensional coordinates of such chimeras. For example, if there are problems obtaining or crystallizing MurGs from other organisms, the present invention

provides information that makes it possible to make chimaeric proteins containing the donor or acceptor binding site from *E. coli* MurG and the corresponding acceptor or donor binding site from another organism. Chimaeric proteins could be easier to express, handle, or crystallize. For example, we have found that *E. faecalis* MurG is more difficult to solubilize than *E. coli* MurG (requiring more detergent). It is believed that the problems are related to the acceptor binding domain having a stronger affinity for the bacterial membranes. To overcome this problem, one can attach the donor binding domain of *E. faecalis* to the *E. coli* acceptor binding site and determine structure to see details of *E. faecalis* donor binding domain.

According to the present invention, crystalline MurG can be used to determine the ability of a chemical compound to bind to a MurG protein in a manner predicted by a structure based drug design method of the present invention. Preferably, a MurG crystal is soaked in a solution containing a chemical compound of the present invention. Binding of the chemical compound to the crystal is then determined by methods standard in the art. Thereby, the co-crystal of MurG and a compound of interest is determined.

METHODS OF CRYSTALLIZATION

The present invention includes a method for producing crystals of MurG proteins, comprising: combining MurG protein with a reservoir solution and inducing crystal formation to produce MurG crystals. Another embodiment of the present invention, a method for producing crystals of MurG protein comprises combining MurG protein with UDP-GlcNAc in a 1:3 ratio and with a reservoir solution and inducing crystal formation to produce MurG crystals.

Preferably, crystals of MurG are formed using a solution containing a range of MurG protein from about 1 mg/ml to about 20 mg/ml, more preferably above 5 mg/ml, limited only by the solubility of the protein, which may vary depending on the specific amino acid sequence.

A reservoir solution contains the buffer, the precipitant, and additives if necessary. A suitable reservoir buffer of the present invention comprises NaMES (2-[N-morpholino]ethanesulfonic acid, sodium salt) buffer, NaHEPES (N-[2-hydroxyethyl]piperazine-N'-[2-ethanesulfonic acid, sodium salt) buffer, Tris (tris[hydroxymethyl]aminomethane) buffer, and any buffer which has the PKa between

5.5 and 8.0. A suitable NaMES buffer solution has a pH range from about 5.6-6.5. Most preferably, the NaMES buffer has a pH of about 6.5. The precipitant comprises ammonium sulfate, saturated sodium and potassium tartrate and polyethylene glycol. A suitable concentration of ammonium sulfate can range from 0.8 M to 1.5 M. Most preferably, the ammonium sulfate concentration is about 0.96 M. A suitable additive comprises detergents like Triton X-100 and n-octyl-beta-glucoside. The concentration of Triton X-100 can range from 0.1% to 1%. Most preferably, the concentration of Triton X-100 is 0.4%.

In a preferred embodiment, MurG crystals are produced by a method comprising concentrating MurG protein in a buffer solution, mixing the protein concentrate with UDP-GlcNAc in a 1:3 molar ratio, mixing equal volumes of protein solution with a reservoir solution, and inducing crystal formation to produce MurG crystals.

In a particular embodiment of the invention, MurG crystals are produced by a method comprising concentrating MurG protein to 10 mg/ml in a buffer of 20 mM Tris-HCl, pH 7.9/150mM NaCl and 50 mM EDTA; mixing the protein concentrate with UDP-GlcNAc in a 1:3 molar ratio; mixing equal volumes of protein solution with a reservoir solution comprising (0.1 M NaMES, pH 6.5, 0.96 M $(\text{NH}_4)_2\text{SO}_4$, 0.4% TRITON® X-100, and 10 mM dithiolthreitol (DTT)), and inducing crystal formation using hanging drop vapor-diffusion.. This preferred method is described in greater detail in Example 1.

Supersaturated solutions of MurG protein can be induced to crystallize by several methods including, but not limited to, vapor diffusion, liquid diffusion, batch crystallization, constant temperature and temperature induction or a combination thereof. Preferably, supersaturated solutions of MurG protein are induced to crystallize by vapor diffusion (i.e., hanging drop method). In a vapor diffusion method, a MurG protein solution is combined with a reservoir solution of the present invention that will cause the MurG protein solution to become supersaturated and form MurG crystals at a constant temperature. Vapor diffusion is preferably performed under a controlled temperature in the range of from about 15°C to about 30°C, more preferably from about 20°C to about 25°C, and most preferably at a constant temperature of about 22°C.

In another preferred embodiment, the present invention includes a method to produce crystals of MurG protein comprising the steps of: (a) preparing an about 10

mg/ml solution of MurG protein in a Tris-HCl buffer, (b) mixing UDP-GlcNAc with the MurG protein solution in a 3:1 molar ratio, (c) dropping 2 μ l droplet of this protein sample onto a coverslip, (d) adding an equal volume of reservoir solution to this droplet and inverting this over a well containing about 1 ml of the reservoir solution; and (e) incubating until crystals of MurG form.

Any isolated MurG protein can be used with the present method. An isolated MurG protein can be isolated from its natural milieu or produced using recombinant DNA technology (e.g., polymerase chain reaction (PCR) amplification, cloning) or chemical synthesis. To produce recombinant MurG protein, a nucleic acid molecule encoding a MurG protein can be inserted into any vector capable of expressing the nucleic acid in a host cell. Suitable and preferred nucleic acid molecules to include in recombinant vectors of the present invention are as disclosed herein. Such suitable and preferred nucleic acid molecules include numerous MurG encoding genes that have been isolated to date; and that will be isolated in the future. A preferred nucleic acid molecule of the present invention encodes a homologue of MurG. Homologues of MurG can be recognized by the presence of certain conserved amino acid residues or sequences.

A sequence alignment for six MurG sequences is shown in fig. 3A. Highlighted residues include those that are invariant or almost invariant across all MurG proteins. A nucleic acid molecule of the present invention can encode any portion of a MurG protein, preferably a full-length MurG protein or either of the two domains. A more preferred nucleic acid molecule to include in a recombinant vector, and particularly in a recombinant molecule, includes a nucleic acid molecule encoding a protein having the amino acid sequence represented by amino acid sequences of MurG proteins as deposited in the NCBI database and are identified with Accession Nos. CAB51993, A71316, E70579, C71699, F70195, A43727, JC1275, BVECMG, CEECAM, O83535, Q9ZK59, CAB85280, AAF39020, BAA18775, AAD26629, CAB73295, P37585, Q9ZHA9, Q9ZHDC0, Q9ZBA5, Q9X4H4, Q9WY74, P74657, O06224, Q9Z702, O84766, O69552, J67238, O51708, O25770, O07670, O07109, P45065, CAB66324, AAC68356, AAF06830, P18579, P17443, P17952, P16457, P07862, AAE23178, AAD53936, CAA18668, CAA38869, CAA38868, CAA38867, CAA38866, AAD08196, BAA01453, BAA01455, BAA01454, AAD19042, CAA45558, CAA74235, AAD10537, AAD06652, AAC95450, CAA14869, AAC73201, AAC65509, AAC67113, AAC45636, CAB08640,

AAC22793, AAC07193, BAA24357, CAB13395, BAA01355, AAB35538, 1904153C, 1808265B, 1808265A, CAA36866, CAA36869, CAA36868, CAA36867, CAA36776, and AAA99436. Further, examples of nucleic acid molecules encoding MurG proteins have been deposited in NCBI, Genbank, and have Accession Nos. AL162758, AE002281, D90917, AF110367, AL139077, AJ242646, AE000520, AE000511, L42023, U00096, NC-000922, AE000783, AE000657, AE001348, AF099188, AR048673, AR048672, AF179611, AL022602, AL109663, X55034, AE000621, D10602, AE001670, X64259, Y13922, U10879, AE001535, AF068902, AJ235271, AE000118, AE001227, AE001176, U94707, Z95388, U32793, AE000727, D84504, Z99111, D10483, X52644, X52540, and L24773. These sequences are known and are publicly available. Further, as additional genomes and genes are sequenced, more MurG encoding nucleotide sequences will become available, and can be used in the present invention.

In specific embodiments of the invention, the protein sequence of *E. coli* MurG was reported in 1990 (Ikeda et al. Nucleic Acids Res. 1990, 19:4014; and Mengin-Lecreux, D. et al., Nucleic Acids Res. 1990, 18:2810.). *E. coli* genomic DNA can be purified from *E. coli* or purchased from ATCC, or the gene for *E. coli* MurG is cloned into a plasmid can be obtained from numerous sources. Primers were designed to the portions of the gene corresponding to the N and C termini of the protein. The primers also encoded restriction enzyme sites outside the protein coding region. The gene sequence was amplified; the corresponding double stranded nucleic acid molecule was cut with appropriate restriction enzymes for cloning into a commercially available expression vector (pET expression vectors available from Novagen provide for numerous variations of MurG protein – wild-type or fusion proteins or proteins with affinity tags at N or C terminus. We have worked with several constructs but found that MurG with a His-tag at C-terminus crystallized best; the protein sequence contained an extra methionine at N-terminus and eight extra residues at C terminus, six of which were histidines. The vector used was pET21b. (as described in Ha et al. J. Am. Chem. Soc. 121, (1999) 8415-8426 hereby incorporated by reference in its entirety).

A recombinant vector of the present invention can be either RNA (probably not) or DNA, and typically includes, but is not limited to, a virus or plasmid. Any recombinant vector and host cell that provides for expression of a MurG protein

encoding nucleic acid sequence can be used in the present invention to express MurG protein for crystallization. Preferred vectors are engineered for high level expression in *E. coli* such as, but not limited to, pET vectors. We have found that over-expression of MurG from either *E. coli* or *E. faecalis* in *E. coli* cells is not toxic and, thus, this approach will work for other MurG proteins.

As used herein, an expression vector is a DNA vector that is capable of transforming a host cell and of affecting expression of a specified nucleic acid molecule. Expression vectors of the present invention include any vectors that function (i.e., direct gene expression) in recombinant cells of the present invention, including bacterial, fungal, and other microorganisms cells. Preferred expression vectors of the present invention direct expression in bacterial cells from a plasmid. A preferred recombinant molecule of the present invention comprises pET21b with *E. coli* MurG gene cloned into the NdeI and XhoI sites.

An expression vector of the present invention can be transformed into any suitable host cell to form a recombinant cell. A suitable host cell includes any cell capable of expressing a nucleic acid molecule inserted into the expression vector. For example, a procaryotic expression vector can be transformed into a bacterial host cell. If the expression vector contains a T7 promoter then a source of T7 RNA polymerase must be provided to induce expression. Some host cells contain the T7 RNA polymerase gene in a repressed state. Expression of T7 RNA polymerase can be induced with a chemical signal such as IPTG or heat. Alternatively, a source of T7 RNA polymerase can be introduced at the appropriate time by infection with a phage containing a copy of T7 RNA polymerase. A wide range of hosts strains can be infected with a suitable phage. Some host strains have been engineered to contain inducible copies of T7 RNA polymerase gene. Such host strains include BL21(DE3) and derivatives thereof. A preferred host strain of the present invention is BL21(DE3)pLysS or BL21(DE3)pLysE, which are commercially available from Novagen and can be readily transformed with a DNA plasmid vector containing a MurG gene under the control of the T7 promoter. As already stated above, a preferred vector is a pET vector, preferably containing a restriction enzyme site permitting cloning of the gene as a fusion containing a C-terminal his tag.

In a preferred embodiment, one method to isolate MurG protein useful for producing MurG crystals includes recovery of MurG protein having a C-terminal LEHHHHHH (His tag) sequence purified as described in Ha *et al.* (1999, J. Amer. Chem. Soc. 121:8415-8426). One of skill in the art is able to modify this procedure in order to purify other proteins can be produced as C-terminal histadine (his) tags. The purification conditions for specific MurG proteins will vary depending upon the particular characteristics of the proteins such as their isoelectric point, molecular weight, etc. It is known that the isoelectric points of different Murg homologues vary a bit, although they are generally relatively high. Also, some Murg homologues may be more hydrophobic than others, which will mean differences in amount of detergent necessary for purification. It is likely that all the Murg homologues can be purified over nickel affinity columns using the C-terminal his-tag as a handle. Those skilled in the art of protein purification will know how to modify purification parameters depending upon the protein characteristics, in order to purify the protein for crystallization.

STRUCTURE OF MURG PROTEIN

One embodiment of the present invention includes a model of a MurG protein, in which the model represents a three dimensional structure of a MurG protein. Another embodiment of the present invention includes the three dimensional structure of a MurG protein. A three dimensional structure of a MurG protein encompassed by the present invention substantially conforms with the atomic coordinates represented in Table 1. According to the present invention, the use of the term "substantially conforms" refers to at least a portion of a three dimensional structure of a MurG protein which is sufficiently spatially similar to at least a portion of a specified three-dimensional configuration of a particular set of atomic coordinates (e.g., those represented by Table 1) to allow the three dimensional structure of another MurG protein to be modeled or calculated using the particular set of atomic coordinates defining the three dimensional configuration of the MurG protein. For example, but not meant to be a limitation, homology modeling can be done using the linear sequence of a different MurG and *E. coli* coordinates; molecular replacement can allow the solution of a different MurG structure using the *E. coli* MurG coordinates and experimental data such as x-ray diffraction pattern from a different MurG crystal. According to the present invention, a three dimensional structure of a

given portion or chain of a first MurG protein can substantially conform to at least a portion of the atomic coordinates which represent a three dimensional configuration of a second MurG.

More particularly, a structure that substantially conforms to a given set of atomic coordinates is a structure wherein at least about 50% of such structure has an average root-mean-square deviation (RMSD) of less than about 2.5 Å for the α -carbon or C-alpha backbone atoms in secondary structure elements in each domain, and more preferably, less than about 2.0 Å for the C-alpha backbone atoms in secondary structure elements in each domain, and, in increasing preference, less than about 1.5 Å, less than about 1.0 Å, less than about 0.7 Å, and more preferably, less than about 0.5 Å for the C-alpha backbone atoms in secondary structure elements in each domain. In a more preferred embodiment, a structure that substantially conforms to a given set of atomic coordinates is a structure wherein at least about 75% of such structure has the recited average root-mean-square deviation (RMSD) value, and more preferably, at least about 90% of such structure has the recited average RMSD value, and most preferably, about 100% of such structure has the recited average RMSD value.

In an even more preferred embodiment, the above definition of "substantially conforms" can be extended to include atoms of amino acid side chains. As used herein, the phrase "common amino acid side chains" refers to amino acid side chains that are common to both the structure which substantially conforms to a given set of atomic coordinates and the structure that is actually represented by such atomic coordinates. Preferably, a three dimensional structure that substantially conforms to a given set of atomic coordinates is a structure wherein at least about 50% of the common amino acid side chains have an average RMSD value of less than about 1.5 Å, and more preferably, less than about 1.3 Å, and in increasing preference, less than about 1.0 Å, less than about 0.7 Å, and most preferably, less than about 0.3 Å.

In a more preferred embodiment, a structure that substantially conforms to a given set of atomic coordinates is a structure wherein at least about 75% of the common amino acid side chains have the recited average RMSD value, and more preferably, at least about 90% of the common amino acid side chains have the recited average RMSD value, and most preferably, about 100% of the common amino acid side chains have the recited average RMSD value.

In more preferred embodiments of the present invention, a large number of different "rotamers" or "rotational isomers" of the MurG protein are encompassed by three dimensional structures of the invention in which the amino acid side chains are at a variety of positions in crystalline forms of the protein or for the protein in solution. Different rotamers refer to molecules of identical configuration may be distinguished as having different conformations after rotation about the various molecular bonds. Therefore, while the same or similar amino acids may be present, the exact location will vary depending upon the freedom of rotation of the bonds due to hydrogen bonding, and other molecular forces.

STRUCTURE OF THE α -CARBON BACKBONE OF MURG AND THE α -CARBON BACKBONE AND CONSERVED AMINO ACID RESIDUES

The present invention includes the three dimensional structure of the α -carbon or C-alpha backbone of a MurG protein, in particular the *E. coli* MurG protein. A three dimensional structure of the C-alpha backbone of the MurG protein encompassed by the present invention substantially conforms with the atomic coordinates represented in Table 2.

More particularly, a structure that substantially conforms to a given set of atomic coordinates is a structure wherein at least about 50% of such structure has an average root-mean-square deviation (RMSD) of less than about 2.5 Å for the C-alpha backbone atoms in secondary structure elements in each domain, and more preferably, less than about 2.0 Å for the C-alpha backbone atoms in secondary structure elements in each domain, and, in increasing preference, less than about 1.5 Å, less than about 1.0 Å, less than about 0.7 Å, and more preferably, less than about 0.5 Å for the C-alpha backbone atoms in secondary structure elements in each domain. In a more preferred embodiment, a structure that substantially conforms to a given set of atomic coordinates is a structure wherein at least about 75% of such structure has the recited average root-mean-square deviation (RMSD) value, and more preferably, at least about 90% of such structure has the recited average RMSD value, and most preferably, about 100% of such structure has the recited average RMSD value. The C-alpha backbone of MurG proteins is expected to be more conserved than the location of the particular amino acid residue side chains.

The present invention also includes the three dimensional structure of the α -carbon or C-alpha backbone and conserved or invariant amino acid residue side chains of a MurG protein, in particular the *E. coli* MurG protein. A three dimensional structure of the C-alpha backbone and conserved amino acid residues of the MurG protein encompassed by the present invention substantially conforms with the atomic coordinates represented in Table 3. The conserved amino acids are highlighted in blue in Figure 3a and include G14, G15, G18, H19, G104, H124, E125, G190, G191, S192, G194, A195, R261, G263, A264, E269, P281, Q289, N292 and A293 (as numbered in the *E. coli* MurG sequence set forth in Figure 3a).

More particularly, a structure that substantially conforms to a given set of atomic coordinates is a structure wherein at least about 50% of such structure has an average root-mean-square deviation (RMSD) of less than about 2.5 Å for the C-alpha backbone and conserved amino acid residue atoms in secondary structure elements in each domain, and more preferably, less than about 2.0 Å for the backbone atoms in secondary structure elements in each domain, and, in increasing preference, less than about 1.5 Å, less than about 1.0 Å, less than about 0.7 Å, and more preferably, less than about 0.5 Å for the backbone atoms in secondary structure elements in each domain. In a more preferred embodiment, a structure that substantially conforms to a given set of atomic coordinates is a structure wherein at least about 75% of such structure has the recited average root-mean-square deviation (RMSD) value, and more preferably, at least about 90% of such structure has the recited average RMSD value, and most preferably, about 100% of such structure has the recited average RMSD value.

STRUCTURE OF THE DONOR NUCLEOTIDE BINDING SITE OF MURG PROTEINS

An embodiment of the present invention includes the three dimensional structure of a donor nucleotide binding site of a MurG protein, in particular an *E. coli* MurG protein. A more preferred embodiment of the present invention includes a three dimensional structure of a donor nucleotide binding site of a MurG protein wherein the three dimensional structure of the donor nucleotide binding site substantially conforms to the atomic coordinates in Table 4. In a preferred embodiment, the donor nucleotide binding site is a UDP-GlcNAc binding site of a MurG protein.

As described in Example 1, the donor nucleotide binding site is located in the C-terminal domain (see Fig. 4a). This binding site is based on the comparison of β -glucosyltransferase (BGT) and *E. coli* MurG and based on experiments done in our laboratory showing that the isolated C domain binds to a UDP-hexose column (See Example 1). The atomic coordinates of Table 4 set forth the donor nucleotide binding site three dimensional structure without a donor nucleotide such as UDP-GlcNAc bound to the MurG protein.

According to the present invention, the use of the term "substantially conforms" refers to at least a portion of a three dimensional structure of a donor nucleotide binding site of a MurG protein which is sufficiently spatially similar to at least a portion of a specified three-dimensional configuration of a particular set of atomic coordinates (e.g., those represented by Table 4) to allow the three dimensional structure of the donor nucleotide binding domain to be modeled or calculated (i.e., by molecular replacement) using the particular set of atomic coordinates defining the three dimensional configuration of the donor nucleotide binding site of a MurG protein. According to the present invention, a three dimensional structure of a given donor nucleotide binding site of a first MurG protein can substantially conform to at least a portion of the atomic coordinates which represent a three dimensional configuration of a second MurG. Since the atomic coordinates of Table 4 were obtained from the *E. coli* MurG crystal protein without a donor nucleotide bound, there will be some variation from the atomic coordinates of the donor nucleotide binding site when a nucleotide is bound vs. unbound. Therefore, a structure "substantially conforming" to that represented by the atomic coordinates in Table 4, will include a structure obtained from co-crystallization of the protein with a donor nucleotide.

More particularly, a structure that substantially conforms to a given set of atomic coordinates is a structure wherein at least about 50% of such structure has an average root-mean-square deviation (RMSD) of less than about 1.5 Å for the C-alpha backbone atoms in secondary structure elements in each domain, and more preferably, less than about 1.3 Å for the C-alpha backbone atoms in secondary structure elements in each domain, and, in increasing preference, less than about 1.0 Å, less than about 0.7 Å, and more preferably less than about 0.5 Å for the C-alpha backbone atoms in secondary structure elements in each domain. In a more preferred embodiment, a structure that

substantially conforms to a given set of atomic coordinates is a structure wherein at least about 75% of such structure has the recited average root-mean-square deviation (RMSD) value, and more preferably, at least about 90% of such structure has the recited average RMSD value.

In an even more preferred embodiment, the above definition of "substantially conforms" can be extended to include atoms of the conserved or invariant amino acid side chains located within the binding site. As used herein, the phrase "conserved amino acid side chains" refers to amino acid side chains that are conserved between MurG proteins within the donor nucleotide binding site. The conserved amino acid residues of the donor nucleotide binding site have been identified as I125, R261, G263, A264, E269, P281, Q289, N292 and A293 (as numbered in the *E. coli* MurG sequence set forth in Figure 3a) and the G loop found between residues numbered 190-195 having residues G190, G191, S192, G194, and A195. Some or all of these conserved residues are necessary for binding the nucleotide donor.

Preferably, a three dimensional structure that substantially conforms to a given set of atomic coordinates is a structure wherein at least about 50% of the conserved amino acid side chains have an average RMSD value of less than about 1.5 Å, and more preferably, less than about 1.3 Å, and in increasing preference, less than about 1.0 Å, less than about 0.7 Å, and most preferably, less than about 0.3 Å. In a more preferred embodiment, a structure that substantially conforms to a given set of atomic coordinates is a structure wherein at least about 75% of the conserved amino acid side chains have the recited average RMSD value, and more preferably, at least about 90% of the conserved amino acid side chains have the recited average RMSD value, and most preferably, about 100% of the conserved amino acid side chains have the recited average RMSD value.

STRUCTURE OF THE ACCEPTOR BINDING SITE OF MURG PROTEIN

An embodiment of the present invention includes the three dimensional structure of an acceptor binding site of a MurG protein. A three dimensional structure of a acceptor binding site of a MurG protein encompassed by the present invention substantially conforms with the atomic coordinates represented in Table 5. A more preferred embodiment of the present invention includes a three dimensional structure of an

acceptor binding site of a MurG protein wherein the three dimensional structure of the acceptor binding site substantially conforms to the atomic coordinates Table 5.

According to the present invention, the use of the term "acceptors" refers to Lipid I and analogues thereof. For the purposes of obtaining co-crystals containing acceptor analogues bound to the acceptor binding site better, the analogues need not be functional acceptors in a MurG assay. In particular embodiments of the present invention, the acceptor is selected from the group consisting of, but not limited to Lipid I, and analogs of Lipid I (see compounds described in Ha et al., J. Amer. Chem. Soc. 1999, vol. 121:8415-26, incorporated by herein by reference in its entirety).

As described in Example 1, the acceptor binding site is located in the N-terminal domain of a MurG protein (see Fig. 3a and 4c). The acceptor binding site or domain is characterized by three highly conserved regions, two of which are glycine-rich loops (also referred to as "G loops") that face the cleft between the C-terminal and N-terminal domains. The conserved residues of the acceptor binding site comprise G14, G15, G18, H19, G104, H124, and E125 (as numbered in the *E. coli* MurG sequence set forth in Figure 3a) and two conserved G loop structures.

According to the present invention, the use of the term "substantially conforms" refers to at least a portion of a three dimensional structure of an acceptor binding site of a MurG protein which is sufficiently spatially similar to at least a portion of a specified three-dimensional configuration of a particular set of atomic coordinates (e.g., those represented by Table 5) to allow the three dimensional structure of the acceptor binding site to be modeled or calculated (i.e., by homology modeling) using the particular set of atomic coordinates defining the three dimensional configuration of the acceptor binding site of a MurG protein. According to the present invention, a three dimensional structure of a given acceptor binding site of a first MurG protein can substantially conform to at least a portion of the atomic coordinates which represent a three dimensional configuration of a second MurG.

In an even more preferred embodiment, the above definition of "substantially conforms" can be extended to include atoms of the conserved amino acid side chains. As used herein, the phrase "conserved amino acid side chains" refers to the conserved or invariant amino acid side chains that are common to MurG proteins. Preferably, a three dimensional structure that substantially conforms to a given set of atomic coordinates is a

structure wherein at least about 50% of the conserved amino acid side chains have an average RMSD value of less than about 1.5 Å, and more preferably, less than about 1.3 Å, and in increasing preference, less than about 1.0 Å, less than about 0.7 Å, and most preferably, less than about 0.3 Å. In a more preferred embodiment, a structure that substantially conforms to a given set of atomic coordinates is a structure wherein at least about 75% of the conserved amino acid side chains have the recited average RMSD value, and more preferably, at least about 90% of the conserved amino acid side chains have the recited average RMSD value, and most preferably, about 100% of the conserved amino acid side chains have the recited average RMSD value.

STRUCTURE OF A MEMBRANE ASSOCIATION SITE OF MurG PROTEIN

An embodiment of the present invention includes the three dimensional structure of a membrane association site of a MurG protein. A three dimensional structure of a membrane association site of a MurG protein encompassed by the present invention substantially conforms with the atomic coordinates represented in Table 6. A more preferred embodiment of the present invention includes a three dimensional structure of an acceptor binding site of a MurG protein wherein the three dimensional structure of the acceptor binding site substantially conforms to the atomic coordinates in Table 6.

According to the present invention, the use of the term "membrane association site" refers to the region of a MurG protein that associates with cytoplasmic surface of bacterial membranes where it performs the reaction of coupling a soluble donor sugar to the membrane anchored acceptor sugar, Lipid I. Analysis of the *E. coli* MurG protein structure shows a hydrophobic patch consisting of residues I75, L79, F82, W85, and W116 in the N-domain. The membrane association site is where the MurG protein associates with the bacterial membranes, and that it is target for inhibitors if we find that a) we can bind to it with another molecule; b) we can disrupt membrane association by binding to it; or c) disrupting membrane association inhibits activity.

As described in Example 1, the membrane association site is located in the N-terminal domain of a MurG protein (see Fig. 4c). The location of the membrane association site is in close proximity to the acceptor binding site and membrane

association in this patch would bring the two M-terminal G-loops close to the membrane surface where the diphosphate portion of the acceptor is located.

According to the present invention, the use of the term "substantially conforms" refers to at least a portion of a three dimensional structure of a membrane association site of a MurG protein which is sufficiently spatially similar to at least a portion of a specified three-dimensional configuration of a particular set of atomic coordinates (e.g., those represented by Table 6) to allow the three dimensional structure of the membrane association site to be modeled or calculated (i.e., by molecular replacement) using the particular set of atomic coordinates defining the three dimensional configuration of the membrane association site of a MurG protein. According to the present invention, a three dimensional structure of a given membrane association site of a first MurG protein can substantially conform to at least a portion of the atomic coordinates which represent a three dimensional configuration of a second MurG.

More particularly, a structure that substantially conforms to a given set of atomic coordinates is a structure wherein at least about 50% of such structure has an average root-mean-square deviation (RMSD) of less than about 1.5 Å for the structural elements in the site, and more preferably, less than about 1.3 Å for the structure elements in each site, and, in increasing preference, less than about 1.0 Å, less than about 0.7 Å, less than about 0.5 Å, and more preferably, less than about 0.3 Å for the structural elements in each site. In a more preferred embodiment, a structure that substantially conforms to a given set of atomic coordinates is a structure wherein at least about 75% of such structure has the recited average root-mean-square deviation (RMSD) value, and more preferably, at least about 90% of such structure has the recited average RMSD value, and most preferably, about 100% of such structure has the recited average RMSD value.

In an even more preferred embodiment, the above definition of "substantially conforms" can be extended to include atoms of α -carbon backbone and conserved amino acid side chains. As used herein, the phrase "conserved amino acid side chains" refers to amino acid side chains that are conserved between MurG proteins. Preferably, a three dimensional structure that substantially conforms to a given set of atomic coordinates is a structure wherein at least about 50% of the conserved α -carbon backbone and conserved amino acid side chains have an average RMSD value of less than about 1.5 Å, and more preferably, less than about 1.3 Å, and in increasing preference, less than about 1.0 Å, less

than about 0.7 Å, and most preferably, less than about 0.3 Å. In a more preferred embodiment, a structure that substantially conforms to a given set of atomic coordinates is a structure wherein at least about 75% of the α -carbon backbone and conserved amino acid side chains have the recited average RMSD value, and more preferably, at least about 90% of the α -carbon backbone and conserved acid side chains have the recited average RMSD value, and most preferably, about 100% of the α -carbon and conserved amino acid side chains have the recited average RMSD value.

COMPUTER READABLE MEDIUM

Another embodiment of the present invention relates to a computer-readable medium encoded with a set three dimensional coordinates selected from the group consisting of the three dimensional coordinates represented in Table 1, the three dimensional coordinates represented in Table 2, the three dimensional coordinates represented in Table 3, the three dimensional coordinates represented in Table 4, the three dimensional coordinates represented in Table 5, or the three dimensional coordinates represented in Table 6, wherein using a graphical display software program, the three dimensional coordinates create an electronic file that can be visualized on a computer capable of representing said electronic file as a three dimensional image. Preferably, the three dimensional image is of a MurG protein, the α -carbon backbone of MurG, the α -carbon backbone and conserved amino acid residue sidechains of MurG, the donor nucleotide binding site of MurG, the acceptor binding site of MurG, or the membrane association site of MurG.

Yet another embodiment of the present invention relates to a computer-readable medium encoded with a set of three dimensional coordinates of a three dimensional structure which substantially conforms to the three dimensional coordinates represented in Table 1, wherein using a graphical display software program, the three dimensional coordinates create an electronic file that can be visualized on a computer capable of representing said electronic file as a three dimensional image. In other embodiments, the present invention relates to a computer-readable medium encoded with a set of three dimensional coordinates of a three dimensional structure which substantially conforms to the three dimensional coordinates represented in Table 2, Table 3, Table 4, Table 5 or Table 6, wherein using a graphical display software program, the three dimensional

coordinates create an electronic file that can be visualized on a computer capable of representing said electronic file as a three dimensional image. Preferably, the three dimensional image is of a MurG protein, the α -carbon backbone of MurG, the α -carbon backbone and conserved amino acid residue sidechains of MurG, the donor nucleotide binding site of MurG, the acceptor binding site of MurG, or the membrane association site of MurG.

IMAGES

One embodiment of the present invention relates to a two dimensional image of an *E. coli* MurG protein including those illustrated in Figures 3-4. Most of these figures were drawn with the MOLSCRIPT program. Preferably, the two dimensional image is of a MurG protein, the α -carbon backbone of MurG, the α -carbon backbone and conserved amino acid residue sidechains of MurG, the donor nucleotide binding site of MurG, the acceptor binding site of MurG, or the membrane association site of MurG.

Another embodiment of the present invention includes a three dimensional computer image of the three dimensional structure of a MurG protein, preferably the *E. coli* MurG protein. Suitable structures of which to produce three dimensional computer images are disclosed herein. Preferably, a computer image is created to a structure substantially conforming with the three dimensional coordinates represented in Table 1.

Another embodiment of the present invention includes an image of an MurG protein that is generated when a set of three dimensional coordinates comprising the three dimensional coordinates represented in Table 1 are analyzed on a computer using a graphical display software program to create an electronic file of the image and visualizing the electronic file as a three dimensional image. Suitable structures to image are disclosed herein. Preferably, the three dimensional structures are of a MurG protein, the α -carbon backbone of MurG, the α -carbon backbone and conserved amino acid residue sidechains of MurG, the donor nucleotide binding site of MurG, the acceptor binding site of MurG, or the membrane association site of MurG. Most preferably, the MurG protein is the *E. coli* MurG protein described herein. A computer image of the present invention can be produced using any suitable software program, including, but not limited to, MOLSCRIPT 2.0 (Avatar Software AB, Helenebrgsgatan 21C, SE-11713, Stockholm, Sweden), the graphical display program O (Jones et al., Acta

Crystallography, vol. A47, p. 110, 1991), or the graphical display program GRASP. Suitable computer hardware useful for producing an image of the present invention are known to those of skill in the art. Preferred computer hardware includes a Silicon Graphics Workstation.

MODELS OF MURG PROTEINS AND BINDING SITES

According to the present invention, a three dimensional structure of the *E. coli* MurG protein and its binding sites of the present invention can be used to derive a model of the three dimensional structure of another MurG protein and its binding sites (i.e., a structure to be modeled). As used herein, a "structure" of a protein refers to the components and the manner of arrangement of the components to constitute a protein or binding site. Also, as used herein, the term "model" refers to a representation of a tangible medium of the three dimensional structure of a protein, polypeptide or peptide, or binding site of a protein. For example, a model can be a representation of the three dimensional structure in a electronic file, on a computer screen, on a piece of paper (i.e., on a two dimensional medium), and/or as a ball-and-stick figure. Physical three-dimensional models are tangible and include, but are not limited to, stick models and space-filling models. The phrase "imaging the model on a computer screen" refers to the ability to express (or represent) and manipulate the model on a computer screen using appropriate computer hardware and software technology known to those skilled in the art. Such technology is available from a variety of sources including, for example, Evans and Sutherland, Salt Lake City, Utah, and Biosym Technologies, San Diego, CA. The phrase "providing a picture of the model" refers to the ability to generate a "hard copy" of the model. Computer screen images and pictures of the model can be visualized in a number of formats including space-filling representations, α carbon traces, ribbon diagrams and electron density maps.

Suitable target MurG proteins and their associated binding sites to model using a method of the present invention include any MurG protein and binding sites that are at least in part structurally related to the *E. coli* MurG protein or its binding sites. A preferred target MurG structure that is at least in part structurally related includes a target MurG structure having an amino acid sequence that is at least about 25%, preferably at least about 30%, more preferably at least about 36%, more preferably at least about 40%,

even more preferably at least about 50%, more preferably at least about 60%, more preferably at least about 70%, more preferably at least about 80%, and more preferably at least about 90% identical to an amino acid sequence of the *E. coli* MurG protein, across the full-length of the target MurG structure sequence when using, for example, a sequence alignment program such as DNAsis™ program (available from Hitachi Software, San Bruno, CA) or the MacVector™ program (available from the Eastman Kodak Company, New Haven, CT) or the GCy™ program (available from the "GCy", University of Wisconsin, Madison, WI), such alignment being performed for example, using the standard default values accompanying such alignment programs.

Preferred MurG proteins and their binding sites are set forth in the amino acid sequences of MurG proteins as deposited in the NCBI database and are identified with Accession Nos. CAB51993, A71316, E70579, C71699, F70195, A43727, JC1275, BVECMG, CEECAM, O83535, Q9ZK59, CAB85280, AAF39020, BAA18775, AAD26629, CAB73295, P37585, Q9ZHA9, Q9ZHDC0, Q9ZBA5, Q9X4H4, Q9WY74, P74657, O06224, Q9Z702, O84766, O69552, O67238, O51708, O25770, O07670, O07109, P45065, CAB66324, AAC68356, AAF06830, P18579, P17443, P17952, P16457, P07862, AAE23178, AAD53936, CAA18668, CAA38869, CAA38868, CAA38867, CAA38866, AAD08196, BAA01453, BAA01455, BAA01454, AAD19042, CAA45558, CAA74235, AAD10537, AAD06652, AAC95450, CAA14869, AAC73201, AAC65509, AAC67113, AAC45636, CAB08640, AAC22793, AAC07193, BAA24357, CAB13395, BAA01355, AAB35538, 1904153C, 1808265B, 1808265A, CAA36866, CAA36869, CAA36868, CAA36867, CAA36776, and AAA99436. The amino acid sequences are publicly available.

A variety of MurG proteins from numerous organisms can be used to prepare models of MurG proteins and binding sites, including but not limited to, microorganisms such as bacteria, higher-order bacteria, thermal stable bacteria, spirochetes, small pathogenic organisms, fungi, protozoa, cyanobacteria, and trypanosomes. More particularly, bacteria such as but not limited to, *Escherichia coli*, *Bacillus subtilis*, *Aquefex aeolicus*, *Borrelia burgdorferi*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Enterococcus faecalis*, *Enterococcus hirae*, *Haemophilus influenzae*, *Helicobacter pylori* J99, *Helicobacter pylori*, *Mycobacterium tuberculosis*, *Porphyromonas gingivalis*, *Rickettsia prowazekii*, *Streptomyces coelicolor*, *Streptomyces collinus*, *Streptococcus*

pneumoniae, *Synechocystis* sp. (strain PCC6803), *Thermotoga maritime*, and *Treponema pallidum*. It is noted that nucleotide and amino acid sequences for many of the above identified organisms are known and publicly available.

Preferred target MurG proteins and binding site structures to model also include, but are not limited to, derivatives of MurG proteins, such as a MurG protein having one or more amino acid residues substituted, deleted or added (referred to herein as MurG mutants), or proteins encoded by natural variants of a nucleic acid molecule encoding a MurG.

In another embodiment of the invention, the process of building a homology model for a protein is divided into the following steps:

- (1) Determine which proteins are related to the model protein;
- (2) Determine structurally conserved regions (SCRs);
- (3) Align the amino acid sequence of the unknown protein with those of the reference protein(s) within the SCRs;
- (4) Assign coordinates in the conserved regions;
- (5) Predict conformations for the rest of the peptide chain, including loops between the SCRs and possibly the N- and C-termini;
- (6) Search for the optimum side chain conformations for residues that differ from those in the reference proteins; and
- (7) Use energy minimization and molecular dynamics to refine the molecular structure so that steric strain introduced during the model-building process can be relieved.

Published sequences are readily available through on-line databases on the Internet, such as SwissProt (<http://www.expasy.ch/sprot/sprot-top.html>). MurG specific and related sequences are obtained for use for building homology models by text-based or sequence similarity searching. SCRs for MurG is the entire protein, considering the *E. coli* MurG crystal structure is the only similar sequence with structural data. Alignment of the sequences using an appropriate alignment program and algorithm, such as Clustal W, allows appropriate assignment of the *E. coli* protein coordinates to a MurG sequence of unknown structure. The Modeler program performs the conformational predictions

for the peptide chain and side chains. Dynamics and minimization using an appropriate program and algorithm, such as Discover.

Modeler Description:

Modeler is an automated homology-modeling scheme designed to find the most probable three-dimensional structure of a protein, given its amino acid sequence and its alignment with related structures. It derives 3D protein models without the time consuming separate stages of core region identification and loop region building or searching that is inherent to manual homology modeling schemes. The related or reference protein structures are used to derive spatial restraints expressed as probability density functions (PDFs) for each of the restrained features of the model. As an example, the main chain conformation of a given residue in the model will be described by restraints that depend upon the residue type, the main chain conformation of equivalent residues in the reference proteins and the local sequence similarity. The probability distribution functions that are used in restraining the model structure are derived from correlations between structural features in a database of families of homologous proteins aligned on the basis of their 3D structure. These functions are used to restrain C-C distances, main chain N--O distances, main chain and side chain dihedral angles, etc. The individual restraints are assembled into a single molecular probability density function (MPDF). The three-dimensional protein model is then obtained by an optimization of this MPDF. The optimization procedure itself consists of a variable target function method (Braun and Go, 1985) with conjugate gradient minimization scheme followed by an optional restrained simulated annealing molecular dynamics scheme.

While several reference structures are used in the traditional homology model building process, only one set of coordinates can be used in any one peptide segment. Modeler is able to simultaneously incorporate structural data from one or more reference proteins. Structural features in the reference proteins are used to derive spatial restraints which in turn are used to generate model protein structures using conjugate gradient and simulated annealing optimization procedures.

Clustal W description:

Clustal W aligns multiple sequences using a progressive pairwise alignment algorithm. It first generates all possible pairwise alignments for a list of sequences and then builds the guide tree based on their pairwise sequence identity, aligning the sequences following the order of the guide tree.

Several unique features in Clustal W improve the sensitivity of the alignment of divergent protein sequences (Thompson et al, 1994a).

- (1) Individual weights are assigned to each sequence in a partial alignment in order to downweight near-duplicate sequences and upweight the most divergent ones.
- (2) Amino acid substitution matrices are varied at different alignment stages according to the divergence of the sequences to be aligned.
- (3) Residue-specific gap penalties and locally reduced gap penalties in hydrophilic regions encourage new gaps in potential loop regions rather than regular secondary structure.
- (4) Positions in early alignments, where gaps have been opened, receive locally reduced gap penalties to encourage the opening of new gaps at these positions.

Discover Description:

The Discover program performs energy minimization, template forcing, torsion forcing, and dynamic trajectories and calculates properties such as interaction energies, derivatives, mean square displacements, and vibrational frequencies. It provides tools for performing simulations under various conditions including constant temperature, constant pressure, constant stress, periodic boundaries, and fixed and restrained atoms.

Homology modeling methods are known to those skilled in the art and are described in the following homology references:

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STRUCTURE BASED DRUG DESIGN

The present invention relates to the use of the crystal structure of the *E. coli* MurG protein represented by the atomic coordinates in Table 1 to make models of MurG proteins and binding sites thereof. The present invention also relates to the use of the crystal structure, α -carbon backbone, α -carbon backbone plus conserved amino acid residue side chains or binding sites of the *E. coli* MurG protein to construct models of these structures in other MurG proteins.

For the first time, the present invention permits the use of molecular design techniques to design, select and synthesize chemical entities and compounds, including inhibitory compounds, capable of binding to the active site or accessory binding site of MURG, in whole or in part.

One approach enabled by this invention, is to use the structure coordinates of MURG to design compounds that bind to the enzyme and alter the physical properties of

the compounds in different ways, e.g., solubility. For example, this invention enables the design of compounds that act as inhibitors of the MURG enzyme by binding to, all or a portion of, the active site of MURG.

A second design approach is to probe a MurG crystal with molecules composed of a variety of different chemical entities to determine optimal sites for interaction between candidate MURG inhibitors and the enzyme. For example, high resolution X-ray diffraction data collected from crystals saturated with solvent allows the determination of where each type of solvent molecule sticks. Small molecules that bind tightly to those sites can then be designed and synthesized and tested for their MURG inhibitor activity. Travis, J., *Science*, 262, p. 1374 (1993).

This invention also enables the development of compounds that can isomerize to short-lived reaction intermediates in the chemical reaction of a substrate or other compound that binds to MURG, with MURG. Thus, the time-dependent analysis of structural changes in MURG during its interaction with other molecules is enabled. The reaction intermediates of MURG can also be deduced from the reaction product in co-complex with MURG. Such information is useful to design improved analogues of known MURG inhibitors or to design novel classes of inhibitors based on the reaction intermediates of the MURG enzyme and MURG-inhibitor co-complex. This provides a novel route for designing MURG inhibitors with both high specificity and stability.

Another approach made possible and enabled by this invention, is to screen computationally small molecule data bases for chemical entities or compounds that can bind in whole, or in part, to the MURG enzyme. In this screening, the quality of fit of such entities or compounds to the binding site may be judged either by shape complementarity or by estimated interaction energy. Meng, E. C. et al., *J. Comp. Chem.*, 13, pp. 505-524 (1992).

Because MURG may crystallize in more than one crystal form, the structure coordinates of MURG, or portions thereof, as provided by this invention are particularly useful to solve the structure of those other crystal forms of MURG. They may also be used to solve the structure of MURG mutants, MURG co-complexes, or of the crystalline form of any other protein with significant amino acid sequence homology to any functional domain of MURG.

One method that may be employed for this purpose is molecular replacement. In this method, the unknown crystal structure, whether it is another crystal form of MURG, a MurG mutant, or a MurG co-complex, or the crystal of some other protein with significant amino acid sequence homology to any functional domain of MURG, may be determined using the MURG structure coordinates of this invention as provided in Tables 1-6. This method will provide an accurate structural form for the unknown crystal more quickly and efficiently than attempting to determine such information ab initio.

In addition, in accordance with this invention, MURG mutants may be crystallized in co-complex with known MURG inhibitors. The crystal structures of a series of such complexes may then be solved by molecular replacement and compared with that of wild-type MURG. Potential sites for modification within the various binding sites of the enzyme may thus be identified. This information provides an additional tool for determining the most efficient binding interactions, for example, increased hydrophobic interactions, between MURG and a chemical entity or compound.

All of the complexes referred to above may be studied using well-known X-ray diffraction techniques and may be refined versus 2-3 Å resolution X-ray data to an R value of about 0.20 or less using computer software, such as X-PLOR (Yale University, COPYRIGHT 1992, distributed by Molecular Simulations, Inc.). See, e.g., Blundel & Johnson, *supra*, Methods in Enzymology, vol. 114 & 115, H. W. Wyckoff et al., eds., Academic Press (1985). This information may thus be used to design, synthesize and optimize novel classes of MURG inhibitors.

The structure coordinates of MURG mutants provided in this invention also facilitate the identification of related proteins or enzymes analogous to MURG in function, structure or both, thereby further leading to novel therapeutic modes for treating or preventing UDP-glycosyltransferase mediated diseases.

The design of compounds that bind to or inhibit MURG according to this invention generally involves consideration of two factors. First, the compound must be capable of physically and structurally associating with MURG. Non-covalent molecular interactions important in the association of MURG with its substrate include hydrogen bonding, van der Waals and hydrophobic interactions.

Second, the compound must be able to assume a conformation that allows it to associate with MURG. Although certain portions of the compound will not directly

participate in this association with MURG, those portions may still influence the overall conformation of the molecule. This, in turn, may have a significant impact on potency. Such conformational requirements include the overall three-dimensional structure and orientation of the chemical entity or compound in relation to all or a portion of the binding site, e.g., active site or accessory binding site of MURG, or the spacing between functional groups of a compound comprising several chemical entities that directly interact with MURG.

The potential inhibitory or binding effect of a chemical compound on MURG may be analyzed prior to its actual synthesis and testing by the use of computer modelling techniques. If the theoretical structure of the given compound suggests insufficient interaction and association between it and MURG, synthesis and testing of the compound is obviated. However, if computer modelling indicates a strong interaction, the molecule may then be synthesized and tested for its ability to bind to MURG and inhibit using the assay of Walker et al. patents (cited supra). In this manner, synthesis of inoperative compounds may be avoided.

An inhibitory or other binding compound of MURG may be computationally evaluated and designed by means of a series of steps in which chemical entities or fragments are screened and selected for their ability to associate with the individual binding pockets or other areas of MURG.

One skilled in the art may use one of several methods to screen chemical entities or fragments for their ability to associate with MURG and more particularly with the individual binding pockets of the MURG donor nucleotide binding site, acceptor binding site or membrane association site. This process may begin by visual inspection of, for example, the binding sites on the computer screen based on the MURG coordinates in Tables 1-6. Selected fragments or chemical entities may then be positioned in a variety of orientations, or docked, within an individual binding pocket of MURG as defined supra. Docking may be accomplished using software such as Quanta and Sybyl, followed by energy minimization and molecular dynamics with standard molecular mechanics forcefields, such as CHARMM and AMBER.

Specialized computer programs may also assist in the process of selecting fragments or chemical entities, including but not limited to:

1. GRID (Goodford, P. J., "A Computational Procedure for Determining Energetically Favorable Binding Sites on Biologically Important Macromolecules" J. Med. Chem., 28, pp. 849-857 (1985)). GRID is available from Oxford University, Oxford, UK.
2. MCSS (Miranker, A. and M. Karplus, "Functionality Maps of Binding Sites: A Multiple Copy Simultaneous Search Method." Proteins: Structure, Function and Genetics, 11, pp. 29-34 (1991)). MCSS is available from Molecular Simulations, Burlington, Mass.
3. AUTODOCK (Goodsell, D. S. and A. J. Olsen, "Automated Docking of Substrates to Proteins by Simulated Annealing" Proteins: Structure, Function, and Genetics, 8, pp. 195-202 (1990)) (AUTODOCK is available from Scripps Research Institute, La Jolla, Calif.).
4. DOCK (Kuntz, I. D. et al., "A Geometric Approach to Macromolecule-Ligand Interactions" J. Mol. Biol., 161, pp. 269-288 (1982)). DOCK is available from University of California, San Francisco, Calif.

Once suitable chemical entities or fragments have been selected, they can be assembled into a single compound or inhibitor. Assembly may be proceed by visual inspection of the relationship of the fragments to each other on the three-dimensional image displayed on a computer screen in relation to the structure coordinates of MURG. This would be followed by manual model building using software such as Quanta or Sybyl.

Useful programs to aid one of skill in the art in connecting the individual chemical entities or fragments include, but are not limited to:

1. CAVEAT (Bartlett, P. A. et al, "CAVEAT: A Program to Facilitate the Structure-Derived Design of Biologically Active Molecules". In Molecular Recognition in Chemical and Biological Problems", Special Pub., Royal Chem. Soc., 78, pp. 182-196 (1989)). CAVEAT is available from the University of California, Berkeley, Calif.

2. 3D Database systems such as MACCS-3D (MDL Information Systems, San Leandro, Calif.). This area is reviewed in Martin, Y. C., "3D Database Searching in Drug Design", J. Med. Chem., 35, pp. 2145-2154 (1992)).
3. HOOK (available from Molecular Simulations, Burlington, Mass.).

Instead of proceeding to build a MurG inhibitor in a step-wise fashion one fragment or chemical entity at a time as described above, inhibitory or other MURG binding compounds may be designed as a whole or "de novo" using either an empty active site or optionally including some portion(s) of a known inhibitor(s). These methods include, but are not limited to:

1. LUDI (Bohm, H.-J., "The Computer Program LUDI: A New Method for the De Novo Design of Enzyme Inhibitors", J. ComR. Aid. Molec. Design, 6, pp. 61-78 (1992)). LUDI is available from Biosym Technologies, San Diego, Calif.
2. LEGEND (Nishibata, Y. and A. Itai, Tetrahedron, 47, p. 8985 (1991)). LEGEND is available from Molecular Simulations, Burlington, Mass.
3. LeapFrog (available from Tripos Associates, St. Louis, Mo.).

Other molecular modeling techniques may also be employed in accordance with this invention. See, e.g., Cohen, N. C. et al., "Molecular Modeling Software and Methods for Medicinal Chemistry, J. Med. Chem., 33, pp. 883-894 (1990). See also, Navia, M. A. and M. A. Murcko, "The Use of Structural Information in Drug Design", Current Opinions in Structural Biology, 2, pp. 202-210 (1992).

Once a compound has been designed or selected by the above methods, the efficiency with which that compound may bind to MURG may be tested and optimized by computational evaluation. For example, a compound that has been designed or selected to function as a MurG-inhibitor must also preferably traverse a volume not overlapping that occupied by the active site when it is bound to the native substrate. An effective MURG inhibitor must preferably demonstrate a relatively small difference in

energy between its bound and free states (i.e., a small deformation energy of binding). Thus, the most efficient MURG inhibitors should preferably be designed with a deformation energy of binding of not greater than about 10 kcal/mole, preferably, not greater than 7 kcal/mole. MURG inhibitors may interact with the enzyme in more than one conformation that is similar in overall binding energy. In those cases, the deformation energy of binding is taken to be the difference between the energy of the free compound and the average energy of the conformations observed when the inhibitor binds to the enzyme.

A compound designed or selected as binding to MURG may be further computationally optimized so that in its bound state it would preferably lack repulsive electrostatic interaction with the target enzyme. Such non-complementary (e.g., electrostatic) interactions include repulsive charge-charge, dipole-dipole and charge-dipole interactions. Specifically, the sum of all electrostatic interactions between the inhibitor and the enzyme when the inhibitor is bound to MURG, preferably make a neutral or favorable contribution to the enthalpy of binding.

Specific computer software is available in the art to evaluate compound deformation energy and electrostatic interaction. Examples of programs designed for such uses include, but are not limited to: Gaussian.92, revision C [M. J. Frisch, Gaussian, Inc., Pittsburgh, Pa. .COPYRIGHT.1992]; AMBER, version 4.0 [P. A. Kollman, University of California at San Francisco, .COPYRIGHT.1994]; QUANTA/CHARMM [Molecular Simulations, Inc., Burlington, Mass. .COPYRIGHT.1994]; and Insight II/Discover (Biosysm Technologies Inc., San Diego, Calif. .COPYRIGHT.1994). These programs may be implemented, for instance, using a Silicon Graphics workstation, IRIS Octane or IBM RISC/6000 workstation. Other hardware systems and software packages will be known to those skilled in the art.

Once a MurG-binding compound has been optimally selected or designed, as described above, substitutions may then be made in some of its atoms or side groups in order to improve or modify its binding properties. Generally, initial substitutions are conservative, i.e., the replacement group will have approximately the same size, shape, hydrophobicity and charge as the original group. It should, of course, be understood that components known in the art to alter conformation should be avoided. Such substituted

chemical compounds may then be analyzed for efficiency of fit to MURG by the same computer methods described in detail, above.

COMPOUNDS AND COMPOSITIONS COMPRISING COMPOUNDS DERIVED FROM STRUCTURE BASED DRUG DESIGN

One embodiment of the present invention is a compound that is capable of binding to a MurG protein, inhibiting the activity of a MurG protein, or stimulating the activity of a MurG protein. Suitable inhibitory compounds of the present invention can: (1) inhibit (i.e., prevent or block) the activity of MurG enzyme by binding to a MurG donor nucleotide binding site and interfering with the binding of the donor nucleotide molecule; (2) inhibit the activity of MurG enzyme by binding to the MurG acceptor binding site and interfering with the binding of the acceptor molecule; (3) inhibit the activity of a MurG enzyme by binding to the membrane association site and interfering with the association of the protein with the bacterial membrane and/or acceptor molecule.

Another embodiment of the present invention is a compound that is capable of stimulating MurG activity. Suitable stimulatory compounds of the present invention can stimulate the activity of a MurG enzyme by binding to the protein at a binding site and causing an increase in enzymatic activity, for example, by increasing the enzymes affinity to bind a donor nucleotide, an acceptor molecule or improve the enzymes stability or increasing the binding affinity of a molecule to MurG.

Such compounds that bind to, inhibit or stimulate activity of a MurG protein include, for example, compounds that mimic donor nucleotide molecules. In preferred embodiments, the compound includes, for example, pyrimidine nucleoside analogues. In yet another preferred embodiment, the compounds include compounds comprising a pyrimidine nucleoside with a substituent containing at least one heteroatom attached to the C5 hydroxyl. In more particular embodiments, pyrimidine derivatives make complementary hydrogen bonding contacts to the amide backbone segment containing Ile 245 and also contact glutamate 269.

Another embodiment of the present invention is a compound that binds to the acceptor binding site of the MurG protein, hereinafter referred to as acceptor analogs. An acceptor analog refers to a compound that interacts with (e.g., binds to, associates with, modifies) the acceptor binding site of a MurG protein. An acceptor analog, for example,

is a compound that mimics the natural acceptor molecule, Lipid I. Examples of such acceptor analogs are set forth in Ha et al., J. Amer. Chem. Soc. 1999, and PCT/US99/02187, U.S. Provisional Application No. 60/073,376 filed February 2, 1998, incorporated herein by reference.

Another embodiment of the present invention is a compound that binds to the MurG protein, that are enzyme-product analogs, hereinafter referred to as Lipid II analogs. A Lipid II analog refers to a compound that interacts with (i.e., binds to, associates with, modifies) the acceptor binding site of a Mur G protein which mimics the product of the transglycosylase reaction.

Inhibitory and stimulatory compounds of the present invention can be identified by various means known to those of skill in the art. For example, binding of an inhibitory compound to, or otherwise interaction with, a MurG protein, can be determined with MurG in solution, for example, using assays described in PCT/US99/02187, U.S. Provisional Application No. 60/073,376 filed February 2, 1998, and PCT/US00/05554, U.S. Provisional Application Nos. 60/122,966 and 60/137,696, incorporated herein by reference.

According to the present invention, suitable compounds of the present invention include peptides or other organic molecules, and inorganic molecules. Suitable organic molecules include small organic molecules. Preferably, a compound of the present invention is not harmful (i.e., toxic) to an animal when administered to an animal.

Compounds of the present invention also can be identified using structure based drug design techniques known to those skilled in the art and described herein above.

Also according to the present invention, compounds are suitable for use in the inhibition of bacterial or microbial growth in an animal, and for example, function as an antibiotic for treatment of bacterial infections in animals.

The present invention also includes compositions comprising compounds of the present invention that inhibit or stimulate MurG activity which function as antibiotics or antimicrobial agents in animals. Compositions of the present invention can be used therapeutically or diagnostically in an animal. Compositions of the present invention comprises at least one compound of the present invention. In a preferred embodiment, compositions of the present invention further comprise a carrier. More particularly, a suitable carrier is a pharmaceutically acceptable carrier known to those skilled in the art.

TABLE 1- ATOMIC COORDINATES OF E. COLI MURG PROTEIN

REMARK coordinates from minimization refinementREMARK refinement
 resolution: 40.0 - 1.9 AREMARK starting r= 0.2200 free_r= 0.2466REMARK
 final r= 0.2200 free_r= 0.2466REMARK rmsd bonds= 0.005558 rmsd
 angles= 1.29505REMARK wa= 1.08391REMARK target= mlf cycles= 1 steps= 30
 REMARK sg= P1 a= 60.613 b= 66.356 c= 67.902 alpha= 64.294 beta= 83.520
 gamma= 65.448REMARK parameter file 1 :
 CNS_TOPPAR:protein_rep.paramREMARK parameter file 2 :
 CNS_TOPPAR:water_rep.paramREMARK parameter file 3 :
 CNS_TOPPAR:ion.paramREMARK molecular structure file: gen.mtfREMARK
 input coordinates: gen.pdbREMARK reflection file= native.cvREMARK ncs=
 noneREMARK B-correction resolution: 6.0 - 1.9REMARK initial B-factor
 correction applied to fobs :REMARK B11= 0.747 B22= 2.098 B33= -
 2.845REMARK B12= -1.847 B13= -3.752 B23= 6.401REMARK B-factor
 correction applied to coordinate array B: 0.038REMARK bulk solvent:
 density level= 0.351665 e/A³, B-factor= 43.8282 A²REMARK reflections
 with |Fobs|/sigma_F < 2.0 rejectedREMARK reflections with |Fobs| >
 10000 * rms(Fobs) rejectedREMARK theoretical total number of refl. in
 resol. range:68102 (100.0%)REMARK number of unobserved reflections (no
 entry or |F|=0):2825(4.1%) REMARK number of reflections rejected:
 3288 (4.8 %)REMARK total number of reflections used:
 61989 91.0%)REMARK number of reflections in working set:
 55765 (81.9%)REMARK number of reflections in test set:
 6224 (9.1%)CRYST1 60.613 66.356 67.902 64.29 83.52 65.45 P 1
 REMARK FILENAME="minimize5.pdb"REMARK DATE:14-Jan-00 15:25:36
 created by user: shaREMARK VERSION:
 0.5

ATOM	1	CB	LYS A	7	0.142	3.434	35.023	1.00	43.02	AAAA
ATOM	2	CG	LYS A	7	1.076	4.457	35.641	1.00	46.34	AAAA
ATOM	3	CD	LYS A	7	0.452	5.841	35.634	1.00	47.39	AAAA
ATOM	4	CE	LYS A	7	1.345	6.846	36.332	1.00	48.65	AAAA
ATOM	5	NZ	LYS A	7	0.780	8.221	36.276	1.00	51.04	AAAA
ATOM	6	C	LYS A	7	-2.239	2.733	34.833	1.00	39.64	AAAA
ATOM	7	O	LYS A	7	-2.050	1.717	34.160	1.00	39.64	AAAA
ATOM	8	N	LYS A	7	-0.974	2.320	36.947	1.00	42.05	AAAA
ATOM	9	CA	LYS A	7	-1.170	3.245	35.788	1.00	41.31	AAAA
ATOM	10	N	ARG A	8	-3.357	3.451	34.773	1.00	37.24	AAAA
ATOM	11	CA	ARG A	8	-4.469	3.076	33.906	1.00	34.91	AAAA
ATOM	12	CB	ARG A	8	-5.782	3.109	34.686	1.00	36.65	AAAA
ATOM	13	CG	ARG A	8	-5.950	2.017	35.721	1.00	39.89	AAAA
ATOM	14	CD	ARG A	8	-7.323	2.124	36.356	1.00	42.12	AAAA
ATOM	15	NE	ARG A	8	-7.663	0.960	37.163	1.00	45.03	AAAA
ATOM	16	CZ	ARG A	8	-7.031	0.610	38.279	1.00	46.29	AAAA
ATOM	17	NH1	ARG A	8	-6.015	1.337	38.725	1.00	46.88	AAAA
ATOM	18	NH2	ARG A	8	-7.420	-0.466	38.952	1.00	47.41	AAAA
ATOM	19	C	ARG A	8	-4.584	3.999	32.696	1.00	32.27	AAAA
ATOM	20	O	ARG A	8	-4.602	5.224	32.832	1.00	31.60	AAAA
ATOM	21	N	LEU A	9	-4.663	3.403	31.512	1.00	29.57	AAAA
ATOM	22	CA	LEU A	9	-4.792	4.171	30.283	1.00	27.45	AAAA
ATOM	23	CB	LEU A	9	-3.581	3.954	29.362	1.00	26.31	AAAA
ATOM	24	CG	LEU A	9	-3.752	4.466	27.916	1.00	25.77	AAAA
ATOM	25	CD1	LEU A	9	-3.670	5.985	27.895	1.00	24.31	AAAA

ATOM	26	CD2	LEU	A	9	-2.679	3.878	26.993	1.00	26.22	AAAA
ATOM	27	C	LEU	A	9	-6.038	3.762	29.523	1.00	25.97	AAAA
ATOM	28	O	LEU	A	9	-6.397	2.587	29.485	1.00	25.57	AAAA
ATOM	29	N	MET	A	10	-6.713	4.738	28.928	1.00	25.37	AAAA
ATOM	30	CA	MET	A	10	-7.866	4.429	28.101	1.00	24.70	AAAA
ATOM	31	CB	MET	A	10	-9.142	5.101	28.612	1.00	25.60	AAAA
ATOM	32	CG	MET	A	10	-10.323	4.873	27.675	1.00	25.77	AAAA
ATOM	33	SD	MET	A	10	-11.916	4.958	28.492	1.00	26.63	AAAA
ATOM	34	CE	MET	A	10	-12.197	3.222	28.862	1.00	25.72	AAAA
ATOM	35	C	MET	A	10	-7.528	4.943	26.715	1.00	23.31	AAAA
ATOM	36	O	MET	A	10	-7.198	6.116	26.544	1.00	24.02	AAAA
ATOM	37	N	VAL	A	11	-7.574	4.059	25.727	1.00	22.25	AAAA
ATOM	38	CA	VAL	A	11	-7.278	4.461	24.359	1.00	22.34	AAAA
ATOM	39	CB	VAL	A	11	-6.444	3.386	23.624	1.00	22.75	AAAA
ATOM	40	CG1	VAL	A	11	-6.256	3.768	22.158	1.00	20.51	AAAA
ATOM	41	CG2	VAL	A	11	-5.082	3.239	24.310	1.00	21.75	AAAA
ATOM	42	C	VAL	A	11	-8.612	4.654	23.646	1.00	22.94	AAAA
ATOM	43	O	VAL	A	11	-9.525	3.843	23.804	1.00	23.37	AAAA
ATOM	44	N	MET	A	12	-8.722	5.734	22.878	1.00	22.18	AAAA
ATOM	45	CA	MET	A	12	-9.949	6.034	22.146	1.00	23.10	AAAA
ATOM	46	CB	MET	A	12	-10.496	7.399	22.589	1.00	22.78	AAAA
ATOM	47	CG	MET	A	12	-10.359	7.655	24.096	1.00	23.92	AAAA
ATOM	48	SD	MET	A	12	-10.955	9.279	24.657	1.00	25.51	AAAA
ATOM	49	CE	MET	A	12	-9.641	10.349	24.162	1.00	22.79	AAAA
ATOM	50	C	MET	A	12	-9.582	6.072	20.673	1.00	22.97	AAAA
ATOM	51	O	MET	A	12	-8.917	6.997	20.226	1.00	21.16	AAAA
ATOM	52	N	ALA	A	13	-9.992	5.057	19.921	1.00	26.97	AAAA
ATOM	53	CA	ALA	A	13	-9.665	5.008	18.498	1.00	30.88	AAAA
ATOM	54	CB	ALA	A	13	-8.381	4.212	18.288	1.00	31.18	AAAA
ATOM	55	C	ALA	A	13	-10.813	4.412	17.685	1.00	34.35	AAAA
ATOM	56	O	ALA	A	13	-11.328	3.335	18.006	1.00	35.86	AAAA
ATOM	57	N	GLY	A	14	-11.176	5.127	16.622	1.00	37.37	AAAA
ATOM	58	CA	GLY	A	14	-12.287	4.762	15.757	1.00	40.54	AAAA
ATOM	59	C	GLY	A	14	-12.239	3.583	14.808	1.00	41.52	AAAA
ATOM	60	O	GLY	A	14	-11.267	2.831	14.755	1.00	43.26	AAAA
ATOM	61	N	GLY	A	15	-13.322	3.451	14.042	1.00	42.70	AAAA
ATOM	62	CA	GLY	A	15	-13.491	2.363	13.094	1.00	43.13	AAAA
ATOM	63	C	GLY	A	15	-12.660	2.286	11.825	1.00	43.41	AAAA
ATOM	64	O	GLY	A	15	-13.212	2.187	10.730	1.00	44.39	AAAA
ATOM	65	N	THR	A	16	-11.340	2.333	11.966	1.00	43.38	AAAA
ATOM	66	CA	THR	A	16	-10.426	2.204	10.833	1.00	43.22	AAAA
ATOM	67	CB	THR	A	16	-10.120	3.551	10.110	1.00	44.23	AAAA
ATOM	68	OG1	THR	A	16	-9.302	4.375	10.949	1.00	44.41	AAAA
ATOM	69	CG2	THR	A	16	-11.404	4.286	9.754	1.00	43.74	AAAA
ATOM	70	C	THR	A	16	-9.118	1.679	11.402	1.00	43.06	AAAA
ATOM	71	O	THR	A	16	-8.728	2.042	12.517	1.00	42.99	AAAA
ATOM	72	N	GLY	A	17	-8.453	0.810	10.649	1.00	41.81	AAAA
ATOM	73	CA	GLY	A	17	-7.190	0.268	11.109	1.00	40.71	AAAA
ATOM	74	C	GLY	A	17	-6.202	1.401	11.275	1.00	39.54	AAAA
ATOM	75	O	GLY	A	17	-5.275	1.330	12.085	1.00	39.73	AAAA
ATOM	76	N	GLY	A	18	-6.413	2.460	10.500	1.00	37.79	AAAA
ATOM	77	CA	GLY	A	18	-5.539	3.611	10.572	1.00	35.68	AAAA
ATOM	78	C	GLY	A	18	-5.394	4.116	11.994	1.00	34.88	AAAA
ATOM	79	O	GLY	A	18	-4.285	4.441	12.427	1.00	35.21	AAAA
ATOM	80	N	HIS	A	19	-6.503	4.186	12.728	1.00	32.89	AAAA
ATOM	81	CA	HIS	A	19	-6.454	4.664	14.110	1.00	32.14	AAAA
ATOM	82	CB	HIS	A	19	-7.759	5.371	14.504	1.00	30.28	AAAA
ATOM	83	CG	HIS	A	19	-8.150	6.504	13.605	1.00	28.85	AAAA
ATOM	84	CD2	HIS	A	19	-9.336	6.808	13.027	1.00	27.83	AAAA
ATOM	85	ND1	HIS	A	19	-7.288	7.524	13.265	1.00	28.68	AAAA
ATOM	86	CE1	HIS	A	19	-7.926	8.407	12.517	1.00	28.09	AAAA
ATOM	87	NE2	HIS	A	19	-9.170	7.996	12.358	1.00	27.45	AAAA
ATOM	88	C	HIS	A	19	-6.229	3.533	15.108	1.00	31.91	AAAA
ATOM	89	O	HIS	A	19	-5.480	3.684	16.072	1.00	31.76	AAAA
ATOM	90	N	VAL	A	20	-6.895	2.407	14.881	1.00	31.82	AAAA
ATOM	91	CA	VAL	A	20	-6.813	1.271	15.788	1.00	33.03	AAAA

ATOM	92	CB	VAL	A	20	-7.875	0.215	15.430	1.00	33.31	AAAA
ATOM	93	CG1	VAL	A	20	-7.766	-0.982	16.361	1.00	33.91	AAAA
ATOM	94	CG2	VAL	A	20	-9.260	0.830	15.540	1.00	34.25	AAAA
ATOM	95	C	VAL	A	20	-5.452	0.587	15.898	1.00	33.31	AAAA
ATOM	96	O	VAL	A	20	-4.977	0.337	17.008	1.00	32.99	AAAA
ATOM	97	N	PHE	A	21	-4.823	0.288	14.765	1.00	33.64	AAAA
ATOM	98	CA	PHE	A	21	-3.526	-0.385	14.794	1.00	33.68	AAAA
ATOM	99	CB	PHE	A	21	-3.020	-0.648	13.368	1.00	35.58	AAAA
ATOM	100	CG	PHE	A	21	-3.900	-1.578	12.577	1.00	39.10	AAAA
ATOM	101	CD1	PHE	A	21	-4.463	-2.701	13.174	1.00	40.50	AAAA
ATOM	102	CD2	PHE	A	21	-4.157	-1.338	11.232	1.00	41.05	AAAA
ATOM	103	CE1	PHE	A	21	-5.271	-3.572	12.446	1.00	41.55	AAAA
ATOM	104	CE2	PHE	A	21	-4.964	-2.205	10.492	1.00	41.86	AAAA
ATOM	105	CZ	PHE	A	21	-5.521	-3.323	11.103	1.00	42.12	AAAA
ATOM	106	C	PHE	A	21	-2.456	0.350	15.605	1.00	32.04	AAAA
ATOM	107	O	PHE	A	21	-1.789	-0.257	16.443	1.00	31.30	AAAA
ATOM	108	N	PRO	A	22	-2.277	1.662	15.375	1.00	31.37	AAAA
ATOM	109	CD	PRO	A	22	-2.939	2.544	14.400	1.00	31.41	AAAA
ATOM	110	CA	PRO	A	22	-1.259	2.396	16.139	1.00	30.01	AAAA
ATOM	111	CB	PRO	A	22	-1.301	3.799	15.536	1.00	30.97	AAAA
ATOM	112	CG	PRO	A	22	-1.892	3.592	14.175	1.00	31.19	AAAA
ATOM	113	C	PRO	A	22	-1.620	2.411	17.624	1.00	29.31	AAAA
ATOM	114	O	PRO	A	22	-0.749	2.366	18.489	1.00	27.42	AAAA
ATOM	115	N	GLY	A	23	-2.918	2.483	17.903	1.00	28.99	AAAA
ATOM	116	CA	GLY	A	23	-3.380	2.492	19.277	1.00	28.59	AAAA
ATOM	117	C	GLY	A	23	-3.035	1.196	19.990	1.00	29.00	AAAA
ATOM	118	O	GLY	A	23	-2.649	1.205	21.160	1.00	28.48	AAAA
ATOM	119	N	LEU	A	24	-3.168	0.078	19.282	1.00	28.08	AAAA
ATOM	120	CA	LEU	A	24	-2.863	-1.227	19.859	1.00	28.39	AAAA
ATOM	121	CB	LEU	A	24	-3.306	-2.347	18.913	1.00	28.16	AAAA
ATOM	122	CG	LEU	A	24	-4.811	-2.605	18.843	1.00	28.45	AAAA
ATOM	123	CD1	LEU	A	24	-5.117	-3.583	17.714	1.00	29.25	AAAA
ATOM	124	CD2	LEU	A	24	-5.291	-3.158	20.181	1.00	29.35	AAAA
ATOM	125	C	LEU	A	24	-1.373	-1.350	20.147	1.00	28.37	AAAA
ATOM	126	O	LEU	A	24	-0.966	-1.986	21.126	1.00	28.60	AAAA
ATOM	127	N	ALA	A	25	-0.555	-0.743	19.296	1.00	27.77	AAAA
ATOM	128	CA	ALA	A	25	0.887	-0.795	19.497	1.00	28.98	AAAA
ATOM	129	CB	ALA	A	25	1.616	-0.142	18.321	1.00	27.53	AAAA
ATOM	130	C	ALA	A	25	1.256	-0.093	20.800	1.00	29.10	AAAA
ATOM	131	O	ALA	A	25	2.035	-0.618	21.595	1.00	29.49	AAAA
ATOM	132	N	VAL	A	26	0.694	1.094	21.020	1.00	28.82	AAAA
ATOM	133	CA	VAL	A	26	0.982	1.853	22.233	1.00	28.94	AAAA
ATOM	134	CB	VAL	A	26	0.400	3.290	22.157	1.00	29.74	AAAA
ATOM	135	CG1	VAL	A	26	0.691	4.049	23.454	1.00	29.76	AAAA
ATOM	136	CG2	VAL	A	26	1.009	4.026	20.981	1.00	29.14	AAAA
ATOM	137	C	VAL	A	26	0.409	1.131	23.450	1.00	29.18	AAAA
ATOM	138	O	VAL	A	26	1.020	1.118	24.518	1.00	29.62	AAAA
ATOM	139	N	ALA	A	27	-0.757	0.518	23.286	1.00	27.98	AAAA
ATOM	140	CA	ALA	A	27	-1.371	-0.215	24.382	1.00	29.32	AAAA
ATOM	141	CB	ALA	A	27	-2.719	-0.755	23.950	1.00	28.32	AAAA
ATOM	142	C	ALA	A	27	-0.462	-1.372	24.840	1.00	30.04	AAAA
ATOM	143	O	ALA	A	27	-0.084	-1.454	26.015	1.00	29.89	AAAA
ATOM	144	N	HIS	A	28	-0.120	-2.259	23.907	1.00	30.92	AAAA
ATOM	145	CA	HIS	A	28	0.734	-3.413	24.201	1.00	30.62	AAAA
ATOM	146	CB	HIS	A	28	1.024	-4.214	22.924	1.00	30.20	AAAA
ATOM	147	CG	HIS	A	28	-0.112	-5.080	22.483	1.00	31.65	AAAA
ATOM	148	CD2	HIS	A	28	-0.764	-5.162	21.299	1.00	31.33	AAAA
ATOM	149	ND1	HIS	A	28	-0.717	-5.996	23.319	1.00	31.81	AAAA
ATOM	150	CE1	HIS	A	28	-1.696	-6.600	22.670	1.00	32.38	AAAA
ATOM	151	NE2	HIS	A	28	-1.747	-6.112	21.443	1.00	32.85	AAAA
ATOM	152	C	HIS	A	28	2.054	-2.989	24.823	1.00	30.90	AAAA
ATOM	153	O	HIS	A	28	2.537	-3.601	25.779	1.00	30.92	AAAA
ATOM	154	N	HIS	A	29	2.636	-1.939	24.263	1.00	30.28	AAAA
ATOM	155	CA	HIS	A	29	3.899	-1.415	24.742	1.00	30.76	AAAA
ATOM	156	CB	HIS	A	29	4.276	-0.195	23.911	1.00	31.40	AAAA
ATOM	157	CG	HIS	A	29	5.679	0.274	24.122	1.00	33.14	AAAA

ATOM	158	CD2	HIS	A	29	6.188	1.226	24.939	1.00	33.77	AAAA
ATOM	159	ND1	HIS	A	29	6.748	-0.240	23.420	1.00	34.47	AAAA
ATOM	160	CE1	HIS	A	29	7.855	0.381	23.791	1.00	34.76	AAAA
ATOM	161	NE2	HIS	A	29	7.542	1.275	24.711	1.00	34.09	AAAA
ATOM	162	C	HIS	A	29	3.835	-1.032	26.227	1.00	31.63	AAAA
ATOM	163	O	HIS	A	29	4.763	-1.315	26.990	1.00	30.76	AAAA
ATOM	164	N	LEU	A	30	2.744	-0.388	26.638	1.00	29.72	AAAA
ATOM	165	CA	LEU	A	30	2.603	0.035	28.028	1.00	30.08	AAAA
ATOM	166	CB	LEU	A	30	1.631	1.225	28.126	1.00	29.45	AAAA
ATOM	167	CG	LEU	A	30	2.107	2.503	27.420	1.00	28.69	AAAA
ATOM	168	CD1	LEU	A	30	1.026	3.587	27.477	1.00	27.76	AAAA
ATOM	169	CD2	LEU	A	30	3.383	2.998	28.075	1.00	28.99	AAAA
ATOM	170	C	LEU	A	30	2.153	-1.096	28.950	1.00	30.55	AAAA
ATOM	171	O	LEU	A	30	2.538	-1.136	30.120	1.00	31.28	AAAA
ATOM	172	N	MET	A	31	1.340	-2.012	28.438	1.00	31.26	AAAA
ATOM	173	CA	MET	A	31	0.884	-3.130	29.256	1.00	33.71	AAAA
ATOM	174	CB	MET	A	31	-0.118	-3.999	28.494	1.00	34.12	AAAA
ATOM	175	CG	MET	A	31	-1.452	-3.341	28.249	1.00	34.98	AAAA
ATOM	176	SD	MET	A	31	-2.618	-4.475	27.485	1.00	38.51	AAAA
ATOM	177	CE	MET	A	31	-2.086	-4.401	25.803	1.00	37.49	AAAA
ATOM	178	C	MET	A	31	2.078	-3.987	29.664	1.00	35.03	AAAA
ATOM	179	O	MET	A	31	2.101	-4.548	30.758	1.00	36.09	AAAA
ATOM	180	N	ALA	A	32	3.062	-4.085	28.776	1.00	35.62	AAAA
ATOM	181	CA	ALA	A	32	4.262	-4.871	29.044	1.00	37.61	AAAA
ATOM	182	CB	ALA	A	32	5.049	-5.087	27.755	1.00	37.79	AAAA
ATOM	183	C	ALA	A	32	5.133	-4.158	30.070	1.00	38.72	AAAA
ATOM	184	O	ALA	A	32	6.223	-4.621	30.409	1.00	39.48	AAAA
ATOM	185	N	GLN	A	33	4.654	-3.022	30.560	1.00	38.28	AAAA
ATOM	186	CA	GLN	A	33	5.408	-2.275	31.548	1.00	38.14	AAAA
ATOM	187	CB	GLN	A	33	5.903	-0.969	30.941	1.00	39.68	AAAA
ATOM	188	CG	GLN	A	33	6.856	-1.210	29.791	1.00	42.76	AAAA
ATOM	189	CD	GLN	A	33	7.262	0.061	29.096	1.00	44.20	AAAA
ATOM	190	OE1	GLN	A	33	7.803	0.975	29.717	1.00	46.28	AAAA
ATOM	191	NE2	GLN	A	33	7.002	0.131	27.795	1.00	44.60	AAAA
ATOM	192	C	GLN	A	33	4.576	-2.020	32.787	1.00	36.68	AAAA
ATOM	193	O	GLN	A	33	4.822	-1.075	33.532	1.00	37.34	AAAA
ATOM	194	N	GLY	A	34	3.585	-2.877	33.000	1.00	35.86	AAAA
ATOM	195	CA	GLY	A	34	2.738	-2.755	34.170	1.00	35.52	AAAA
ATOM	196	C	GLY	A	34	1.461	-1.951	34.008	1.00	34.34	AAAA
ATOM	197	O	GLY	A	34	0.611	-1.974	34.897	1.00	33.67	AAAA
ATOM	198	N	TRP	A	35	1.314	-1.248	32.890	1.00	34.23	AAAA
ATOM	199	CA	TRP	A	35	0.121	-0.435	32.661	1.00	33.63	AAAA
ATOM	200	CB	TRP	A	35	0.324	0.509	31.474	1.00	34.84	AAAA
ATOM	201	CG	TRP	A	35	1.150	1.722	31.753	1.00	35.09	AAAA
ATOM	202	CD2	TRP	A	35	0.722	3.087	31.659	1.00	36.11	AAAA
ATOM	203	CE2	TRP	A	35	1.840	3.897	31.957	1.00	36.13	AAAA
ATOM	204	CE3	TRP	A	35	-0.499	3.705	31.350	1.00	37.33	AAAA
ATOM	205	CD1	TRP	A	35	2.469	1.759	32.099	1.00	35.78	AAAA
ATOM	206	NE1	TRP	A	35	2.893	3.062	32.221	1.00	34.49	AAAA
ATOM	207	CZ2	TRP	A	35	1.776	5.293	31.955	1.00	37.71	AAAA
ATOM	208	CZ3	TRP	A	35	-0.563	5.095	31.348	1.00	37.99	AAAA
ATOM	209	CH2	TRP	A	35	0.570	5.874	31.650	1.00	38.17	AAAA
ATOM	210	C	TRP	A	35	-1.153	-1.228	32.402	1.00	33.77	AAAA
ATOM	211	O	TRP	A	35	-1.136	-2.282	31.763	1.00	32.95	AAAA
ATOM	212	N	GLN	A	36	-2.261	-0.704	32.912	1.00	32.90	AAAA
ATOM	213	CA	GLN	A	36	-3.567	-1.301	32.696	1.00	33.08	AAAA
ATOM	214	CB	GLN	A	36	-4.448	-1.160	33.937	1.00	34.93	AAAA
ATOM	215	CG	GLN	A	36	-4.240	-2.228	34.992	1.00	38.58	AAAA
ATOM	216	CD	GLN	A	36	-5.272	-2.143	36.103	1.00	40.36	AAAA
ATOM	217	OE1	GLN	A	36	-5.295	-1.186	36.874	1.00	42.12	AAAA
ATOM	218	NE2	GLN	A	36	-6.140	-3.146	36.181	1.00	42.80	AAAA
ATOM	219	C	GLN	A	36	-4.160	-0.482	31.552	1.00	32.42	AAAA
ATOM	220	O	GLN	A	36	-4.114	0.748	31.583	1.00	31.42	AAAA
ATOM	221	N	VAL	A	37	-4.697	-1.157	30.541	1.00	32.07	AAAA
ATOM	222	CA	VAL	A	37	-5.276	-0.456	29.403	1.00	31.91	AAAA
ATOM	223	CB	VAL	A	37	-4.436	-0.656	28.123	1.00	32.46	AAAA

ATOM	224	CG1	VAL	A	37	-5.010	0.179	26.983	1.00	32.66	AAAA
ATOM	225	CG2	VAL	A	37	-2.994	-0.269	28.379	1.00	31.40	AAAA
ATOM	226	C	VAL	A	37	-6.693	-0.917	29.118	1.00	32.15	AAAA
ATOM	227	O	VAL	A	37	-7.017	-2.104	29.225	1.00	31.04	AAAA
ATOM	228	N	ARG	A	38	-7.532	0.046	28.752	1.00	30.74	AAAA
ATOM	229	CA	ARG	A	38	-8.925	-0.202	28.433	1.00	31.08	AAAA
ATOM	230	CB	ARG	A	38	-9.807	0.325	29.562	1.00	33.01	AAAA
ATOM	231	CG	ARG	A	38	-11.251	-0.116	29.499	1.00	37.13	AAAA
ATOM	232	CD	ARG	A	38	-11.532	-1.185	30.529	1.00	39.30	AAAA
ATOM	233	NE	ARG	A	38	-12.937	-1.567	30.519	1.00	41.65	AAAA
ATOM	234	CZ	ARG	A	38	-13.464	-2.495	31.308	1.00	43.12	AAAA
ATOM	235	NH1	ARG	A	38	-12.697	-3.142	32.176	1.00	43.84	AAAA
ATOM	236	NH2	ARG	A	38	-14.758	-2.773	31.227	1.00	43.90	AAAA
ATOM	237	C	ARG	A	38	-9.196	0.568	27.143	1.00	29.87	AAAA
ATOM	238	O	ARG	A	38	-8.574	1.601	26.883	1.00	28.94	AAAA
ATOM	239	N	TRP	A	39	-10.119	0.072	26.332	1.00	28.69	AAAA
ATOM	240	CA	TRP	A	39	-10.414	0.729	25.071	1.00	28.19	AAAA
ATOM	241	CB	TRP	A	39	-10.321	-0.305	23.939	1.00	29.84	AAAA
ATOM	242	CG	TRP	A	39	-10.046	0.269	22.583	1.00	33.23	AAAA
ATOM	243	CD2	TRP	A	39	-8.774	0.339	21.919	1.00	33.62	AAAA
ATOM	244	CE2	TRP	A	39	-8.995	0.945	20.661	1.00	34.00	AAAA
ATOM	245	CE3	TRP	A	39	-7.470	-0.052	22.261	1.00	33.80	AAAA
ATOM	246	CD1	TRP	A	39	-10.955	0.823	21.729	1.00	34.36	AAAA
ATOM	247	NE1	TRP	A	39	-10.332	1.230	20.573	1.00	33.43	AAAA
ATOM	248	CZ2	TRP	A	39	-7.960	1.171	19.743	1.00	34.56	AAAA
ATOM	249	CZ3	TRP	A	39	-6.442	0.171	21.350	1.00	35.28	AAAA
ATOM	250	CH2	TRP	A	39	-6.695	0.779	20.102	1.00	34.47	AAAA
ATOM	251	C	TRP	A	39	-11.790	1.395	25.081	1.00	26.35	AAAA
ATOM	252	O	TRP	A	39	-12.683	0.994	25.826	1.00	26.68	AAAA
ATOM	253	N	LEU	A	40	-11.935	2.438	24.269	1.00	25.04	AAAA
ATOM	254	CA	LEU	A	40	-13.197	3.159	24.130	1.00	23.18	AAAA
ATOM	255	CB	LEU	A	40	-13.074	4.602	24.637	1.00	22.55	AAAA
ATOM	256	CG	LEU	A	40	-14.395	5.381	24.623	1.00	20.79	AAAA
ATOM	257	CD1	LEU	A	40	-15.314	4.801	25.675	1.00	21.21	AAAA
ATOM	258	CD2	LEU	A	40	-14.149	6.868	24.905	1.00	21.72	AAAA
ATOM	259	C	LEU	A	40	-13.495	3.179	22.634	1.00	22.87	AAAA
ATOM	260	O	LEU	A	40	-12.718	3.721	21.854	1.00	22.99	AAAA
ATOM	261	N	GLY	A	41	-14.608	2.580	22.232	1.00	25.02	AAAA
ATOM	262	CA	GLY	A	41	-14.946	2.553	20.821	1.00	25.95	AAAA
ATOM	263	C	GLY	A	41	-16.426	2.332	20.594	1.00	28.01	AAAA
ATOM	264	O	GLY	A	41	-17.234	2.555	21.494	1.00	28.82	AAAA
ATOM	265	N	THR	A	42	-16.783	1.884	19.395	1.00	29.77	AAAA
ATOM	266	CA	THR	A	42	-18.185	1.641	19.059	1.00	31.41	AAAA
ATOM	267	CB	THR	A	42	-18.603	2.497	17.855	1.00	32.12	AAAA
ATOM	268	OG1	THR	A	42	-18.293	3.871	18.119	1.00	34.95	AAAA
ATOM	269	CG2	THR	A	42	-20.098	2.367	17.611	1.00	34.55	AAAA
ATOM	270	C	THR	A	42	-18.458	0.168	18.741	1.00	32.23	AAAA
ATOM	271	O	THR	A	42	-17.721	-0.463	17.986	1.00	29.57	AAAA
ATOM	272	N	ALA	A	43	-19.541	-0.360	19.306	1.00	34.77	AAAA
ATOM	273	CA	ALA	A	43	-19.920	-1.760	19.127	1.00	37.23	AAAA
ATOM	274	CB	ALA	A	43	-21.173	-2.060	19.948	1.00	37.66	AAAA
ATOM	275	C	ALA	A	43	-20.126	-2.232	17.686	1.00	39.10	AAAA
ATOM	276	O	ALA	A	43	-20.088	-3.434	17.422	1.00	39.09	AAAA
ATOM	277	N	ASP	A	44	-20.333	-1.304	16.757	1.00	40.78	AAAA
ATOM	278	CA	ASP	A	44	-20.557	-1.671	15.361	1.00	42.78	AAAA
ATOM	279	CB	ASP	A	44	-21.678	-0.812	14.774	1.00	44.80	AAAA
ATOM	280	CG	ASP	A	44	-21.438	0.670	14.973	1.00	46.37	AAAA
ATOM	281	OD1	ASP	A	44	-20.464	1.206	14.400	1.00	48.22	AAAA
ATOM	282	OD2	ASP	A	44	-22.220	1.302	15.712	1.00	49.14	AAAA
ATOM	283	C	ASP	A	44	-19.324	-1.559	14.472	1.00	43.14	AAAA
ATOM	284	O	ASP	A	44	-19.320	-2.061	13.349	1.00	44.14	AAAA
ATOM	285	N	ARG	A	45	-18.281	-0.904	14.970	1.00	42.77	AAAA
ATOM	286	CA	ARG	A	45	-17.056	-0.730	14.199	1.00	42.34	AAAA
ATOM	287	CB	ARG	A	45	-16.415	0.614	14.550	1.00	44.43	AAAA
ATOM	288	CG	ARG	A	45	-17.206	1.822	14.056	1.00	48.23	AAAA
ATOM	289	CD	ARG	A	45	-17.272	1.845	12.533	1.00	51.20	AAAA

ATOM	290	NE	ARG	A	45	-17.950	3.029	12.014	1.00	54.35	AAAA
ATOM	291	CZ	ARG	A	45	-17.526	4.279	12.191	1.00	56.26	AAAA
ATOM	292	NH1	ARG	A	45	-16.417	4.522	12.881	1.00	56.45	AAAA
ATOM	293	NH2	ARG	A	45	-18.212	5.290	11.670	1.00	57.50	AAAA
ATOM	294	C	ARG	A	45	-16.054	-1.872	14.401	1.00	41.11	AAAA
ATOM	295	O	ARG	A	45	-16.194	-2.679	15.320	1.00	40.45	AAAA
ATOM	296	N	MET	A	46	-15.041	-1.928	13.543	1.00	39.55	AAAA
ATOM	297	CA	MET	A	46	-14.038	-2.990	13.604	1.00	39.67	AAAA
ATOM	298	CB	MET	A	46	-13.041	-2.839	12.444	1.00	39.68	AAAA
ATOM	299	CG	MET	A	46	-12.239	-1.544	12.423	1.00	42.15	AAAA
ATOM	300	SD	MET	A	46	-10.690	-1.620	13.352	1.00	44.74	AAAA
ATOM	301	CE	MET	A	46	-9.559	-2.332	12.128	1.00	41.92	AAAA
ATOM	302	C	MET	A	46	-13.279	-3.148	14.926	1.00	38.68	AAAA
ATOM	303	O	MET	A	46	-12.772	-4.232	15.219	1.00	38.02	AAAA
ATOM	304	N	GLU	A	47	-13.198	-2.092	15.730	1.00	37.48	AAAA
ATOM	305	CA	GLU	A	47	-12.486	-2.198	17.002	1.00	36.91	AAAA
ATOM	306	CB	GLU	A	47	-12.309	-0.820	17.650	1.00	35.19	AAAA
ATOM	307	CG	GLU	A	47	-13.615	-0.150	18.058	1.00	34.12	AAAA
ATOM	308	CD	GLU	A	47	-14.142	0.807	17.003	1.00	34.06	AAAA
ATOM	309	OE1	GLU	A	47	-13.712	0.707	15.832	1.00	33.13	AAAA
ATOM	310	OE2	GLU	A	47	-14.995	1.652	17.350	1.00	32.08	AAAA
ATOM	311	C	GLU	A	47	-13.225	-3.123	17.972	1.00	36.96	AAAA
ATOM	312	O	GLU	A	47	-12.612	-3.744	18.842	1.00	37.00	AAAA
ATOM	313	N	ALA	A	48	-14.541	-3.222	17.818	1.00	36.76	AAAA
ATOM	314	CA	ALA	A	48	-15.342	-4.066	18.700	1.00	36.98	AAAA
ATOM	315	CB	ALA	A	48	-16.823	-3.917	18.365	1.00	37.33	AAAA
ATOM	316	C	ALA	A	48	-14.943	-5.533	18.623	1.00	38.23	AAAA
ATOM	317	O	ALA	A	48	-15.100	-6.281	19.590	1.00	37.91	AAAA
ATOM	318	N	ASP	A	49	-14.430	-5.947	17.470	1.00	39.31	AAAA
ATOM	319	CA	ASP	A	49	-14.027	-7.332	17.286	1.00	40.97	AAAA
ATOM	320	CB	ASP	A	49	-14.477	-7.832	15.909	1.00	42.68	AAAA
ATOM	321	CG	ASP	A	49	-15.988	-7.912	15.783	1.00	44.91	AAAA
ATOM	322	OD1	ASP	A	49	-16.612	-8.681	16.549	1.00	45.64	AAAA
ATOM	323	OD2	ASP	A	49	-16.552	-7.205	14.918	1.00	46.44	AAAA
ATOM	324	C	ASP	A	49	-12.524	-7.519	17.426	1.00	40.10	AAAA
ATOM	325	O	ASP	A	49	-12.069	-8.518	17.974	1.00	40.92	AAAA
ATOM	326	N	LEU	A	50	-11.761	-6.549	16.940	1.00	39.40	AAAA
ATOM	327	CA	LEU	A	50	-10.306	-6.623	16.982	1.00	39.05	AAAA
ATOM	328	CB	LEU	A	50	-9.710	-5.578	16.036	1.00	38.17	AAAA
ATOM	329	CG	LEU	A	50	-8.183	-5.562	15.942	1.00	38.18	AAAA
ATOM	330	CD1	LEU	A	50	-7.685	-6.916	15.462	1.00	37.91	AAAA
ATOM	331	CD2	LEU	A	50	-7.740	-4.460	14.999	1.00	37.50	AAAA
ATOM	332	C	LEU	A	50	-9.666	-6.486	18.365	1.00	39.12	AAAA
ATOM	333	O	LEU	A	50	-8.805	-7.286	18.732	1.00	38.56	AAAA
ATOM	334	N	VAL	A	51	-10.084	-5.483	19.132	1.00	38.79	AAAA
ATOM	335	CA	VAL	A	51	-9.516	-5.257	20.459	1.00	37.64	AAAA
ATOM	336	CB	VAL	A	51	-10.127	-3.989	21.111	1.00	36.87	AAAA
ATOM	337	CG1	VAL	A	51	-9.571	-3.795	22.523	1.00	35.15	AAAA
ATOM	338	CG2	VAL	A	51	-9.810	-2.777	20.256	1.00	34.42	AAAA
ATOM	339	C	VAL	A	51	-9.647	-6.449	21.415	1.00	37.87	AAAA
ATOM	340	O	VAL	A	51	-8.695	-6.790	22.115	1.00	37.54	AAAA
ATOM	341	N	PRO	A	52	-10.825	-7.093	21.465	1.00	38.44	AAAA
ATOM	342	CD	PRO	A	52	-12.141	-6.700	20.932	1.00	38.92	AAAA
ATOM	343	CA	PRO	A	52	-10.959	-8.237	22.373	1.00	39.32	AAAA
ATOM	344	CB	PRO	A	52	-12.436	-8.602	22.253	1.00	39.97	AAAA
ATOM	345	CG	PRO	A	52	-13.080	-7.277	21.962	1.00	38.98	AAAA
ATOM	346	C	PRO	A	52	-10.035	-9.392	21.974	1.00	40.07	AAAA
ATOM	347	O	PRO	A	52	-9.685	-10.232	22.805	1.00	40.30	AAAA
ATOM	348	N	LYS	A	53	-9.649	-9.427	20.699	1.00	40.35	AAAA
ATOM	349	CA	LYS	A	53	-8.752	-10.463	20.193	1.00	40.58	AAAA
ATOM	350	CB	LYS	A	53	-8.812	-10.541	18.661	1.00	41.25	AAAA
ATOM	351	CG	LYS	A	53	-10.093	-11.169	18.129	1.00	43.24	AAAA
ATOM	352	CD	LYS	A	53	-10.033	-11.383	16.627	1.00	44.40	AAAA
ATOM	353	CE	LYS	A	53	-11.280	-12.102	16.133	1.00	45.87	AAAA
ATOM	354	NZ	LYS	A	53	-11.250	-12.342	14.659	1.00	47.88	AAAA
ATOM	355	C	LYS	A	53	-7.323	-10.184	20.636	1.00	39.99	AAAA

ATOM	356	O	LYS	A	53	-6.426	-11.006	20.432	1.00	39.70	AAAA
ATOM	357	N	HIS	A	54	-7.112	-9.014	21.231	1.00	38.65	AAAA
ATOM	358	CA	HIS	A	54	-5.790	-8.642	21.727	1.00	37.71	AAAA
ATOM	359	CB	HIS	A	54	-5.408	-7.233	21.272	1.00	37.50	AAAA
ATOM	360	CG	HIS	A	54	-4.903	-7.164	19.864	1.00	37.59	AAAA
ATOM	361	CD2	HIS	A	54	-5.483	-7.502	18.687	1.00	37.67	AAAA
ATOM	362	ND1	HIS	A	54	-3.658	-6.666	19.546	1.00	37.90	AAAA
ATOM	363	CE1	HIS	A	54	-3.492	-6.698	18.235	1.00	37.11	AAAA
ATOM	364	NE2	HIS	A	54	-4.586	-7.202	17.691	1.00	36.75	AAAA
ATOM	365	C	HIS	A	54	-5.788	-8.711	23.248	1.00	37.10	AAAA
ATOM	366	O	HIS	A	54	-4.871	-8.214	23.899	1.00	37.35	AAAA
ATOM	367	N	GLY	A	55	-6.828	-9.331	23.800	1.00	36.15	AAAA
ATOM	368	CA	GLY	A	55	-6.948	-9.477	25.240	1.00	36.70	AAAA
ATOM	369	C	GLY	A	55	-7.266	-8.200	25.997	1.00	36.66	AAAA
ATOM	370	O	GLY	A	55	-7.145	-8.157	27.222	1.00	36.89	AAAA
ATOM	371	N	ILE	A	56	-7.686	-7.163	25.277	1.00	35.61	AAAA
ATOM	372	CA	ILE	A	56	-8.009	-5.885	25.900	1.00	34.03	AAAA
ATOM	373	CB	ILE	A	56	-7.389	-4.723	25.100	1.00	32.39	AAAA
ATOM	374	CG2	ILE	A	56	-7.748	-3.386	25.750	1.00	31.80	AAAA
ATOM	375	CG1	ILE	A	56	-5.869	-4.904	25.031	1.00	31.50	AAAA
ATOM	376	CD1	ILE	A	56	-5.149	-3.900	24.144	1.00	30.46	AAAA
ATOM	377	C	ILE	A	56	-9.516	-5.668	26.017	1.00	34.37	AAAA
ATOM	378	O	ILE	A	56	-10.263	-5.908	25.067	1.00	34.29	AAAA
ATOM	379	N	GLU	A	57	-9.955	-5.224	27.193	1.00	34.18	AAAA
ATOM	380	CA	GLU	A	57	-11.370	-4.969	27.432	1.00	34.19	AAAA
ATOM	381	CB	GLU	A	57	-11.638	-4.733	28.922	1.00	37.08	AAAA
ATOM	382	CG	GLU	A	57	-11.301	-5.913	29.837	1.00	41.06	AAAA
ATOM	383	CD	GLU	A	57	-12.180	-7.127	29.591	1.00	44.07	AAAA
ATOM	384	OE1	GLU	A	57	-12.011	-8.135	30.313	1.00	45.83	AAAA
ATOM	385	OE2	GLU	A	57	-13.040	-7.078	28.682	1.00	46.00	AAAA
ATOM	386	C	GLU	A	57	-11.751	-3.723	26.645	1.00	32.88	AAAA
ATOM	387	O	GLU	A	57	-10.905	-2.870	26.368	1.00	31.69	AAAA
ATOM	388	N	ILE	A	58	-13.022	-3.611	26.285	1.00	31.36	AAAA
ATOM	389	CA	ILE	A	58	-13.454	-2.454	25.529	1.00	29.92	AAAA
ATOM	390	CB	ILE	A	58	-13.390	-2.749	24.009	1.00	29.51	AAAA
ATOM	391	CG2	ILE	A	58	-14.175	-4.015	23.689	1.00	28.67	AAAA
ATOM	392	CG1	ILE	A	58	-13.895	-1.543	23.216	1.00	29.61	AAAA
ATOM	393	CD1	ILE	A	58	-13.578	-1.623	21.734	1.00	29.09	AAAA
ATOM	394	C	ILE	A	58	-14.843	-1.984	25.927	1.00	29.49	AAAA
ATOM	395	O	ILE	A	58	-15.791	-2.764	25.968	1.00	27.83	AAAA
ATOM	396	N	ASP	A	59	-14.939	-0.700	26.252	1.00	29.28	AAAA
ATOM	397	CA	ASP	A	59	-16.202	-0.091	26.626	1.00	29.70	AAAA
ATOM	398	CB	ASP	A	59	-15.999	0.916	27.759	1.00	30.90	AAAA
ATOM	399	CG	ASP	A	59	-15.676	0.245	29.083	1.00	32.17	AAAA
ATOM	400	OD1	ASP	A	59	-16.485	-0.591	29.540	1.00	33.00	AAAA
ATOM	401	OD2	ASP	A	59	-14.615	0.554	29.664	1.00	33.03	AAAA
ATOM	402	C	ASP	A	59	-16.723	0.608	25.378	1.00	30.39	AAAA
ATOM	403	O	ASP	A	59	-15.947	1.165	24.600	1.00	30.45	AAAA
ATOM	404	N	PHE	A	60	-18.033	0.570	25.180	1.00	31.29	AAAA
ATOM	405	CA	PHE	A	60	-18.612	1.183	24.000	1.00	32.36	AAAA
ATOM	406	CB	PHE	A	60	-19.469	0.166	23.239	1.00	33.01	AAAA
ATOM	407	CG	PHE	A	60	-18.720	-1.056	22.793	1.00	33.55	AAAA
ATOM	408	CD1	PHE	A	60	-19.033	-2.307	23.318	1.00	34.07	AAAA
ATOM	409	CD2	PHE	A	60	-17.720	-0.964	21.832	1.00	34.02	AAAA
ATOM	410	CE1	PHE	A	60	-18.362	-3.451	22.890	1.00	33.73	AAAA
ATOM	411	CE2	PHE	A	60	-17.042	-2.104	21.397	1.00	34.93	AAAA
ATOM	412	CZ	PHE	A	60	-17.366	-3.348	21.928	1.00	34.12	AAAA
ATOM	413	C	PHE	A	60	-19.469	2.395	24.300	1.00	32.89	AAAA
ATOM	414	O	PHE	A	60	-20.062	2.508	25.372	1.00	33.13	AAAA
ATOM	415	N	ILE	A	61	-19.502	3.309	23.338	1.00	34.43	AAAA
ATOM	416	CA	ILE	A	61	-20.326	4.500	23.421	1.00	36.08	AAAA
ATOM	417	CB	ILE	A	61	-19.545	5.785	23.056	1.00	36.15	AAAA
ATOM	418	CG2	ILE	A	61	-20.511	6.957	22.913	1.00	36.47	AAAA
ATOM	419	CG1	ILE	A	61	-18.504	6.092	24.136	1.00	37.27	AAAA
ATOM	420	CD1	ILE	A	61	-17.711	7.360	23.875	1.00	38.32	AAAA
ATOM	421	C	ILE	A	61	-21.380	4.230	22.353	1.00	37.27	AAAA

ATOM	422	O	ILE	A	61	-21.050	3.901	21.215	1.00	36.29	AAAA
ATOM	423	N	ARG	A	62	-22.644	4.337	22.728	1.00	39.91	AAAA
ATOM	424	CA	ARG	A	62	-23.732	4.087	21.797	1.00	43.16	AAAA
ATOM	425	CB	ARG	A	62	-24.818	3.268	22.494	1.00	44.19	AAAA
ATOM	426	CG	ARG	A	62	-26.183	3.312	21.825	1.00	48.33	AAAA
ATOM	427	CD	ARG	A	62	-27.207	2.581	22.680	1.00	50.28	AAAA
ATOM	428	NE	ARG	A	62	-28.584	2.906	22.319	1.00	52.71	AAAA
ATOM	429	CZ	ARG	A	62	-29.646	2.419	22.951	1.00	53.14	AAAA
ATOM	430	NH1	ARG	A	62	-29.482	1.586	23.968	1.00	54.03	AAAA
ATOM	431	NH2	ARG	A	62	-30.870	2.767	22.573	1.00	53.49	AAAA
ATOM	432	C	ARG	A	62	-24.302	5.400	21.280	1.00	44.33	AAAA
ATOM	433	O	ARG	A	62	-24.942	6.140	22.021	1.00	43.98	AAAA
ATOM	434	N	ILE	A	63	-24.053	5.686	20.005	1.00	46.60	AAAA
ATOM	435	CA	ILE	A	63	-24.537	6.912	19.378	1.00	49.26	AAAA
ATOM	436	CB	ILE	A	63	-23.369	7.834	18.965	1.00	49.17	AAAA
ATOM	437	CG2	ILE	A	63	-23.903	9.208	18.593	1.00	50.31	AAAA
ATOM	438	CG1	ILE	A	63	-22.368	7.967	20.113	1.00	49.48	AAAA
ATOM	439	CD1	ILE	A	63	-21.158	8.822	19.775	1.00	49.03	AAAA
ATOM	440	C	ILE	A	63	-25.316	6.540	18.123	1.00	50.72	AAAA
ATOM	441	O	ILE	A	63	-24.724	6.219	17.093	1.00	50.90	AAAA
ATOM	442	N	SER	A	64	-26.639	6.591	18.209	1.00	52.58	AAAA
ATOM	443	CA	SER	A	64	-27.488	6.235	17.078	1.00	54.45	AAAA
ATOM	444	CB	SER	A	64	-28.731	5.491	17.574	1.00	54.65	AAAA
ATOM	445	OG	SER	A	64	-29.528	6.329	18.391	1.00	55.29	AAAA
ATOM	446	C	SER	A	64	-27.927	7.433	16.242	1.00	55.33	AAAA
ATOM	447	O	SER	A	64	-27.919	8.571	16.713	1.00	55.34	AAAA
ATOM	448	N	GLY	A	65	-28.301	7.158	14.993	1.00	56.31	AAAA
ATOM	449	CA	GLY	A	65	-28.774	8.196	14.090	1.00	57.42	AAAA
ATOM	450	C	GLY	A	65	-27.751	9.156	13.508	1.00	58.34	AAAA
ATOM	451	O	GLY	A	65	-28.052	10.333	13.315	1.00	58.53	AAAA
ATOM	452	N	LEU	A	66	-26.552	8.668	13.207	1.00	59.08	AAAA
ATOM	453	CA	LEU	A	66	-25.514	9.530	12.648	1.00	59.80	AAAA
ATOM	454	CB	LEU	A	66	-24.147	9.153	13.229	1.00	59.99	AAAA
ATOM	455	CG	LEU	A	66	-23.927	9.513	14.704	1.00	60.38	AAAA
ATOM	456	CD1	LEU	A	66	-23.983	11.026	14.877	1.00	60.37	AAAA
ATOM	457	CD2	LEU	A	66	-24.983	8.840	15.565	1.00	60.47	AAAA
ATOM	458	C	LEU	A	66	-25.467	9.497	11.121	1.00	60.04	AAAA
ATOM	459	O	LEU	A	66	-25.049	10.466	10.484	1.00	59.29	AAAA
ATOM	460	N	ARG	A	67	-25.892	8.378	10.541	1.00	60.97	AAAA
ATOM	461	CA	ARG	A	67	-25.923	8.224	9.089	1.00	61.57	AAAA
ATOM	462	CB	ARG	A	67	-26.860	9.273	8.484	1.00	62.96	AAAA
ATOM	463	CG	ARG	A	67	-28.340	8.984	8.698	1.00	65.29	AAAA
ATOM	464	CD	ARG	A	67	-29.138	10.270	8.842	1.00	66.93	AAAA
ATOM	465	NE	ARG	A	67	-30.566	10.067	8.611	1.00	68.58	AAAA
ATOM	466	CZ	ARG	A	67	-31.514	10.924	8.980	1.00	69.56	AAAA
ATOM	467	NH1	ARG	A	67	-31.192	12.048	9.607	1.00	69.39	AAAA
ATOM	468	NH2	ARG	A	67	-32.788	10.665	8.709	1.00	69.97	AAAA
ATOM	469	C	ARG	A	67	-24.558	8.301	8.409	1.00	61.08	AAAA
ATOM	470	O	ARG	A	67	-24.474	8.448	7.191	1.00	61.57	AAAA
ATOM	471	N	GLY	A	68	-23.489	8.204	9.189	1.00	60.22	AAAA
ATOM	472	CA	GLY	A	68	-22.161	8.249	8.605	1.00	58.95	AAAA
ATOM	473	C	GLY	A	68	-21.531	9.627	8.541	1.00	58.19	AAAA
ATOM	474	O	GLY	A	68	-20.373	9.763	8.140	1.00	58.31	AAAA
ATOM	475	N	LYS	A	69	-22.282	10.655	8.921	1.00	57.03	AAAA
ATOM	476	CA	LYS	A	69	-21.746	12.009	8.904	1.00	55.91	AAAA
ATOM	477	CB	LYS	A	69	-22.812	13.015	9.349	1.00	56.90	AAAA
ATOM	478	CG	LYS	A	69	-23.827	13.368	8.264	1.00	57.91	AAAA
ATOM	479	CD	LYS	A	69	-23.167	14.147	7.133	1.00	58.56	AAAA
ATOM	480	CE	LYS	A	69	-24.163	14.517	6.044	1.00	59.37	AAAA
ATOM	481	NZ	LYS	A	69	-23.522	15.327	4.965	1.00	59.41	AAAA
ATOM	482	C	LYS	A	69	-20.527	12.078	9.818	1.00	54.19	AAAA
ATOM	483	O	LYS	A	69	-19.447	12.480	9.392	1.00	54.69	AAAA
ATOM	484	N	GLY	A	70	-20.697	11.676	11.072	1.00	51.77	AAAA
ATOM	485	CA	GLY	A	70	-19.575	11.692	11.991	1.00	48.95	AAAA
ATOM	486	C	GLY	A	70	-19.668	12.687	13.129	1.00	46.84	AAAA
ATOM	487	O	GLY	A	70	-20.754	12.975	13.629	1.00	46.29	AAAA

ATOM	488	N	ILE	A	71	-18.515	13.221	13.523	1.00	45.26	AAAA
ATOM	489	CA	ILE	A	71	-18.415	14.174	14.623	1.00	43.82	AAAA
ATOM	490	CB	ILE	A	71	-16.936	14.463	14.959	1.00	42.91	AAAA
ATOM	491	CG2	ILE	A	71	-16.262	15.142	13.786	1.00	42.86	AAAA
ATOM	492	CG1	ILE	A	71	-16.839	15.325	16.217	1.00	41.89	AAAA
ATOM	493	CD1	ILE	A	71	-17.324	14.619	17.471	1.00	42.12	AAAA
ATOM	494	C	ILE	A	71	-19.127	15.501	14.367	1.00	43.91	AAAA
ATOM	495	O	ILE	A	71	-19.635	16.125	15.296	1.00	43.71	AAAA
ATOM	496	N	LYS	A	72	-19.154	15.935	13.112	1.00	43.92	AAAA
ATOM	497	CA	LYS	A	72	-19.815	17.188	12.757	1.00	43.85	AAAA
ATOM	498	CB	LYS	A	72	-19.559	17.526	11.284	1.00	45.17	AAAA
ATOM	499	CG	LYS	A	72	-20.140	16.517	10.297	1.00	46.64	AAAA
ATOM	500	CD	LYS	A	72	-19.590	15.112	10.516	1.00	47.65	AAAA
ATOM	501	CE	LYS	A	72	-18.070	15.074	10.388	1.00	47.12	AAAA
ATOM	502	NZ	LYS	A	72	-17.533	13.692	10.506	1.00	46.69	AAAA
ATOM	503	C	LYS	A	72	-21.318	17.073	13.003	1.00	42.82	AAAA
ATOM	504	O	LYS	A	72	-21.969	18.035	13.414	1.00	43.31	AAAA
ATOM	505	N	ALA	A	73	-21.862	15.889	12.752	1.00	41.38	AAAA
ATOM	506	CA	ALA	A	73	-23.282	15.650	12.954	1.00	39.79	AAAA
ATOM	507	CB	ALA	A	73	-23.700	14.379	12.238	1.00	39.55	AAAA
ATOM	508	C	ALA	A	73	-23.575	15.524	14.438	1.00	39.28	AAAA
ATOM	509	O	ALA	A	73	-24.509	16.132	14.959	1.00	37.60	AAAA
ATOM	510	N	LEU	A	74	-22.760	14.725	15.116	1.00	38.96	AAAA
ATOM	511	CA	LEU	A	74	-22.933	14.498	16.541	1.00	38.75	AAAA
ATOM	512	CB	LEU	A	74	-21.817	13.575	17.055	1.00	39.47	AAAA
ATOM	513	CG	LEU	A	74	-21.826	13.192	18.536	1.00	39.30	AAAA
ATOM	514	CD1	LEU	A	74	-21.439	14.383	19.366	1.00	40.12	AAAA
ATOM	515	CD2	LEU	A	74	-23.199	12.673	18.936	1.00	39.66	AAAA
ATOM	516	C	LEU	A	74	-22.938	15.808	17.317	1.00	38.15	AAAA
ATOM	517	O	LEU	A	74	-23.768	16.012	18.206	1.00	37.74	AAAA
ATOM	518	N	ILE	A	75	-22.014	16.699	16.982	1.00	38.08	AAAA
ATOM	519	CA	ILE	A	75	-21.923	17.975	17.678	1.00	39.02	AAAA
ATOM	520	CB	ILE	A	75	-20.605	18.707	17.319	1.00	40.76	AAAA
ATOM	521	CG2	ILE	A	75	-20.616	19.109	15.856	1.00	41.16	AAAA
ATOM	522	CG1	ILE	A	75	-20.426	19.938	18.209	1.00	42.50	AAAA
ATOM	523	CD1	ILE	A	75	-20.302	19.616	19.690	1.00	44.15	AAAA
ATOM	524	C	ILE	A	75	-23.114	18.886	17.377	1.00	38.41	AAAA
ATOM	525	O	ILE	A	75	-23.396	19.818	18.130	1.00	38.12	AAAA
ATOM	526	N	ALA	A	76	-23.816	18.602	16.283	1.00	38.04	AAAA
ATOM	527	CA	ALA	A	76	-24.971	19.399	15.878	1.00	37.19	AAAA
ATOM	528	CB	ALA	A	76	-25.060	19.454	14.350	1.00	37.36	AAAA
ATOM	529	C	ALA	A	76	-26.268	18.847	16.455	1.00	36.15	AAAA
ATOM	530	O	ALA	A	76	-27.352	19.323	16.124	1.00	35.97	AAAA
ATOM	531	N	ALA	A	77	-26.156	17.834	17.309	1.00	34.42	AAAA
ATOM	532	CA	ALA	A	77	-27.326	17.225	17.935	1.00	33.14	AAAA
ATOM	533	CB	ALA	A	77	-27.460	15.780	17.499	1.00	33.13	AAAA
ATOM	534	C	ALA	A	77	-27.125	17.311	19.443	1.00	32.59	AAAA
ATOM	535	O	ALA	A	77	-26.502	16.436	20.042	1.00	31.09	AAAA
ATOM	536	N	PRO	A	78	-27.664	18.372	20.073	1.00	32.06	AAAA
ATOM	537	CD	PRO	A	78	-28.619	19.290	19.423	1.00	31.98	AAAA
ATOM	538	CA	PRO	A	78	-27.577	18.653	21.514	1.00	31.07	AAAA
ATOM	539	CB	PRO	A	78	-28.671	19.701	21.727	1.00	32.32	AAAA
ATOM	540	CG	PRO	A	78	-28.703	20.427	20.414	1.00	32.04	AAAA
ATOM	541	C	PRO	A	78	-27.748	17.450	22.443	1.00	30.50	AAAA
ATOM	542	O	PRO	A	78	-26.874	17.155	23.257	1.00	29.52	AAAA
ATOM	543	N	LEU	A	79	-28.878	16.766	22.334	1.00	28.95	AAAA
ATOM	544	CA	LEU	A	79	-29.130	15.619	23.194	1.00	29.33	AAAA
ATOM	545	CB	LEU	A	79	-30.573	15.137	23.023	1.00	29.48	AAAA
ATOM	546	CG	LEU	A	79	-31.644	16.154	23.435	1.00	30.82	AAAA
ATOM	547	CD1	LEU	A	79	-33.025	15.542	23.234	1.00	31.23	AAAA
ATOM	548	CD2	LEU	A	79	-31.450	16.558	24.901	1.00	30.46	AAAA
ATOM	549	C	LEU	A	79	-28.160	14.465	22.950	1.00	28.58	AAAA
ATOM	550	O	LEU	A	79	-27.745	13.795	23.898	1.00	27.00	AAAA
ATOM	551	N	ARG	A	80	-27.794	14.240	21.689	1.00	27.70	AAAA
ATOM	552	CA	ARG	A	80	-26.877	13.156	21.348	1.00	28.33	AAAA
ATOM	553	CB	ARG	A	80	-26.813	12.941	19.836	1.00	30.44	AAAA

ATOM	554	CG	ARG	A	80	-28.037	12.294	19.222	1.00	36.59	AAAA
ATOM	555	CD	ARG	A	80	-27.657	11.616	17.915	1.00	38.91	AAAA
ATOM	556	NE	ARG	A	80	-28.821	11.189	17.151	1.00	43.51	AAAA
ATOM	557	CZ	ARG	A	80	-29.537	11.991	16.370	1.00	44.36	AAAA
ATOM	558	NH1	ARG	A	80	-29.207	13.270	16.244	1.00	45.19	AAAA
ATOM	559	NH2	ARG	A	80	-30.589	11.513	15.721	1.00	45.91	AAAA
ATOM	560	C	ARG	A	80	-25.464	13.384	21.871	1.00	27.39	AAAA
ATOM	561	O	ARG	A	80	-24.835	12.455	22.392	1.00	26.07	AAAA
ATOM	562	N	ILE	A	81	-24.950	14.603	21.719	1.00	26.19	AAAA
ATOM	563	CA	ILE	A	81	-23.608	14.886	22.217	1.00	24.89	AAAA
ATOM	564	CB	ILE	A	81	-23.081	16.269	21.702	1.00	25.72	AAAA
ATOM	565	CG2	ILE	A	81	-24.069	17.373	22.021	1.00	26.90	AAAA
ATOM	566	CG1	ILE	A	81	-21.722	16.584	22.332	1.00	25.98	AAAA
ATOM	567	CD1	ILE	A	81	-20.696	15.474	22.169	1.00	26.39	AAAA
ATOM	568	C	ILE	A	81	-23.609	14.832	23.752	1.00	24.30	AAAA
ATOM	569	O	ILE	A	81	-22.669	14.315	24.365	1.00	22.57	AAAA
ATOM	570	N	PHE	A	82	-24.672	15.344	24.367	1.00	22.71	AAAA
ATOM	571	CA	PHE	A	82	-24.800	15.333	25.827	1.00	22.28	AAAA
ATOM	572	CB	PHE	A	82	-26.099	16.029	26.236	1.00	21.54	AAAA
ATOM	573	CG	PHE	A	82	-26.281	16.184	27.730	1.00	20.67	AAAA
ATOM	574	CD1	PHE	A	82	-25.244	16.644	28.538	1.00	21.08	AAAA
ATOM	575	CD2	PHE	A	82	-27.512	15.907	28.318	1.00	21.44	AAAA
ATOM	576	CE1	PHE	A	82	-25.430	16.831	29.916	1.00	20.18	AAAA
ATOM	577	CE2	PHE	A	82	-27.719	16.093	29.700	1.00	19.77	AAAA
ATOM	578	CZ	PHE	A	82	-26.678	16.555	30.497	1.00	20.80	AAAA
ATOM	579	C	PHE	A	82	-24.797	13.887	26.330	1.00	21.61	AAAA
ATOM	580	O	PHE	A	82	-24.091	13.536	27.285	1.00	21.05	AAAA
ATOM	581	N	ASN	A	83	-25.577	13.042	25.669	1.00	21.80	AAAA
ATOM	582	CA	ASN	A	83	-25.648	11.640	26.045	1.00	22.62	AAAA
ATOM	583	CB	ASN	A	83	-26.806	10.969	25.296	1.00	22.62	AAAA
ATOM	584	CG	ASN	A	83	-26.921	9.495	25.612	1.00	25.00	AAAA
ATOM	585	OD1	ASN	A	83	-26.227	8.677	25.031	1.00	26.80	AAAA
ATOM	586	ND2	ASN	A	83	-27.791	9.153	26.548	1.00	28.27	AAAA
ATOM	587	C	ASN	A	83	-24.324	10.888	25.805	1.00	21.61	AAAA
ATOM	588	O	ASN	A	83	-23.903	10.080	26.639	1.00	22.04	AAAA
ATOM	589	N	ALA	A	84	-23.658	11.150	24.686	1.00	19.98	AAAA
ATOM	590	CA	ALA	A	84	-22.383	10.480	24.401	1.00	19.25	AAAA
ATOM	591	CB	ALA	A	84	-21.912	10.817	22.981	1.00	20.79	AAAA
ATOM	592	C	ALA	A	84	-21.318	10.906	25.424	1.00	19.48	AAAA
ATOM	593	O	ALA	A	84	-20.509	10.095	25.880	1.00	18.26	AAAA
ATOM	594	N	TRP	A	85	-21.322	12.188	25.769	1.00	17.57	AAAA
ATOM	595	CA	TRP	A	85	-20.390	12.736	26.749	1.00	18.15	AAAA
ATOM	596	CB	TRP	A	85	-20.561	14.260	26.781	1.00	17.16	AAAA
ATOM	597	CG	TRP	A	85	-19.863	15.007	27.892	1.00	16.32	AAAA
ATOM	598	CD2	TRP	A	85	-20.300	16.233	28.472	1.00	16.29	AAAA
ATOM	599	CE2	TRP	A	85	-19.340	16.605	29.445	1.00	15.39	AAAA
ATOM	600	CE3	TRP	A	85	-21.413	17.062	28.266	1.00	16.28	AAAA
ATOM	601	CD1	TRP	A	85	-18.677	14.682	28.519	1.00	15.58	AAAA
ATOM	602	NE1	TRP	A	85	-18.364	15.639	29.454	1.00	14.76	AAAA
ATOM	603	CZ2	TRP	A	85	-19.458	17.762	30.204	1.00	14.50	AAAA
ATOM	604	CZ3	TRP	A	85	-21.530	18.218	29.027	1.00	16.55	AAAA
ATOM	605	CH2	TRP	A	85	-20.553	18.558	29.988	1.00	15.65	AAAA
ATOM	606	C	TRP	A	85	-20.639	12.099	28.125	1.00	19.04	AAAA
ATOM	607	O	TRP	A	85	-19.696	11.691	28.820	1.00	17.64	AAAA
ATOM	608	N	ARG	A	86	-21.903	11.986	28.516	1.00	18.52	AAAA
ATOM	609	CA	ARG	A	86	-22.216	11.375	29.803	1.00	19.34	AAAA
ATOM	610	CB	ARG	A	86	-23.675	11.654	30.181	1.00	19.24	AAAA
ATOM	611	CG	ARG	A	86	-23.892	13.104	30.660	1.00	18.36	AAAA
ATOM	612	CD	ARG	A	86	-25.318	13.357	31.154	1.00	19.61	AAAA
ATOM	613	NE	ARG	A	86	-26.303	13.245	30.072	1.00	19.64	AAAA
ATOM	614	CZ	ARG	A	86	-27.021	12.156	29.807	1.00	21.06	AAAA
ATOM	615	NH1	ARG	A	86	-26.880	11.063	30.548	1.00	19.09	AAAA
ATOM	616	NH2	ARG	A	86	-27.879	12.156	28.787	1.00	18.59	AAAA
ATOM	627	O	GLN	A	87	-19.846	6.687	29.576	1.00	18.93	AAAA
ATOM	628	N	ALA	A	88	-19.471	8.479	28.255	1.00	20.24	AAAA
ATOM	629	CA	ALA	A	88	-18.023	8.436	28.412	1.00	20.23	AAAA

ATOM	630	CB	ALA	A	88	-17.355	9.386	27.419	1.00	18.84	AAAA
ATOM	631	C	ALA	A	88	-17.622	8.787	29.841	1.00	20.11	AAAA
ATOM	632	O	ALA	A	88	-16.687	8.202	30.388	1.00	20.39	AAAA
ATOM	633	N	ARG	A	89	-18.309	9.745	30.454	1.00	18.15	AAAA
ATOM	634	CA	ARG	A	89	-17.985	10.091	31.836	1.00	19.16	AAAA
ATOM	635	CB	ARG	A	89	-18.797	11.302	32.313	1.00	16.58	AAAA
ATOM	636	CG	ARG	A	89	-18.225	12.657	31.896	1.00	17.41	AAAA
ATOM	637	CD	ARG	A	89	-19.196	13.769	32.284	1.00	15.10	AAAA
ATOM	638	NE	ARG	A	89	-19.437	13.835	33.729	1.00	16.60	AAAA
ATOM	639	CZ	ARG	A	89	-18.675	14.506	34.587	1.00	16.76	AAAA
ATOM	640	NH1	ARG	A	89	-17.609	15.173	34.157	1.00	16.02	AAAA
ATOM	641	NH2	ARG	A	89	-18.990	14.531	35.877	1.00	15.64	AAAA
ATOM	642	C	ARG	A	89	-18.258	8.902	32.764	1.00	19.91	AAAA
ATOM	643	O	ARG	A	89	-17.469	8.618	33.674	1.00	18.92	AAAA
ATOM	644	N	ALA	A	90	-19.371	8.213	32.544	1.00	21.12	AAAA
ATOM	645	CA	ALA	A	90	-19.719	7.063	33.386	1.00	23.31	AAAA
ATOM	646	CB	ALA	A	90	-21.080	6.502	32.976	1.00	24.02	AAAA
ATOM	647	C	ALA	A	90	-18.640	5.990	33.257	1.00	24.57	AAAA
ATOM	648	O	ALA	A	90	-18.236	5.367	34.243	1.00	24.35	AAAA
ATOM	649	N	ILE	A	91	-18.173	5.790	32.031	1.00	24.03	AAAA
ATOM	650	CA	ILE	A	91	-17.135	4.816	31.746	1.00	24.73	AAAA
ATOM	651	CB	ILE	A	91	-16.922	4.699	30.209	1.00	25.99	AAAA
ATOM	652	CG2	ILE	A	91	-15.547	4.086	29.890	1.00	25.27	AAAA
ATOM	653	CG1	ILE	A	91	-18.061	3.875	29.601	1.00	25.74	AAAA
ATOM	654	CD1	ILE	A	91	-18.123	3.931	28.085	1.00	25.37	AAAA
ATOM	655	C	ILE	A	91	-15.823	5.196	32.436	1.00	25.69	AAAA
ATOM	656	O	ILE	A	91	-15.133	4.339	32.991	1.00	25.17	AAAA
ATOM	657	N	MET	A	92	-15.482	6.481	32.410	1.00	24.39	AAAA
ATOM	658	CA	MET	A	92	-14.243	6.933	33.024	1.00	24.61	AAAA
ATOM	659	CB	MET	A	92	-13.798	8.258	32.391	1.00	23.19	AAAA
ATOM	660	CG	MET	A	92	-13.480	8.088	30.908	1.00	21.54	AAAA
ATOM	661	SD	MET	A	92	-12.816	9.554	30.108	1.00	21.51	AAAA
ATOM	662	CE	MET	A	92	-12.756	9.008	28.463	1.00	17.14	AAAA
ATOM	663	C	MET	A	92	-14.325	7.041	34.545	1.00	24.72	AAAA
ATOM	664	O	MET	A	92	-13.311	6.918	35.236	1.00	24.71	AAAA
ATOM	665	N	LYS	A	93	-15.524	7.262	35.070	1.00	24.64	AAAA
ATOM	666	CA	LYS	A	93	-15.700	7.337	36.517	1.00	26.89	AAAA
ATOM	667	CB	LYS	A	93	-17.102	7.840	36.864	1.00	27.06	AAAA
ATOM	668	CG	LYS	A	93	-17.269	9.345	36.831	1.00	26.10	AAAA
ATOM	669	CD	LYS	A	93	-18.641	9.742	37.366	1.00	28.56	AAAA
ATOM	670	CE	LYS	A	93	-18.762	11.251	37.483	1.00	28.03	AAAA
ATOM	671	NZ	LYS	A	93	-20.068	11.663	38.060	1.00	29.77	AAAA
ATOM	672	C	LYS	A	93	-15.495	5.938	37.119	1.00	28.19	AAAA
ATOM	673	O	LYS	A	93	-14.994	5.792	38.238	1.00	28.43	AAAA
ATOM	674	N	ALA	A	94	-15.880	4.912	36.367	1.00	29.30	AAAA
ATOM	675	CA	ALA	A	94	-15.736	3.532	36.831	1.00	30.63	AAAA
ATOM	676	CB	ALA	A	94	-16.750	2.635	36.131	1.00	30.03	AAAA
ATOM	677	C	ALA	A	94	-14.325	2.981	36.622	1.00	30.40	AAAA
ATOM	678	O	ALA	A	94	-13.778	2.322	37.507	1.00	30.67	AAAA
ATOM	679	N	TYR	A	95	-13.735	3.255	35.462	1.00	29.39	AAAA
ATOM	680	CA	TYR	A	95	-12.394	2.764	35.163	1.00	29.94	AAAA
ATOM	681	CB	TYR	A	95	-12.189	2.685	33.648	1.00	29.85	AAAA
ATOM	682	CG	TYR	A	95	-10.838	2.151	33.224	1.00	31.64	AAAA
ATOM	683	CD1	TYR	A	95	-10.382	0.907	33.669	1.00	31.90	AAAA
ATOM	684	CE1	TYR	A	95	-9.139	0.414	33.270	1.00	32.14	AAAA
ATOM	685	CD2	TYR	A	95	-10.015	2.886	32.370	1.00	30.90	AAAA
ATOM	686	CE2	TYR	A	95	-8.779	2.405	31.969	1.00	31.95	AAAA
ATOM	687	CZ	TYR	A	95	-8.345	1.167	32.423	1.00	32.95	AAAA
ATOM	688	OH	TYR	A	95	-7.120	0.687	32.019	1.00	33.09	AAAA
ATOM	689	C	TYR	A	95	-11.312	3.633	35.791	1.00	29.90	AAAA
ATOM	690	O	TYR	A	95	-10.253	3.137	36.190	1.00	28.99	AAAA
ATOM	691	N	LYS	A	96	-11.584	4.930	35.871	1.00	23.94	AAAA
ATOM	692	CA	LYS	A	96	-10.658	5.893	36.452	1.00	29.17	AAAA
ATOM	693	CB	LYS	A	96	-10.543	5.658	37.966	1.00	32.14	AAAA
ATOM	694	CG	LYS	A	96	-11.871	5.829	38.690	1.00	35.57	AAAA
ATOM	695	CD	LYS	A	96	-11.784	5.541	40.183	1.00	38.37	AAAA

ATOM	697	CE	LYS	A	96	-13.158	5.72	40.828	1.00	39.96	AAAA
ATOM	697	NZ	LYS	A	96	-13.170	5.428	42.295	1.00	42.96	AAAA
ATOM	698	C	LYS	A	96	-9.274	5.884	35.817	1.00	27.78	AAAA
ATOM	699	O	LYS	A	96	-8.281	5.608	36.482	1.00	28.12	AAAA
ATOM	700	N	PRO	A	97	-9.187	6.185	34.509	1.00	26.15	AAAA
ATOM	701	CD	PRO	A	97	-10.258	6.519	33.547	1.00	24.76	AAAA
ATOM	702	CA	PRO	A	97	-7.867	6.191	33.868	1.00	24.70	AAAA
ATOM	703	CB	PRO	A	97	-8.202	6.241	32.381	1.00	23.96	AAAA
ATOM	704	CG	PRO	A	97	-9.477	7.078	32.362	1.00	24.55	AAAA
ATOM	705	C	PRO	A	97	-7.060	7.408	34.320	1.00	24.77	AAAA
ATOM	706	O	PRO	A	97	-7.628	8.438	34.684	1.00	23.93	AAAA
ATOM	707	N	ASP	A	98	-5.737	7.288	34.314	1.00	24.94	AAAA
ATOM	708	CA	ASP	A	98	-4.890	8.404	34.717	1.00	24.75	AAAA
ATOM	709	CB	ASP	A	98	-3.554	7.891	35.261	1.00	26.69	AAAA
ATOM	710	CG	ASP	A	98	-3.725	7.040	36.509	1.00	28.25	AAAA
ATOM	711	OD1	ASP	A	98	-3.546	5.808	36.426	1.00	28.34	AAAA
ATOM	712	OD2	ASP	A	98	-4.053	7.603	37.569	1.00	29.50	AAAA
ATOM	713	C	ASP	A	98	-4.654	9.328	33.529	1.00	23.89	AAAA
ATOM	714	O	ASP	A	98	-4.267	10.486	33.681	1.00	22.57	AAAA
ATOM	715	N	VAL	A	99	-4.918	8.807	32.339	1.00	24.10	AAAA
ATOM	716	CA	VAL	A	99	-4.740	9.569	31.111	1.00	23.85	AAAA
ATOM	717	CB	VAL	A	99	-3.237	9.633	30.730	1.00	25.11	AAAA
ATOM	718	CG1	VAL	A	99	-2.684	8.220	30.614	1.00	25.72	AAAA
ATOM	719	CG2	VAL	A	99	-3.044	10.372	29.420	1.00	24.76	AAAA
ATOM	720	C	VAL	A	99	-5.498	8.865	29.989	1.00	22.90	AAAA
ATOM	721	O	VAL	A	99	-5.767	7.667	30.073	1.00	22.05	AAAA
ATOM	722	N	VAL	A	100	-5.869	9.613	28.951	1.00	22.07	AAAA
ATOM	723	CA	VAL	A	100	-6.544	9.008	27.808	1.00	21.38	AAAA
ATOM	724	CB	VAL	A	100	-8.038	9.451	27.663	1.00	21.17	AAAA
ATOM	725	CG1	VAL	A	100	-8.804	9.095	28.914	1.00	21.06	AAAA
ATOM	726	CG2	VAL	A	100	-8.139	10.942	27.354	1.00	22.14	AAAA
ATOM	727	C	VAL	A	100	-5.777	9.398	26.559	1.00	21.31	AAAA
ATOM	728	O	VAL	A	100	-5.244	10.505	26.464	1.00	21.01	AAAA
ATOM	729	N	LEU	A	101	-5.701	8.468	25.612	1.00	21.54	AAAA
ATOM	730	CA	LEU	A	101	-4.994	8.697	24.362	1.00	22.01	AAAA
ATOM	731	CB	LEU	A	101	-3.944	7.599	24.139	1.00	23.42	AAAA
ATOM	732	CG	LEU	A	101	-2.691	7.856	23.288	1.00	25.21	AAAA
ATOM	733	CD1	LEU	A	101	-2.230	6.515	22.696	1.00	25.87	AAAA
ATOM	734	CD2	LEU	A	101	-2.930	8.854	22.187	1.00	26.43	AAAA
ATOM	735	C	LEU	A	101	-6.006	8.644	23.222	1.00	21.51	AAAA
ATOM	736	O	LEU	A	101	-6.667	7.625	23.029	1.00	21.94	AAAA
ATOM	737	N	GLY	A	102	-6.127	9.742	22.484	1.00	21.18	AAAA
ATOM	738	CA	GLY	A	102	-7.043	9.780	21.358	1.00	21.84	AAAA
ATOM	739	C	GLY	A	102	-6.246	9.586	20.079	1.00	21.20	AAAA
ATOM	740	O	GLY	A	102	-5.294	10.324	19.837	1.00	22.62	AAAA
ATOM	741	N	MET	A	103	-6.627	8.599	19.270	1.00	21.18	AAAA
ATOM	742	CA	MET	A	103	-5.933	8.312	18.015	1.00	22.83	AAAA
ATOM	743	CB	MET	A	103	-5.715	6.805	17.865	1.00	23.16	AAAA
ATOM	744	CG	MET	A	103	-4.978	6.140	19.030	1.00	24.31	AAAA
ATOM	745	SD	MET	A	103	-3.333	6.804	19.308	1.00	27.62	AAAA
ATOM	746	CE	MET	A	103	-2.455	6.156	17.873	1.00	26.43	AAAA
ATOM	747	C	MET	A	103	-6.709	8.823	16.795	1.00	23.47	AAAA
ATOM	748	O	MET	A	103	-6.351	8.532	15.653	1.00	23.75	AAAA
ATOM	749	N	GLY	A	104	-7.767	9.590	17.043	1.00	25.38	AAAA
ATOM	750	CA	GLY	A	104	-8.585	10.114	15.959	1.00	25.56	AAAA
ATOM	751	C	GLY	A	104	-9.878	9.326	15.833	1.00	25.55	AAAA
ATOM	752	O	GLY	A	104	-10.004	8.241	16.404	1.00	26.58	AAAA
ATOM	753	N	GLY	A	105	-10.840	9.854	15.082	1.00	26.06	AAAA
ATOM	754	CA	GLY	A	105	-12.107	9.159	14.930	1.00	26.21	AAAA
ATOM	755	C	GLY	A	105	-13.140	9.819	15.823	1.00	26.96	AAAA
ATOM	756	O	GLY	A	105	-12.810	10.258	16.926	1.00	25.49	AAAA
ATOM	757	N	TYR	A	106	-14.393	9.863	15.376	1.00	27.65	AAAA
ATOM	758	CA	TYR	A	106	-15.434	10.534	16.145	1.00	28.10	AAAA
ATOM	759	CB	TYR	A	106	-16.759	10.556	15.362	1.00	31.05	AAAA
ATOM	760	CG	TYR	A	106	-17.536	9.257	15.303	1.00	33.49	AAAA
ATOM	761	CD1	TYR	A	106	-18.269	8.802	16.400	1.00	34.81	AAAA

ATOM	762	CE1	TYR	A	106	-19.038	7.634	16.323	1.00	36.18	AAAA
ATOM	763	CD2	TYR	A	106	-17.581	8.509	14.123	1.00	35.64	AAAA
ATOM	764	CE2	TYR	A	106	-18.343	7.344	14.032	1.00	36.47	AAAA
ATOM	765	CZ	TYR	A	106	-19.069	6.912	15.133	1.00	37.27	AAAA
ATOM	766	OH	TYR	A	106	-19.829	5.766	15.027	1.00	38.99	AAAA
ATOM	767	C	TYR	A	106	-15.678	10.072	17.576	1.00	26.46	AAAA
ATOM	768	O	TYR	A	106	-15.976	10.897	18.430	1.00	26.55	AAAA
ATOM	769	N	VAL	A	107	-15.549	8.780	17.858	1.00	25.31	AAAA
ATOM	770	CA	VAL	A	107	-15.783	8.318	19.223	1.00	23.91	AAAA
ATOM	771	CB	VAL	A	107	-15.659	6.772	19.335	1.00	25.47	AAAA
ATOM	772	CG1	VAL	A	107	-14.224	6.327	19.076	1.00	26.57	AAAA
ATOM	773	CG2	VAL	A	107	-16.126	6.315	20.711	1.00	24.96	AAAA
ATOM	774	C	VAL	A	107	-14.836	8.993	20.223	1.00	23.22	AAAA
ATOM	775	O	VAL	A	107	-15.190	9.190	21.389	1.00	23.17	AAAA
ATOM	776	N	SER	A	108	-13.650	9.381	19.765	1.00	23.13	AAAA
ATOM	777	CA	SER	A	108	-12.676	10.029	20.643	1.00	23.40	AAAA
ATOM	778	CB	SER	A	108	-11.301	10.108	19.967	1.00	23.85	AAAA
ATOM	779	OG	SER	A	108	-11.292	11.038	18.899	1.00	25.04	AAAA
ATOM	780	C	SER	A	108	-13.121	11.430	21.044	1.00	23.03	AAAA
ATOM	781	O	SER	A	108	-12.592	12.009	21.993	1.00	22.32	AAAA
ATOM	782	N	GLY	A	109	-14.089	11.979	20.310	1.00	21.84	AAAA
ATOM	783	CA	GLY	A	109	-14.583	13.307	20.627	1.00	21.98	AAAA
ATOM	784	C	GLY	A	109	-15.297	13.342	21.972	1.00	20.30	AAAA
ATOM	785	O	GLY	A	109	-14.898	14.088	22.856	1.00	21.37	AAAA
ATOM	786	N	PRO	A	110	-16.369	12.557	22.155	1.00	20.07	AAAA
ATOM	787	CD	PRO	A	110	-16.992	11.637	21.191	1.00	20.80	AAAA
ATOM	788	CA	PRO	A	110	-17.085	12.550	23.436	1.00	19.58	AAAA
ATOM	789	CB	PRO	A	110	-18.232	11.569	23.199	1.00	20.85	AAAA
ATOM	790	CG	PRO	A	110	-18.398	11.548	21.702	1.00	22.43	AAAA
ATOM	791	C	PRO	A	110	-16.136	12.031	24.524	1.00	18.52	AAAA
ATOM	792	O	PRO	A	110	-16.184	12.462	25.675	1.00	19.12	AAAA
ATOM	793	N	GLY	A	111	-15.286	11.086	24.140	1.00	19.12	AAAA
ATOM	794	CA	GLY	A	111	-14.332	10.525	25.087	1.00	18.87	AAAA
ATOM	795	C	GLY	A	111	-13.402	11.601	25.612	1.00	17.97	AAAA
ATOM	796	O	GLY	A	111	-13.208	11.730	26.813	1.00	19.32	AAAA
ATOM	797	N	GLY	A	112	-12.822	12.380	24.704	1.00	18.62	AAAA
ATOM	798	CA	GLY	A	112	-11.925	13.451	25.105	1.00	17.38	AAAA
ATOM	799	C	GLY	A	112	-12.610	14.509	25.957	1.00	17.36	AAAA
ATOM	800	O	GLY	A	112	-12.035	14.997	26.936	1.00	16.49	AAAA
ATOM	801	N	LEU	A	113	-13.837	14.864	25.583	1.00	16.45	AAAA
ATOM	802	CA	LEU	A	113	-14.611	15.866	26.314	1.00	17.35	AAAA
ATOM	803	CB	LEU	A	113	-15.974	16.079	25.640	1.00	17.68	AAAA
ATOM	804	CG	LEU	A	113	-16.735	17.409	25.805	1.00	21.99	AAAA
ATOM	805	CD1	LEU	A	113	-18.205	17.154	25.511	1.00	20.80	AAAA
ATOM	806	CD2	LEU	A	113	-16.570	18.007	27.178	1.00	22.94	AAAA
ATOM	807	C	LEU	A	113	-14.836	15.329	27.725	1.00	16.05	AAAA
ATOM	808	O	LEU	A	113	-14.695	16.045	28.711	1.00	16.63	AAAA
ATOM	809	N	ALA	A	114	-15.199	14.056	27.801	1.00	16.59	AAAA
ATOM	810	CA	ALA	A	114	-15.442	13.416	29.087	1.00	15.95	AAAA
ATOM	811	CB	ALA	A	114	-15.859	11.963	28.868	1.00	17.72	AAAA
ATOM	812	C	ALA	A	114	-14.194	13.492	29.968	1.00	15.37	AAAA
ATOM	813	O	ALA	A	114	-14.260	13.952	31.105	1.00	15.94	AAAA
ATOM	814	N	ALA	A	115	-13.053	13.050	29.452	1.00	16.63	AAAA
ATOM	815	CA	ALA	A	115	-11.820	13.098	30.251	1.00	15.65	AAAA
ATOM	816	CB	ALA	A	115	-10.641	12.518	29.450	1.00	15.52	AAAA
ATOM	817	C	ALA	A	115	-11.506	14.530	30.693	1.00	16.10	AAAA
ATOM	818	O	ALA	A	115	-11.141	14.777	31.841	1.00	15.67	AAAA
ATOM	819	N	TRP	A	116	-11.650	15.480	29.778	1.00	16.71	AAAA
ATOM	820	CA	TRP	A	116	-11.380	16.873	30.100	1.00	17.31	AAAA
ATOM	821	CB	TRP	A	116	-11.542	17.723	28.835	1.00	18.91	AAAA
ATOM	822	CG	TRP	A	116	-11.172	19.155	29.003	1.00	21.69	AAAA
ATOM	823	CD2	TRP	A	116	-12.008	20.277	28.740	1.00	23.65	AAAA
ATOM	824	CE2	TRP	A	116	-11.262	21.438	29.048	1.00	25.14	AAAA
ATOM	825	CE3	TRP	A	116	-13.321	20.418	28.268	1.00	26.49	AAAA
ATOM	826	CD1	TRP	A	116	-9.979	19.658	29.447	1.00	23.00	AAAA
ATOM	827	NE1	TRP	A	116	-10.025	21.032	29.479	1.00	24.96	AAAA

ATOM	828	CZ2	TRP	A	116	-11.785	22.724	28.902	1.00	26.16	AAAA
ATOM	829	CZ3	TRP	A	116	-13.842	21.702	28.122	1.00	26.44	AAAA
ATOM	830	CH2	TRP	A	116	-13.072	22.834	28.439	1.00	25.35	AAAA
ATOM	831	C	TRP	A	116	-12.292	17.377	31.233	1.00	16.50	AAAA
ATOM	832	O	TRP	A	116	-11.835	18.080	32.137	1.00	16.03	AAAA
ATOM	833	N	SER	A	117	-13.565	16.990	31.200	1.00	16.73	AAAA
ATOM	834	CA	SER	A	117	-14.528	17.399	32.229	1.00	17.06	AAAA
ATOM	835	CB	SER	A	117	-15.961	17.116	31.762	1.00	16.18	AAAA
ATOM	836	OG	SER	A	117	-16.270	15.731	31.743	1.00	18.31	AAAA
ATOM	837	C	SER	A	117	-14.289	16.720	33.586	1.00	18.05	AAAA
ATOM	838	O	SER	A	117	-14.837	17.147	34.605	1.00	17.79	AAAA
ATOM	839	N	LEU	A	118	-13.466	15.678	33.594	1.00	18.13	AAAA
ATOM	840	CA	LEU	A	118	-13.146	14.950	34.827	1.00	19.26	AAAA
ATOM	841	CB	LEU	A	118	-13.262	13.441	34.587	1.00	18.09	AAAA
ATOM	842	CG	LEU	A	118	-14.686	12.932	34.353	1.00	20.04	AAAA
ATOM	843	CD1	LEU	A	118	-14.659	11.484	33.869	1.00	20.30	AAAA
ATOM	844	CD2	LEU	A	118	-15.480	13.064	35.646	1.00	20.40	AAAA
ATOM	845	C	LEU	A	118	-11.736	15.283	35.305	1.00	20.78	AAAA
ATOM	846	O	LEU	A	118	-11.267	14.763	36.321	1.00	20.64	AAAA
ATOM	847	N	GLY	A	119	-11.057	16.152	34.566	1.00	21.27	AAAA
ATOM	848	CA	GLY	A	119	-9.706	16.537	34.943	1.00	21.97	AAAA
ATOM	849	C	GLY	A	119	-8.648	15.519	34.550	1.00	21.55	AAAA
ATOM	850	O	GLY	A	119	-7.515	15.582	35.034	1.00	21.92	AAAA
ATOM	851	N	ILE	A	120	-9.009	14.584	33.678	1.00	20.43	AAAA
ATOM	852	CA	ILE	A	120	-8.082	13.548	33.214	1.00	21.09	AAAA
ATOM	853	CB	ILE	A	120	-8.853	12.270	32.836	1.00	20.95	AAAA
ATOM	854	CG2	ILE	A	120	-7.902	11.226	32.275	1.00	22.20	AAAA
ATOM	855	CG1	ILE	A	120	-9.624	11.748	34.051	1.00	22.05	AAAA
ATOM	856	CD1	ILE	A	120	-10.688	10.709	33.689	1.00	21.95	AAAA
ATOM	857	C	ILE	A	120	-7.358	14.088	31.978	1.00	20.81	AAAA
ATOM	858	O	ILE	A	120	-8.001	14.465	31.004	1.00	21.35	AAAA
ATOM	859	N	PRO	A	121	-6.013	14.131	31.999	1.00	20.67	AAAA
ATOM	860	CD	PRO	A	121	-5.052	13.722	33.040	1.00	20.88	AAAA
ATOM	861	CA	PRO	A	121	-5.320	14.658	30.819	1.00	20.52	AAAA
ATOM	862	CB	PRO	A	121	-3.842	14.649	31.237	1.00	21.37	AAAA
ATOM	863	CG	PRO	A	121	-3.777	13.532	32.240	1.00	22.04	AAAA
ATOM	864	C	PRO	A	121	-5.580	13.893	29.536	1.00	19.38	AAAA
ATOM	865	O	PRO	A	121	-5.717	12.671	29.538	1.00	18.17	AAAA
ATOM	866	N	VAL	A	122	-5.647	14.645	28.442	1.00	20.01	AAAA
ATOM	867	CA	VAL	A	122	-5.903	14.102	27.120	1.00	19.76	AAAA
ATOM	868	CB	VAL	A	122	-7.047	14.866	26.421	1.00	18.63	AAAA
ATOM	869	CG1	VAL	A	122	-7.286	14.281	25.033	1.00	20.46	AAAA
ATOM	870	CG2	VAL	A	122	-8.320	14.790	27.264	1.00	20.31	AAAA
ATOM	871	C	VAL	A	122	-4.672	14.205	26.223	1.00	19.39	AAAA
ATOM	872	O	VAL	A	122	-4.096	15.282	26.069	1.00	19.66	AAAA
ATOM	873	N	VAL	A	123	-4.284	13.079	25.634	1.00	19.86	AAAA
ATOM	874	CA	VAL	A	123	-3.134	13.029	24.734	1.00	20.22	AAAA
ATOM	875	CB	VAL	A	123	-2.086	11.982	25.200	1.00	20.59	AAAA
ATOM	876	CG1	VAL	A	123	-0.898	11.957	24.226	1.00	20.51	AAAA
ATOM	877	CG2	VAL	A	123	-1.602	12.317	26.606	1.00	17.21	AAAA
ATOM	878	C	VAL	A	123	-3.684	12.600	23.381	1.00	21.06	AAAA
ATOM	879	O	VAL	A	123	-4.482	11.666	23.300	1.00	22.10	AAAA
ATOM	880	N	LEU	A	124	-3.269	13.284	22.325	1.00	21.08	AAAA
ATOM	881	CA	LEU	A	124	-3.746	12.952	20.989	1.00	21.68	AAAA
ATOM	882	CB	LEU	A	124	-4.463	14.149	20.366	1.00	21.81	AAAA
ATOM	883	CG	LEU	A	124	-5.629	14.805	21.105	1.00	21.93	AAAA
ATOM	884	CD1	LEU	A	124	-6.133	15.980	20.268	1.00	22.15	AAAA
ATOM	885	CD2	LEU	A	124	-6.737	13.787	21.337	1.00	21.49	AAAA
ATOM	886	C	LEU	A	124	-2.628	12.558	20.038	1.00	21.67	AAAA
ATOM	887	O	LEU	A	124	-1.493	13.011	20.170	1.00	22.39	AAAA
ATOM	888	N	HIS	A	125	-2.964	11.713	19.075	1.00	22.63	AAAA
ATOM	889	CA	HIS	A	125	-2.014	11.336	18.036	1.00	24.74	AAAA
ATOM	890	CB	HIS	A	125	-1.429	9.939	18.244	1.00	24.62	AAAA
ATOM	891	CG	HIS	A	125	-0.471	9.540	17.162	1.00	27.30	AAAA
ATOM	892	CD2	HIS	A	125	-0.629	8.744	16.079	1.00	27.23	AAAA
ATOM	893	ND1	HIS	A	125	0.806	10.057	17.072	1.00	29.96	AAAA

ATOM	894	CE1	HIS	A	125	1.391	9.597	15.979	1.00	27.40	AAAA
ATOM	895	NE2	HIS	A	125	0.541	8.799	15.358	1.00	28.94	AAAA
ATOM	896	C	HIS	A	125	-2.763	11.364	16.705	1.00	24.38	AAAA
ATOM	897	O	HIS	A	125	-3.813	10.741	16.565	1.00	23.93	AAAA
ATOM	898	N	GLU	A	126	-2.233	12.111	15.744	1.00	24.36	AAAA
ATOM	899	CA	GLU	A	126	-2.836	12.199	14.420	1.00	26.31	AAAA
ATOM	900	CB	GLU	A	126	-2.992	13.664	14.005	1.00	25.81	AAAA
ATOM	901	CG	GLU	A	126	-3.465	13.861	12.567	1.00	26.62	AAAA
ATOM	902	CD	GLU	A	126	-4.795	13.196	12.288	1.00	27.69	AAAA
ATOM	903	OE1	GLU	A	126	-5.785	13.544	12.965	1.00	27.90	AAAA
ATOM	904	OE2	GLU	A	126	-4.855	12.326	11.391	1.00	27.53	AAAA
ATOM	905	C	GLU	A	126	-1.901	11.472	13.456	1.00	27.49	AAAA
ATOM	906	O	GLU	A	126	-0.727	11.819	13.349	1.00	27.87	AAAA
ATOM	907	N	GLN	A	127	-2.423	10.463	12.765	1.00	28.80	AAAA
ATOM	908	CA	GLN	A	127	-1.617	9.682	11.834	1.00	30.09	AAAA
ATOM	909	CB	GLN	A	127	-2.192	8.264	11.688	1.00	28.89	AAAA
ATOM	910	CG	GLN	A	127	-2.184	7.421	12.958	1.00	28.94	AAAA
ATOM	911	CD	GLN	A	127	-3.456	7.578	13.775	1.00	29.34	AAAA
ATOM	912	OE1	GLN	A	127	-4.543	7.207	13.329	1.00	29.36	AAAA
ATOM	913	NE2	GLN	A	127	-3.326	8.131	14.973	1.00	28.70	AAAA
ATOM	914	C	GLN	A	127	-1.455	10.277	10.438	1.00	30.92	AAAA
ATOM	915	O	GLN	A	127	-0.428	10.068	9.794	1.00	31.21	AAAA
ATOM	916	N	ASN	A	128	-2.448	11.038	9.986	1.00	32.48	AAAA
ATOM	917	CA	ASN	A	128	-2.434	11.596	8.634	1.00	33.12	AAAA
ATOM	918	CB	ASN	A	128	-3.864	11.589	8.083	1.00	32.20	AAAA
ATOM	919	CG	ASN	A	128	-4.606	10.312	8.424	1.00	33.05	AAAA
ATOM	920	OD1	ASN	A	128	-5.296	10.236	9.445	1.00	33.34	AAAA
ATOM	921	ND2	ASN	A	128	-4.454	9.292	7.584	1.00	31.22	AAAA
ATOM	922	C	ASN	A	128	-1.809	12.971	8.394	1.00	33.60	AAAA
ATOM	923	O	ASN	A	128	-1.571	13.744	9.327	1.00	34.03	AAAA
ATOM	924	N	GLY	A	129	-1.550	13.256	7.117	1.00	33.69	AAAA
ATOM	925	CA	GLY	A	129	-0.959	14.524	6.718	1.00	33.68	AAAA
ATOM	926	C	GLY	A	129	-1.903	15.682	6.972	1.00	33.41	AAAA
ATOM	927	O	GLY	A	129	-1.482	16.834	7.057	1.00	32.92	AAAA
ATOM	928	N	ILE	A	130	-3.192	15.374	7.070	1.00	33.49	AAAA
ATOM	929	CA	ILE	A	130	-4.205	16.383	7.361	1.00	33.06	AAAA
ATOM	930	CB	ILE	A	130	-5.204	16.570	6.206	1.00	33.49	AAAA
ATOM	931	CG2	ILE	A	130	-4.548	17.358	5.083	1.00	35.66	AAAA
ATOM	932	CG1	ILE	A	130	-5.736	15.209	5.751	1.00	34.45	AAAA
ATOM	933	CD1	ILE	A	130	-6.775	15.279	4.665	1.00	35.68	AAAA
ATOM	934	C	ILE	A	130	-4.964	15.892	8.584	1.00	32.19	AAAA
ATOM	935	O	ILE	A	130	-5.379	14.733	8.644	1.00	32.07	AAAA
ATOM	936	N	ALA	A	131	-5.135	16.771	9.561	1.00	31.26	AAAA
ATOM	937	CA	ALA	A	131	-5.832	16.404	10.788	1.00	30.63	AAAA
ATOM	938	CB	ALA	A	131	-5.735	17.547	11.800	1.00	30.70	AAAA
ATOM	939	C	ALA	A	131	-7.292	16.038	10.556	1.00	30.27	AAAA
ATOM	940	O	ALA	A	131	-7.992	16.682	9.774	1.00	30.54	AAAA
ATOM	941	N	GLY	A	132	-7.743	14.987	11.232	1.00	29.03	AAAA
ATOM	942	CA	GLY	A	132	-9.131	14.587	11.119	1.00	27.98	AAAA
ATOM	943	C	GLY	A	132	-9.902	15.678	11.837	1.00	26.80	AAAA
ATOM	944	O	GLY	A	132	-9.326	16.387	12.660	1.00	25.68	AAAA
ATOM	945	N	LEU	A	133	-11.188	15.827	11.543	1.00	26.51	AAAA
ATOM	946	CA	LEU	A	133	-11.973	16.882	12.186	1.00	26.70	AAAA
ATOM	947	CB	LEU	A	133	-13.363	16.967	11.538	1.00	28.16	AAAA
ATOM	948	CG	LEU	A	133	-14.275	18.138	11.936	1.00	28.52	AAAA
ATOM	949	CD1	LEU	A	133	-14.889	17.874	13.280	1.00	32.18	AAAA
ATOM	950	CD2	LEU	A	133	-13.486	19.436	11.960	1.00	30.27	AAAA
ATOM	951	C	LEU	A	133	-12.097	16.713	13.703	1.00	25.88	AAAA
ATOM	952	O	LEU	A	133	-12.063	17.700	14.444	1.00	26.12	AAAA
ATOM	953	N	THR	A	134	-12.240	15.475	14.169	1.00	24.18	AAAA
ATOM	954	CA	THR	A	134	-12.353	15.230	15.608	1.00	23.78	AAAA
ATOM	955	CB	THR	A	134	-12.605	13.729	15.922	1.00	23.18	AAAA
ATOM	956	OG1	THR	A	134	-13.814	13.300	15.285	1.00	23.74	AAAA
ATOM	957	CG2	THR	A	134	-12.751	13.511	17.433	1.00	23.66	AAAA
ATOM	958	C	THR	A	134	-11.071	15.671	16.315	1.00	22.68	AAAA
ATOM	959	O	THR	A	134	-11.116	16.368	17.328	1.00	21.38	AAAA

ATOM	960	N	ASN	A	135	-9.927	15.267	15.771	1.00	23.98	AAAA
ATOM	961	CA	ASN	A	135	-8.636	15.623	16.358	1.00	24.64	AAAA
ATOM	962	CB	ASN	A	135	-7.488	14.936	15.597	1.00	24.49	AAAA
ATOM	963	CG	ASN	A	135	-7.020	13.638	16.264	1.00	25.25	AAAA
ATOM	964	OD1	ASN	A	135	-6.267	12.856	15.668	1.00	25.70	AAAA
ATOM	965	ND2	ASN	A	135	-7.445	13.415	17.504	1.00	22.51	AAAA
ATOM	966	C	ASN	A	135	-8.421	17.135	16.349	1.00	25.19	AAAA
ATOM	967	O	ASN	A	135	-7.890	17.702	17.301	1.00	24.79	AAAA
ATOM	968	N	LYS	A	136	-8.839	17.792	15.274	1.00	26.78	AAAA
ATOM	969	CA	LYS	A	136	-8.661	19.234	15.177	1.00	28.71	AAAA
ATOM	970	CB	LYS	A	136	-9.165	19.743	13.828	1.00	30.84	AAAA
ATOM	971	CG	LYS	A	136	-8.816	21.195	13.563	1.00	34.68	AAAA
ATOM	972	CD	LYS	A	136	-9.206	21.596	12.148	1.00	36.19	AAAA
ATOM	973	CE	LYS	A	136	-8.810	23.033	11.846	1.00	37.78	AAAA
ATOM	974	NZ	LYS	A	136	-9.124	23.414	10.432	1.00	40.33	AAAA
ATOM	975	C	LYS	A	136	-9.370	19.981	16.304	1.00	28.66	AAAA
ATOM	976	O	LYS	A	136	-8.803	20.900	16.902	1.00	28.47	AAAA
ATOM	977	N	TRP	A	137	-10.606	19.589	16.596	1.00	28.05	AAAA
ATOM	978	CA	TRP	A	137	-11.363	20.243	17.656	1.00	28.85	AAAA
ATOM	979	CB	TRP	A	137	-12.855	19.921	17.516	1.00	31.86	AAAA
ATOM	980	CG	TRP	A	137	-13.485	20.502	16.282	1.00	34.71	AAAA
ATOM	981	CD2	TRP	A	137	-14.788	20.206	15.755	1.00	36.70	AAAA
ATOM	982	CE2	TRP	A	137	-14.982	21.036	14.630	1.00	37.21	AAAA
ATOM	983	CE3	TRP	A	137	-15.811	19.321	16.130	1.00	38.46	AAAA
ATOM	984	CD1	TRP	A	137	-12.959	21.466	15.471	1.00	36.22	AAAA
ATOM	985	NE1	TRP	A	137	-13.851	21.794	14.480	1.00	36.96	AAAA
ATOM	986	CZ2	TRP	A	137	-16.160	21.010	13.869	1.00	38.57	AAAA
ATOM	987	CZ3	TRP	A	137	-16.986	19.295	15.373	1.00	39.12	AAAA
ATOM	988	CH2	TRP	A	137	-17.148	20.136	14.255	1.00	39.31	AAAA
ATOM	989	C	TRP	A	137	-10.868	19.803	19.029	1.00	28.01	AAAA
ATOM	990	O	TRP	A	137	-10.763	20.605	19.955	1.00	27.04	AAAA
ATOM	991	N	LEU	A	138	-10.548	18.520	19.143	1.00	27.31	AAAA
ATOM	992	CA	LEU	A	138	-10.072	17.943	20.393	1.00	26.35	AAAA
ATOM	993	CB	LEU	A	138	-9.879	16.444	20.174	1.00	27.79	AAAA
ATOM	994	CG	LEU	A	138	-10.054	15.384	21.262	1.00	30.24	AAAA
ATOM	995	CD1	LEU	A	138	-11.263	15.650	22.142	1.00	29.67	AAAA
ATOM	996	CD2	LEU	A	138	-10.178	14.036	20.562	1.00	30.06	AAAA
ATOM	997	C	LEU	A	138	-8.772	18.609	20.834	1.00	25.34	AAAA
ATOM	998	O	LEU	A	138	-8.532	18.814	22.030	1.00	23.81	AAAA
ATOM	999	N	ALA	A	139	-7.931	18.953	19.865	1.00	26.03	AAAA
ATOM	1000	CA	ALA	A	139	-6.657	19.595	20.160	1.00	26.05	AAAA
ATOM	1001	CB	ALA	A	139	-5.918	19.934	18.858	1.00	26.98	AAAA
ATOM	1002	C	ALA	A	139	-6.847	20.858	21.002	1.00	26.86	AAAA
ATOM	1003	O	ALA	A	139	-5.929	21.286	21.697	1.00	26.11	AAAA
ATOM	1004	N	LYS	A	140	-8.044	21.439	20.952	1.00	26.32	AAAA
ATOM	1005	CA	LYS	A	140	-8.329	22.649	21.716	1.00	26.90	AAAA
ATOM	1006	CB	LYS	A	140	-9.644	23.276	21.238	1.00	29.14	AAAA
ATOM	1007	CG	LYS	A	140	-9.665	23.595	19.749	1.00	31.62	AAAA
ATOM	1008	CD	LYS	A	140	-8.523	24.513	19.364	1.00	35.02	AAAA
ATOM	1009	CE	LYS	A	140	-8.811	25.975	19.704	1.00	37.44	AAAA
ATOM	1010	NZ	LYS	A	140	-9.865	26.555	18.812	1.00	40.43	AAAA
ATOM	1011	C	LYS	A	140	-8.395	22.414	23.230	1.00	25.59	AAAA
ATOM	1012	O	LYS	A	140	-8.333	23.361	24.004	1.00	24.94	AAAA
ATOM	1013	N	ILE	A	141	-8.526	21.159	23.649	1.00	24.13	AAAA
ATOM	1014	CA	ILE	A	141	-8.587	20.844	25.075	1.00	23.31	AAAA
ATOM	1015	CB	ILE	A	141	-9.971	20.270	25.477	1.00	22.85	AAAA
ATOM	1016	CG2	ILE	A	141	-11.046	21.355	25.372	1.00	23.88	AAAA
ATOM	1017	CG1	ILE	A	141	-10.313	19.071	24.595	1.00	23.34	AAAA
ATOM	1018	CD1	ILE	A	141	-11.574	18.339	25.012	1.00	25.61	AAAA
ATOM	1019	C	ILE	A	141	-7.524	19.822	25.482	1.00	23.06	AAAA
ATOM	1020	O	ILE	A	141	-7.427	19.450	26.655	1.00	22.52	AAAA
ATOM	1021	N	ALA	A	142	-6.724	19.375	24.520	1.00	21.80	AAAA
ATOM	1022	CA	ALA	A	142	-5.695	18.379	24.803	1.00	21.97	AAAA
ATOM	1023	CB	ALA	A	142	-5.231	17.739	23.495	1.00	20.41	AAAA
ATOM	1024	C	ALA	A	142	-4.491	18.924	25.580	1.00	21.11	AAAA
ATOM	1025	O	ALA	A	142	-4.132	20.094	25.465	1.00	22.76	AAAA

ATOM	1026	N	THR	A	143	-3.887	18.056	28.384	1.00	21.92	AAAA
ATOM	1027	CA	THR	A	143	-2.707	18.391	27.178	1.00	22.64	AAAA
ATOM	1028	CB	THR	A	143	-2.598	17.450	28.400	1.00	23.91	AAAA
ATOM	1029	OG1	THR	A	143	-3.751	17.635	29.232	1.00	25.42	AAAA
ATOM	1030	CG2	THR	A	143	-1.329	17.735	29.209	1.00	24.48	AAAA
ATOM	1031	C	THR	A	143	-1.454	18.235	26.312	1.00	22.79	AAAA
ATOM	1032	O	THR	A	143	-0.444	18.910	26.517	1.00	23.30	AAAA
ATOM	1033	N	LYS	A	144	-1.525	17.341	25.335	1.00	23.20	AAAA
ATOM	1034	CA	LYS	A	144	-0.398	17.106	24.440	1.00	25.09	AAAA
ATOM	1035	CB	LYS	A	144	0.565	16.083	25.049	1.00	25.01	AAAA
ATOM	1036	CG	LYS	A	144	1.706	15.658	24.129	1.00	28.28	AAAA
ATOM	1037	CD	LYS	A	144	2.604	16.838	23.747	1.00	27.48	AAAA
ATOM	1038	CE	LYS	A	144	3.818	16.373	22.946	1.00	29.11	AAAA
ATOM	1039	NZ	LYS	A	144	4.722	17.507	22.587	1.00	28.97	AAAA
ATOM	1040	C	LYS	A	144	-0.896	16.595	23.102	1.00	24.77	AAAA
ATOM	1041	O	LYS	A	144	-1.688	15.660	23.039	1.00	24.45	AAAA
ATOM	1042	N	VAL	A	145	-0.432	17.218	22.030	1.00	24.92	AAAA
ATOM	1043	CA	VAL	A	145	-0.830	16.793	20.701	1.00	25.14	AAAA
ATOM	1044	CB	VAL	A	145	-1.510	17.938	19.919	1.00	24.18	AAAA
ATOM	1045	CG1	VAL	A	145	-2.023	17.418	18.591	1.00	24.71	AAAA
ATOM	1046	CG2	VAL	A	145	-2.658	18.528	20.740	1.00	25.82	AAAA
ATOM	1047	C	VAL	A	145	0.420	16.356	19.950	1.00	25.49	AAAA
ATOM	1048	O	VAL	A	145	1.449	17.034	19.995	1.00	25.76	AAAA
ATOM	1049	N	MET	A	146	0.324	15.208	19.289	1.00	26.18	AAAA
ATOM	1050	CA	MET	A	146	1.421	14.654	18.503	1.00	26.41	AAAA
ATOM	1051	CB	MET	A	146	2.000	13.396	19.172	1.00	26.85	AAAA
ATOM	1052	CG	MET	A	146	2.826	13.653	20.430	1.00	25.85	AAAA
ATOM	1053	SD	MET	A	146	3.306	12.116	21.269	1.00	28.45	AAAA
ATOM	1054	CE	MET	A	146	1.827	11.741	22.217	1.00	26.47	AAAA
ATOM	1055	C	MET	A	146	0.860	14.293	17.131	1.00	27.20	AAAA
ATOM	1056	O	MET	A	146	-0.311	13.934	16.998	1.00	25.68	AAAA
ATOM	1057	N	GLN	A	147	1.701	14.395	16.111	1.00	28.03	AAAA
ATOM	1058	CA	GLN	A	147	1.294	14.091	14.748	1.00	28.39	AAAA
ATOM	1059	CB	GLN	A	147	1.067	15.388	13.979	1.00	28.65	AAAA
ATOM	1060	CG	GLN	A	147	2.203	16.371	14.142	1.00	30.13	AAAA
ATOM	1061	CD	GLN	A	147	2.006	17.653	13.360	1.00	29.84	AAAA
ATOM	1062	OE1	GLN	A	147	2.730	18.629	13.565	1.00	32.18	AAAA
ATOM	1063	NE2	GLN	A	147	1.036	17.657	12.453	1.00	29.40	AAAA
ATOM	1064	C	GLN	A	147	2.394	13.274	14.085	1.00	29.45	AAAA
ATOM	1065	O	GLN	A	147	3.570	13.420	14.424	1.00	29.21	AAAA
ATOM	1066	N	ALA	A	148	2.010	12.412	13.150	1.00	29.90	AAAA
ATOM	1067	CA	ALA	A	148	2.975	11.563	12.461	1.00	31.39	AAAA
ATOM	1068	CB	ALA	A	148	2.254	10.468	11.690	1.00	30.97	AAAA
ATOM	1069	C	ALA	A	148	3.846	12.373	11.514	1.00	32.66	AAAA
ATOM	1070	O	ALA	A	148	5.071	12.231	11.517	1.00	32.76	AAAA
ATOM	1071	N	PHE	A	149	3.205	13.220	10.712	1.00	33.44	AAAA
ATOM	1072	CA	PHE	A	149	3.903	14.059	9.744	1.00	35.09	AAAA
ATOM	1073	CB	PHE	A	149	3.367	13.814	8.332	1.00	34.59	AAAA
ATOM	1074	CG	PHE	A	149	3.200	12.367	7.985	1.00	35.35	AAAA
ATOM	1075	CD1	PHE	A	149	1.935	11.789	7.958	1.00	34.17	AAAA
ATOM	1076	CD2	PHE	A	149	4.304	11.579	7.685	1.00	34.88	AAAA
ATOM	1077	CE1	PHE	A	149	1.771	10.448	7.637	1.00	34.20	AAAA
ATOM	1078	CE2	PHE	A	149	4.148	10.236	7.364	1.00	36.09	AAAA
ATOM	1079	CZ	PHE	A	149	2.878	9.670	7.340	1.00	35.09	AAAA
ATOM	1080	C	PHE	A	149	3.719	15.536	10.056	1.00	36.17	AAAA
ATOM	1081	O	PHE	A	149	2.697	15.939	10.606	1.00	37.06	AAAA
ATOM	1082	N	PRO	A	150	4.709	16.370	9.704	1.00	37.23	AAAA
ATOM	1083	CD	PRO	A	150	6.002	16.078	9.056	1.00	37.75	AAAA
ATOM	1084	CA	PRO	A	150	4.569	17.803	9.975	1.00	38.03	AAAA
ATOM	1085	CB	PRO	A	150	5.967	18.341	9.682	1.00	38.69	AAAA
ATOM	1086	CG	PRO	A	150	6.432	17.448	8.569	1.00	38.52	AAAA
ATOM	1087	C	PRO	A	150	3.510	18.369	9.028	1.00	38.18	AAAA
ATOM	1088	O	PRO	A	150	3.355	17.878	7.912	1.00	38.42	AAAA
ATOM	1089	N	GLY	A	151	2.763	19.374	9.475	1.00	38.74	AAAA
ATOM	1090	CA	GLY	A	151	1.749	19.952	8.609	1.00	38.66	AAAA
ATOM	1091	C	GLY	A	151	0.300	19.705	8.996	1.00	38.69	AAAA

ATOM	1092	O	GLY	A	151	-0.571	20.502	8.645	1.00	38.08	AAAA
ATOM	1093	N	ALA	A	152	0.024	18.602	9.689	1.00	38.70	AAAA
ATOM	1094	CA	ALA	A	152	-1.343	18.311	10.112	1.00	38.90	AAAA
ATOM	1095	CB	ALA	A	152	-1.402	16.980	10.859	1.00	38.46	AAAA
ATOM	1096	C	ALA	A	152	-1.729	19.461	11.032	1.00	39.30	AAAA
ATOM	1097	O	ALA	A	152	-2.753	20.114	10.838	1.00	40.05	AAAA
ATOM	1098	N	PHE	A	153	-0.887	19.700	12.031	1.00	39.42	AAAA
ATOM	1099	CA	PHE	A	153	-1.084	20.795	12.971	1.00	39.90	AAAA
ATOM	1100	CB	PHE	A	153	-1.209	20.286	14.409	1.00	39.04	AAAA
ATOM	1101	CG	PHE	A	153	-2.478	19.535	14.685	1.00	38.06	AAAA
ATOM	1102	CD1	PHE	A	153	-2.571	18.175	14.419	1.00	36.71	AAAA
ATOM	1103	CD2	PHE	A	153	-3.582	20.190	15.228	1.00	37.52	AAAA
ATOM	1104	CE1	PHE	A	153	-3.747	17.475	14.692	1.00	36.39	AAAA
ATOM	1105	CE2	PHE	A	153	-4.761	19.500	15.502	1.00	36.08	AAAA
ATOM	1106	CZ	PHE	A	153	-4.842	18.140	15.235	1.00	36.20	AAAA
ATOM	1107	C	PHE	A	153	0.143	21.696	12.865	1.00	40.75	AAAA
ATOM	1108	O	PHE	A	153	1.238	21.228	12.543	1.00	41.03	AAAA
ATOM	1109	N	PRO	A	154	-0.026	23.001	13.128	1.00	41.05	AAAA
ATOM	1110	CD	PRO	A	154	-1.328	23.667	13.304	1.00	41.17	AAAA
ATOM	1111	CA	PRO	A	154	1.052	23.992	13.068	1.00	41.57	AAAA
ATOM	1112	CB	PRO	A	154	0.339	25.292	13.428	1.00	41.69	AAAA
ATOM	1113	CG	PRO	A	154	-1.024	25.081	12.876	1.00	41.76	AAAA
ATOM	1114	C	PRO	A	154	2.260	23.744	13.975	1.00	42.12	AAAA
ATOM	1115	O	PRO	A	154	3.400	23.833	13.515	1.00	43.15	AAAA
ATOM	1116	N	ASN	A	155	2.023	23.432	15.249	1.00	41.75	AAAA
ATOM	1117	CA	ASN	A	155	3.135	23.230	16.180	1.00	41.57	AAAA
ATOM	1118	CB	ASN	A	155	3.180	24.389	17.179	1.00	44.02	AAAA
ATOM	1119	CG	ASN	A	155	2.961	25.736	16.522	1.00	45.69	AAAA
ATOM	1120	OD1	ASN	A	155	1.862	26.045	16.058	1.00	47.64	AAAA
ATOM	1121	ND2	ASN	A	155	4.010	26.545	16.475	1.00	47.43	AAAA
ATOM	1122	C	ASN	A	155	3.193	21.921	16.970	1.00	40.83	AAAA
ATOM	1123	O	ASN	A	155	3.973	21.814	17.917	1.00	41.17	AAAA
ATOM	1124	N	ALA	A	156	2.390	20.929	16.601	1.00	38.83	AAAA
ATOM	1125	CA	ALA	A	156	2.400	19.658	17.326	1.00	37.19	AAAA
ATOM	1126	CB	ALA	A	156	1.203	18.811	16.909	1.00	36.03	AAAA
ATOM	1127	C	ALA	A	156	3.698	18.882	17.090	1.00	35.95	AAAA
ATOM	1128	O	ALA	A	156	4.206	18.834	15.971	1.00	35.55	AAAA
ATOM	1129	N	GLU	A	157	4.233	18.275	18.146	1.00	35.08	AAAA
ATOM	1130	CA	GLU	A	157	5.464	17.505	18.022	1.00	33.77	AAAA
ATOM	1131	CB	GLU	A	157	5.848	16.881	19.373	1.00	34.33	AAAA
ATOM	1132	CG	GLU	A	157	7.175	16.124	19.352	1.00	34.59	AAAA
ATOM	1133	CD	GLU	A	157	7.487	15.430	20.670	1.00	35.45	AAAA
ATOM	1134	OE1	GLU	A	157	8.517	14.729	20.746	1.00	34.09	AAAA
ATOM	1135	OE2	GLU	A	157	6.705	15.582	21.631	1.00	36.21	AAAA
ATOM	1136	C	GLU	A	157	5.282	16.405	16.970	1.00	32.70	AAAA
ATOM	1137	O	GLU	A	157	4.262	15.709	16.952	1.00	31.88	AAAA
ATOM	1138	N	VAL	A	158	6.268	16.265	16.088	1.00	31.00	AAAA
ATOM	1139	CA	VAL	A	158	6.230	15.255	15.032	1.00	30.25	AAAA
ATOM	1140	CB	VAL	A	158	6.926	15.768	13.751	1.00	30.33	AAAA
ATOM	1141	CG1	VAL	A	158	7.013	14.653	12.719	1.00	29.98	AAAA
ATOM	1142	CG2	VAL	A	158	6.147	16.953	13.181	1.00	30.15	AAAA
ATOM	1143	C	VAL	A	158	6.937	13.998	15.529	1.00	29.69	AAAA
ATOM	1144	O	VAL	A	158	8.142	14.020	15.798	1.00	29.80	AAAA
ATOM	1145	N	VAL	A	159	6.182	12.909	15.645	1.00	28.61	AAAA
ATOM	1146	CA	VAL	A	159	6.715	11.647	16.149	1.00	29.00	AAAA
ATOM	1147	CB	VAL	A	159	6.019	11.250	17.469	1.00	28.75	AAAA
ATOM	1148	CG1	VAL	A	159	6.129	12.384	18.482	1.00	28.06	AAAA
ATOM	1149	CG2	VAL	A	159	4.552	10.921	17.197	1.00	28.06	AAAA
ATOM	1150	C	VAL	A	159	6.581	10.469	15.186	1.00	29.32	AAAA
ATOM	1151	O	VAL	A	159	7.066	9.376	15.479	1.00	29.89	AAAA
ATOM	1152	N	GLY	A	160	5.915	10.688	14.054	1.00	30.03	AAAA
ATOM	1153	CA	GLY	A	160	5.727	9.628	13.075	1.00	29.63	AAAA
ATOM	1154	C	GLY	A	160	4.678	8.608	13.483	1.00	29.61	AAAA
ATOM	1155	O	GLY	A	160	3.917	8.849	14.416	1.00	29.30	AAAA
ATOM	1156	N	ASN	A	161	4.635	7.475	12.782	1.00	29.30	AAAA
ATOM	1157	CA	ASN	A	161	3.677	6.401	13.074	1.00	29.78	AAAA

ATOM	1158	CB	ASN	A	161	2.800	6.097	11.858	1.00	30.70	AAAA
ATOM	1159	CG	ASN	A	161	1.755	7.154	11.609	1.00	32.16	AAAA
ATOM	1160	OD1	ASN	A	161	0.951	7.461	12.492	1.00	31.78	AAAA
ATOM	1161	ND2	ASN	A	161	1.750	7.711	10.400	1.00	30.88	AAAA
ATOM	1162	C	ASN	A	161	4.344	5.089	13.462	1.00	29.50	AAAA
ATOM	1163	O	ASN	A	161	5.471	4.810	13.058	1.00	29.61	AAAA
ATOM	1164	N	PRO	A	162	3.648	4.263	14.251	1.00	29.59	AAAA
ATOM	1165	CD	PRO	A	162	2.441	4.571	15.039	1.00	29.95	AAAA
ATOM	1166	CA	PRO	A	162	4.219	2.977	14.650	1.00	29.65	AAAA
ATOM	1167	CB	PRO	A	162	3.143	2.389	15.553	1.00	29.79	AAAA
ATOM	1168	CG	PRO	A	162	2.559	3.608	16.200	1.00	30.38	AAAA
ATOM	1169	C	PRO	A	162	4.423	2.135	13.389	1.00	30.13	AAAA
ATOM	1170	O	PRO	A	162	3.535	2.063	12.531	1.00	28.48	AAAA
ATOM	1171	N	VAL	A	163	5.590	1.508	13.287	1.00	29.92	AAAA
ATOM	1172	CA	VAL	A	163	5.935	0.664	12.149	1.00	29.89	AAAA
ATOM	1173	CB	VAL	A	163	7.182	1.224	11.417	1.00	31.04	AAAA
ATOM	1174	CG1	VAL	A	163	7.571	0.308	10.260	1.00	30.44	AAAA
ATOM	1175	CG2	VAL	A	163	6.902	2.631	10.914	1.00	29.10	AAAA
ATOM	1176	C	VAL	A	163	6.258	-0.744	12.652	1.00	31.06	AAAA
ATOM	1177	O	VAL	A	163	6.884	-0.892	13.706	1.00	29.66	AAAA
ATOM	1178	N	ARG	A	164	5.820	-1.773	11.927	1.00	31.83	AAAA
ATOM	1179	CA	ARG	A	164	6.124	-3.142	12.339	1.00	34.34	AAAA
ATOM	1180	CB	ARG	A	164	5.533	-4.167	11.354	1.00	36.31	AAAA
ATOM	1181	CG	ARG	A	164	5.704	-3.841	9.876	1.00	39.86	AAAA
ATOM	1182	CD	ARG	A	164	4.855	-4.770	8.997	1.00	41.13	AAAA
ATOM	1183	NE	ARG	A	164	5.368	-6.140	8.946	1.00	43.44	AAAA
ATOM	1184	CZ	ARG	A	164	4.765	-7.145	8.311	1.00	44.08	AAAA
ATOM	1185	NH1	ARG	A	164	3.619	-6.940	7.671	1.00	44.91	AAAA
ATOM	1186	NH2	ARG	A	164	5.308	-8.355	8.308	1.00	44.44	AAAA
ATOM	1187	C	ARG	A	164	7.649	-3.248	12.419	1.00	34.72	AAAA
ATOM	1188	O	ARG	A	164	8.364	-2.769	11.537	1.00	33.63	AAAA
ATOM	1189	N	THR	A	165	8.138	-3.855	13.496	1.00	34.72	AAAA
ATOM	1190	CA	THR	A	165	9.567	-3.969	13.730	1.00	34.94	AAAA
ATOM	1191	CB	THR	A	165	9.839	-4.437	15.177	1.00	35.90	AAAA
ATOM	1192	OG1	THR	A	165	9.008	-5.563	15.488	1.00	36.96	AAAA
ATOM	1193	CG2	THR	A	165	9.530	-3.313	16.149	1.00	35.88	AAAA
ATOM	1194	C	THR	A	165	10.373	-4.814	12.749	1.00	34.61	AAAA
ATOM	1195	O	THR	A	165	11.577	-4.603	12.608	1.00	34.56	AAAA
ATOM	1196	N	ASP	A	166	9.739	-5.765	12.068	1.00	34.66	AAAA
ATOM	1197	CA	ASP	A	166	10.492	-6.558	11.103	1.00	34.85	AAAA
ATOM	1198	CB	ASP	A	166	9.697	-7.784	10.642	1.00	36.47	AAAA
ATOM	1199	CG	ASP	A	166	8.341	-7.430	10.089	1.00	37.65	AAAA
ATOM	1200	OD1	ASP	A	166	7.566	-8.365	9.804	1.00	41.03	AAAA
ATOM	1201	OD2	ASP	A	166	8.048	-6.227	9.937	1.00	39.97	AAAA
ATOM	1202	C	ASP	A	166	10.862	-5.667	9.917	1.00	33.70	AAAA
ATOM	1203	O	ASP	A	166	11.846	-5.925	9.224	1.00	34.04	AAAA
ATOM	1204	N	VAL	A	167	10.081	-4.610	9.694	1.00	31.98	AAAA
ATOM	1205	CA	VAL	A	167	10.366	-3.667	8.611	1.00	31.43	AAAA
ATOM	1206	CB	VAL	A	167	9.096	-2.888	8.170	1.00	31.53	AAAA
ATOM	1207	CG1	VAL	A	167	9.485	-1.738	7.248	1.00	30.83	AAAA
ATOM	1208	CG2	VAL	A	167	8.120	-3.825	7.458	1.00	31.61	AAAA
ATOM	1209	C	VAL	A	167	11.400	-2.657	9.108	1.00	31.23	AAAA
ATOM	1210	O	VAL	A	167	12.320	-2.268	8.380	1.00	30.04	AAAA
ATOM	1211	N	LEU	A	168	11.243	-2.238	10.359	1.00	31.72	AAAA
ATOM	1212	CA	LEU	A	168	12.159	-1.277	10.959	1.00	32.61	AAAA
ATOM	1213	CB	LEU	A	168	11.714	-0.942	12.387	1.00	33.77	AAAA

ATOM	1214	CG	LEU A 168	10.490	-0.046	12.562	1.00	34.46
AAAA								
ATOM	1215	CD1	LEU A 168	10.141	0.076	14.041	1.00	35.50
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ATOM	1216	CD2	LEU A 168	10.790	1.338	11.974	1.00	34.18
AAAA								
ATOM	1217	C	LEU A 168	13.594	-1.790	10.986	1.00	32.72
AAAA								
ATOM	1218	O	LEU A 168	14.538	-1.002	10.923	1.00	32.67
AAAA								
ATOM	1219	N	ALA A 169	13.752	-3.109	11.076	1.00	33.35
AAAA								
ATOM	1220	CA	ALA A 169	15.077	-3.725	11.138	1.00	34.36
AAAA								
ATOM	1221	CB	ALA A 169	14.992	-5.054	11.883	1.00	33.96
AAAA								
ATOM	1222	C	ALA A 169	15.746	-3.939	9.777	1.00	35.45
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ATOM	1223	O	ALA A 169	16.905	-4.362	9.713	1.00	36.53
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ATOM	1224	N	LEU A 170	15.030	-3.651	8.695	1.00	34.52
AAAA								
ATOM	1225	CA	LEU A 170	15.590	-3.833	7.358	1.00	34.60
AAAA								
ATOM	1226	CB	LEU A 170	14.577	-3.423	6.281	1.00	34.25
AAAA								
ATOM	1227	CG	LEU A 170	13.363	-4.333	6.071	1.00	33.98
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ATOM	1228	CD1	LEU A 170	12.393	-3.675	5.101	1.00	34.11
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ATOM	1229	CD2	LEU A 170	13.820	-5.688	5.543	1.00	33.52
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ATOM	1230	C	LEU A 170	16.880	-3.042	7.163	1.00	34.41
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ATOM	1231	O	LEU A 170	17.001	-1.902	7.616	1.00	33.45
AAAA								
ATOM	1232	N	PRO A 171	17.867	-3.648	6.486	1.00	34.33
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ATOM	1233	CD	PRO A 171	17.877	-5.028	5.971	1.00	34.76
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ATOM	1234	CA	PRO A 171	19.152	-2.988	6.233	1.00	35.17
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ATOM	1235	CB	PRO A 171	19.897	-4.005	5.366	1.00	34.52
AAAA								
ATOM	1236	CG	PRO A 171	19.361	-5.308	5.844	1.00	34.60
AAAA								
ATOM	1237	C	PRO A 171	18.938	-1.665	5.503	1.00	35.39
AAAA								
ATOM	1238	O	PRO A 171	17.933	-1.485	4.820	1.00	34.32
AAAA								
ATOM	1239	N	LEU A 172	19.884	-0.746	5.654	1.00	36.05
AAAA								
ATOM	1240	CA	LEU A 172	19.801	0.555	4.998	1.00	37.43
AAAA								
ATOM	1241	CB	LEU A 172	20.946	1.458	5.468	1.00	37.48
AAAA								
ATOM	1242	CG	LEU A 172	20.934	1.934	6.925	1.00	38.42
AAAA								
ATOM	1243	CD1	LEU A 172	19.751	2.863	7.158	1.00	37.89
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ATOM	1244	CD2	LEU A 172	20.876	0.735	7.859	1.00	38.70
AAAA								
ATOM	1245	C	LEU A 172	19.865	0.400	3.479	1.00	38.03
AAAA								
ATOM	1246	O	LEU A 172	20.392	-0.591	2.969	1.00	38.19
AAAA								

ATOM	1247	N	PRO A 173	19.329	1.383	2.737	1.00	38.41
AAAA								
ATOM	1248	CD	PRO A 173	18.647	2.586	3.248	1.00	38.12
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ATOM	1249	CA	PRO A 173	19.319	1.367	1.271	1.00	39.54
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ATOM	1250	CB	PRO A 173	18.853	2.778	0.923	1.00	38.97
AAAA								
ATOM	1251	CG	PRO A 173	17.898	3.076	2.029	1.00	38.41
AAAA								
ATOM	1252	C	PRO A 173	20.672	1.027	0.639	1.00	41.06
AAAA								
ATOM	1253	O	PRO A 173	20.751	0.205	-0.276	1.00	41.26
AAAA								
ATOM	1254	N	GLN A 174	21.734	1.659	1.127	1.00	42.31
AAAA								
ATOM	1255	CA	GLN A 174	23.063	1.401	0.591	1.00	43.56
AAAA								
ATOM	1256	CB	GLN A 174	24.118	2.219	1.343	1.00	45.08
AAAA								
ATOM	1257	CG	GLN A 174	24.197	3.672	0.906	1.00	47.91
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ATOM	1258	CD	GLN A 174	25.366	4.413	1.534	1.00	50.04
AAAA								
ATOM	1259	OE1	GLN A 174	25.665	5.552	1.164	1.00	50.92
AAAA								
ATOM	1260	NE2	GLN A 174	26.033	3.771	2.491	1.00	50.23
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ATOM	1261	C	GLN A 174	23.415	-0.076	0.667	1.00	43.25
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ATOM	1262	O	GLN A 174	23.955	-0.641	-0.280	1.00	42.73
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ATOM	1263	N	GLN A 175	23.098	-0.702	1.794	1.00	43.02
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ATOM	1264	CA	GLN A 175	23.398	-2.115	1.981	1.00	43.41
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ATOM	1265	CB	GLN A 175	23.206	-2.505	3.449	1.00	44.88
AAAA								
ATOM	1266	CG	GLN A 175	23.844	-1.544	4.444	1.00	47.91
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ATOM	1267	CD	GLN A 175	25.331	-1.344	4.211	1.00	49.82
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ATOM	1268	OE1	GLN A 175	25.747	-0.765	3.203	1.00	50.30
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ATOM	1269	NE2	GLN A 175	26.145	-1.826	5.148	1.00	51.04
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ATOM	1270	C	GLN A 175	22.521	-2.997	1.097	1.00	42.34
AAAA								
ATOM	1271	O	GLN A 175	22.996	-3.961	0.500	1.00	41.64
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ATOM	1272	N	ARG A 176	21.238	-2.659	1.016	1.00	41.73
AAAA								
ATOM	1273	CA	ARG A 176	20.285	-3.422	0.216	1.00	41.37
AAAA								
ATOM	1274	CB	ARG A 176	18.854	-2.912	0.469	1.00	42.69
AAAA								
ATOM	1275	CG	ARG A 176	17.767	-3.726	-0.232	1.00	44.32
AAAA								
ATOM	1276	CD	ARG A 176	16.338	-3.227	0.066	1.00	46.28
AAAA								
ATOM	1277	NE	ARG A 176	15.922	-2.116	-0.793	1.00	46.82
AAAA								
ATOM	1278	CZ	ARG A 176	16.043	-0.829	-0.479	1.00	47.07
AAAA								
ATOM	1279	NH1	ARG A 176	16.567	-0.471	0.686	1.00	47.74
AAAA								

ATOM	1280	NH2	ARG	A	176	15.645	0.102	-1.337	1.00	46.75
AAAA										
ATOM	1281	C	ARG	A	176	20.574	-3.358	-1.279	1.00	40.60
AAAA										
ATOM	1282	O	ARG	A	176	20.485	-4.366	-1.981	1.00	39.33
AAAA										
ATOM	1283	N	LEU	A	177	20.928	-2.171	-1.757	1.00	40.82
AAAA										
ATOM	1284	CA	LEU	A	177	21.182	-1.957	-3.177	1.00	41.69
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ATOM	1285	CB	LEU	A	177	20.635	-0.587	-3.580	1.00	41.42
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ATOM	1286	CG	LEU	A	177	19.152	-0.376	-3.262	1.00	41.85
AAAA										
ATOM	1287	CD1	LEU	A	177	18.756	1.059	-3.578	1.00	41.44
AAAA										
ATOM	1288	CD2	LEU	A	177	18.311	-1.358	-4.066	1.00	41.27
AAAA										
ATOM	1289	C	LEU	A	177	22.632	-2.080	-3.636	1.00	42.12
AAAA										
ATOM	1290	O	LEU	A	177	22.923	-1.918	-4.822	1.00	42.57
AAAA										
ATOM	1291	N	ALA	A	178	23.536	-2.374	-2.709	1.00	42.36
AAAA										
ATOM	1292	CA	ALA	A	178	24.951	-2.505	-3.047	1.00	41.77
AAAA										
ATOM	1293	CB	ALA	A	178	25.774	-2.711	-1.778	1.00	42.52
AAAA										
ATOM	1294	C	ALA	A	178	25.204	-3.649	-4.024	1.00	41.23
AAAA										
ATOM	1295	O	ALA	A	178	24.981	-4.818	-3.701	1.00	41.31
AAAA										
ATOM	1296	N	GLY	A	179	25.668	-3.299	-5.221	1.00	40.21
AAAA										
ATOM	1297	CA	GLY	A	179	25.960	-4.298	-6.232	1.00	37.93
AAAA										
ATOM	1298	C	GLY	A	179	24.747	-4.873	-6.938	1.00	36.85
AAAA										
ATOM	1299	O	GLY	A	179	24.873	-5.797	-7.744	1.00	36.55
AAAA										
ATOM	1300	N	ARG	A	180	23.566	-4.333	-6.654	1.00	35.52
AAAA										
ATOM	1301	CA	ARG	A	180	22.362	-4.844	-7.289	1.00	34.04
AAAA										
ATOM	1302	CB	ARG	A	180	21.114	-4.428	-6.504	1.00	31.99
AAAA										
ATOM	1303	CG	ARG	A	180	19.840	-5.038	-7.055	1.00	29.72
AAAA										
ATOM	1304	CD	ARG	A	180	18.608	-4.609	-6.268	1.00	27.51
AAAA										
ATOM	1305	NE	ARG	A	180	18.531	-5.233	-4.948	1.00	25.67
AAAA										
ATOM	1306	CZ	ARG	A	180	17.475	-5.139	-4.144	1.00	26.02
AAAA										
ATOM	1307	NH1	ARG	A	180	16.414	-4.441	-4.533	1.00	24.19
AAAA										
ATOM	1308	NH2	ARG	A	180	17.472	-5.749	-2.961	1.00	23.88
AAAA										
ATOM	1309	C	ARG	A	180	22.251	-4.353	-8.726	1.00	34.92
AAAA										
ATOM	1310	O	ARG	A	180	22.348	-3.157	-8.995	1.00	35.69
AAAA										
ATOM	1311	N	GLU	A	181	22.055	-5.290	-9.646	1.00	34.98
AAAA										
ATOM	1312	CA	GLU	A	181	21.917	-4.969	-11.059	1.00	35.58
AAAA										

ATOM	1313	CB	GLU A 181	23.188	-5.354	-11.822	1.00	37.16
AAAA								
ATOM	1314	CG	GLU A 181	24.411	-4.540	-11.436	1.00	40.11
AAAA								
ATOM	1315	CD	GLU A 181	25.666	-4.983	-12.169	1.00	42.11
AAAA								
ATOM	1316	OE1	GLU A 181	26.698	-4.284	-12.056	1.00	42.94
AAAA								
ATOM	1317	OE2	GLU A 181	25.623	-6.033	-12.848	1.00	43.38
AAAA								
ATOM	1318	C	GLU A 181	20.736	-5.745	-11.615	1.00	34.83
AAAA								
ATOM	1319	O	GLU A 181	20.148	-6.577	-10.919	1.00	35.81
AAAA								
ATOM	1320	N	GLY A 182	20.387	-5.469	-12.866	1.00	33.11
AAAA								
ATOM	1321	CA	GLY A 182	19.279	-6.166	-13.489	1.00	31.63
AAAA								
ATOM	1322	C	GLY A 182	17.989	-5.368	-13.523	1.00	30.40
AAAA								
ATOM	1323	O	GLY A 182	17.959	-4.210	-13.106	1.00	28.65
AAAA								
ATOM	1324	N	PRO A 183	16.898	-5.974	-14.015	1.00	29.29
AAAA								
ATOM	1325	CD	PRO A 183	16.829	-7.363	-14.498	1.00	30.43
AAAA								
ATOM	1326	CA	PRO A 183	15.589	-5.327	-14.109	1.00	29.46
AAAA								
ATOM	1327	CB	PRO A 183	14.675	-6.463	-14.560	1.00	29.59
AAAA								
ATOM	1328	CG	PRO A 183	15.597	-7.333	-15.362	1.00	30.17
AAAA								
ATOM	1329	C	PRO A 183	15.159	-4.734	-12.771	1.00	29.01
AAAA								
ATOM	1330	O	PRO A 183	15.455	-5.289	-11.708	1.00	27.87
AAAA								
ATOM	1331	N	VAL A 184	14.483	-3.591	-12.826	1.00	27.36
AAAA								
ATOM	1332	CA	VAL A 184	14.014	-2.942	-11.613	1.00	25.28
AAAA								
ATOM	1333	CB	VAL A 184	13.506	-1.512	-11.912	1.00	26.16
AAAA								
ATOM	1334	CG1	VAL A 184	12.865	-0.901	-10.673	1.00	25.72
AAAA								
ATOM	1335	CG2	VAL A 184	14.670	-0.648	-12.374	1.00	26.35
AAAA								
ATOM	1336	C	VAL A 184	12.896	-3.799	-11.032	1.00	23.68
AAAA								
ATOM	1337	O	VAL A 184	11.971	-4.195	-11.735	1.00	21.69
AAAA								
ATOM	1338	N	ARG A 185	13.003	-4.102	-9.744	1.00	23.12
AAAA								
ATOM	1339	CA	ARG A 185	12.015	-4.931	-9.065	1.00	22.35
AAAA								
ATOM	1340	CB	ARG A 185	12.687	-5.649	-7.897	1.00	23.23
AAAA								
ATOM	1341	CG	ARG A 185	13.910	-6.440	-8.323	1.00	25.75
AAAA								
ATOM	1342	CD	ARG A 185	14.729	-6.847	-7.120	1.00	27.07
AAAA								
ATOM	1343	NE	ARG A 185	15.976	-7.502	-7.495	1.00	28.67
AAAA								
ATOM	1344	CZ	ARG A 185	16.784	-8.093	-6.623	1.00	29.19
AAAA								
ATOM	1345	NH1	ARG A 185	16.462	-8.100	-5.339	1.00	26.72
AAAA								

ATOM	1346	NH2	ARG A 185	17.903	-8.679	-7.032	1.00	31.00
AAAA								
ATOM	1347	C	ARG A 185	10.860	-4.066	-8.574	1.00	21.55
AAAA								
ATOM	1348	O	ARG A 185	11.033	-3.228	-7.693	1.00	21.13
AAAA								
ATOM	1349	N	VAL A 186	9.687	-4.263	-9.166	1.00	21.59
AAAA								
ATOM	1350	CA	VAL A 186	8.515	-3.480	-8.805	1.00	21.51
AAAA								
ATOM	1351	CB	VAL A 186	7.745	-3.005	-10.064	1.00	21.61
AAAA								
ATOM	1352	CG1	VAL A 186	6.574	-2.124	-9.656	1.00	21.27
AAAA								
ATOM	1353	CG2	VAL A 186	8.689	-2.252	-11.001	1.00	22.25
AAAA								
ATOM	1354	C	VAL A 186	7.563	-4.294	-7.942	1.00	20.09
AAAA								
ATOM	1355	O	VAL A 186	7.064	-5.330	-8.361	1.00	20.16
AAAA								
ATOM	1356	N	LEU A 187	7.325	-3.807	-6.735	1.00	20.75
AAAA								
ATOM	1357	CA	LEU A 187	6.421	-4.462	-5.801	1.00	21.10
AAAA								
ATOM	1358	CB	LEU A 187	6.979	-4.363	-4.379	1.00	22.77
AAAA								
ATOM	1359	CG	LEU A 187	6.492	-5.359	-3.316	1.00	24.90
AAAA								
ATOM	1360	CD1	LEU A 187	6.763	-4.768	-1.932	1.00	23.74
AAAA								
ATOM	1361	CD2	LEU A 187	5.027	-5.651	-3.487	1.00	27.67
AAAA								
ATOM	1362	C	LEU A 187	5.104	-3.691	-5.871	1.00	21.37
AAAA								
ATOM	1363	O	LEU A 187	5.078	-2.491	-5.585	1.00	21.09
AAAA								
ATOM	1364	N	VAL A 188	4.034	-4.377	-6.262	1.00	21.43
AAAA								
ATOM	1365	CA	VAL A 188	2.706	-3.774	-6.355	1.00	22.58
AAAA								
ATOM	1366	CB	VAL A 188	1.988	-4.190	-7.657	1.00	22.95
AAAA								
ATOM	1367	CG1	VAL A 188	0.643	-3.488	-7.765	1.00	22.98
AAAA								
ATOM	1368	CG2	VAL A 188	2.853	-3.842	-8.855	1.00	23.03
AAAA								
ATOM	1369	C	VAL A 188	1.891	-4.267	-5.161	1.00	22.98
AAAA								
ATOM	1370	O	VAL A 188	1.603	-5.456	-5.051	1.00	22.38
AAAA								
ATOM	1371	N	VAL A 189	1.534	-3.349	-4.267	1.00	23.91
AAAA								
ATOM	1372	CA	VAL A 189	0.779	-3.706	-3.070	1.00	25.11
AAAA								
ATOM	1373	CB	VAL A 189	1.523	-3.237	-1.800	1.00	25.30
AAAA								
ATOM	1374	CG1	VAL A 189	0.740	-3.635	-0.549	1.00	23.23
AAAA								
ATOM	1375	CG2	VAL A 189	2.915	-3.828	-1.773	1.00	22.20
AAAA								
ATOM	1376	C	VAL A 189	-0.619	-3.096	-3.080	1.00	26.20
AAAA								
ATOM	1377	O	VAL A 189	-0.770	-1.879	-3.186	1.00	26.94
AAAA								
ATOM	1378	N	GLY A 190	-1.629	-3.955	-2.975	1.00	27.50
AAAA								

ATOM	1379	CA	GLY A 190	-3.007	-3.505	-2.966	1.00	30.27
AAAA								
ATOM	1380	C	GLY A 190	-3.720	-3.736	-1.641	1.00	32.15
AAAA								
ATOM	1381	O	GLY A 190	-4.896	-3.403	-1.499	1.00	32.00
AAAA								
ATOM	1382	N	GLY A 191	-3.016	-4.299	-0.664	1.00	32.97
AAAA								
ATOM	1383	CA	GLY A 191	-3.640	-4.550	0.624	1.00	34.29
AAAA								
ATOM	1384	C	GLY A 191	-4.507	-5.794	0.607	1.00	34.92
AAAA								
ATOM	1385	O	GLY A 191	-4.741	-6.388	-0.444	1.00	34.34
AAAA								
ATOM	1386	N	SER A 192	-4.996	-6.183	1.778	1.00	36.47
AAAA								
ATOM	1387	CA	SER A 192	-5.827	-7.377	1.910	1.00	38.39
AAAA								
ATOM	1388	CB	SER A 192	-6.389	-7.460	3.335	1.00	39.07
AAAA								
ATOM	1389	OG	SER A 192	-7.124	-6.291	3.658	1.00	41.25
AAAA								
ATOM	1390	C	SER A 192	-6.974	-7.472	0.903	1.00	38.69
AAAA								
ATOM	1391	O	SER A 192	-7.293	-8.557	0.410	1.00	38.58
AAAA								
ATOM	1392	N	GLN A 193	-7.599	-6.344	0.595	1.00	38.60
AAAA								
ATOM	1393	CA	GLN A 193	-8.715	-6.367	-0.339	1.00	39.91
AAAA								
ATOM	1394	CB	GLN A 193	-9.787	-5.367	0.110	1.00	41.97
AAAA								
ATOM	1395	CG	GLN A 193	-10.354	-5.679	1.497	1.00	43.94
AAAA								
ATOM	1396	CD	GLN A 193	-10.790	-7.135	1.640	1.00	45.71
AAAA								
ATOM	1397	OE1	GLN A 193	-11.677	-7.607	0.922	1.00	46.93
AAAA								
ATOM	1398	NE2	GLN A 193	-10.162	-7.853	2.567	1.00	45.80
AAAA								
ATOM	1399	C	GLN A 193	-8.298	-6.098	-1.781	1.00	39.31
AAAA								
ATOM	1400	O	GLN A 193	-9.076	-6.320	-2.708	1.00	39.52
AAAA								
ATOM	1401	N	GLY A 194	-7.064	-5.642	-1.961	1.00	38.40
AAAA								
ATOM	1402	CA	GLY A 194	-6.560	-5.358	-3.291	1.00	38.11
AAAA								
ATOM	1403	C	GLY A 194	-6.961	-3.987	-3.797	1.00	37.62
AAAA								
ATOM	1404	O	GLY A 194	-7.904	-3.382	-3.291	1.00	37.80
AAAA								
ATOM	1405	N	ALA A 195	-6.228	-3.489	-4.787	1.00	36.62
AAAA								
ATOM	1406	CA	ALA A 195	-6.513	-2.191	-5.387	1.00	36.35
AAAA								
ATOM	1407	CB	ALA A 195	-5.290	-1.291	-5.305	1.00	35.75
AAAA								
ATOM	1408	C	ALA A 195	-6.898	-2.437	-6.842	1.00	36.61
AAAA								
ATOM	1409	O	ALA A 195	-6.038	-2.519	-7.717	1.00	35.93
AAAA								
ATOM	1410	N	ARG A 196	-8.198	-2.566	-7.080	1.00	36.94
AAAA								
ATOM	1411	CA	ARG A 196	-8.741	-2.828	-8.412	1.00	38.03
AAAA								

ATOM	1412	CB	ARG A 196	-10.229	-2.466	-8.450	1.00	40.33
AAAA								
ATOM	1413	CG	ARG A 196	-10.526	-0.968	-8.375	1.00	44.08
AAAA								
ATOM	1414	CD	ARG A 196	-9.935	-0.306	-7.129	1.00	46.46
AAAA								
ATOM	1415	NE	ARG A 196	-10.381	-0.949	-5.894	1.00	48.33
AAAA								
ATOM	1416	CZ	ARG A 196	-10.199	-0.439	-4.682	1.00	48.85
AAAA								
ATOM	1417	NH1	ARG A 196	-9.581	0.725	-4.538	1.00	49.51
AAAA								
ATOM	1418	NH2	ARG A 196	-10.636	-1.093	-3.615	1.00	49.95
AAAA								
ATOM	1419	C	ARG A 196	-8.023	-2.120	-9.558	1.00	37.11
AAAA								
ATOM	1420	O	ARG A 196	-7.729	-2.736	-10.583	1.00	36.96
AAAA								
ATOM	1421	N	ILE A 197	-7.739	-0.834	-9.392	1.00	35.89
AAAA								
ATOM	1422	CA	ILE A 197	-7.071	-0.091	-10.448	1.00	35.67
AAAA								
ATOM	1423	CB	ILE A 197	-7.049	1.427	-10.161	1.00	36.70
AAAA								
ATOM	1424	CG2	ILE A 197	-6.221	1.726	-8.918	1.00	36.91
AAAA								
ATOM	1425	CG1	ILE A 197	-6.485	2.162	-11.381	1.00	36.95
AAAA								
ATOM	1426	CD1	ILE A 197	-6.529	3.661	-11.272	1.00	38.71
AAAA								
ATOM	1427	C	ILE A 197	-5.644	-0.580	-10.694	1.00	34.73
AAAA								
ATOM	1428	O	ILE A 197	-5.178	-0.575	-11.833	1.00	33.53
AAAA								
ATOM	1429	N	LEU A 198	-4.948	-0.992	-9.638	1.00	32.35
AAAA								
ATOM	1430	CA	LEU A 198	-3.588	-1.494	-9.813	1.00	31.48
AAAA								
ATOM	1431	CB	LEU A 198	-2.862	-1.633	-8.467	1.00	31.03
AAAA								
ATOM	1432	CG	LEU A 198	-2.548	-0.342	-7.704	1.00	32.00
AAAA								
ATOM	1433	CD1	LEU A 198	-1.773	-0.688	-6.442	1.00	30.82
AAAA								
ATOM	1434	CD2	LEU A 198	-1.734	0.607	-8.566	1.00	30.86
AAAA								
ATOM	1435	C	LEU A 198	-3.668	-2.850	-10.501	1.00	29.72
AAAA								
ATOM	1436	O	LEU A 198	-2.837	-3.173	-11.344	1.00	29.46
AAAA								
ATOM	1437	N	ASN A 199	-4.678	-3.639	-10.150	1.00	28.63
AAAA								
ATOM	1438	CA	ASN A 199	-4.848	-4.952	-10.758	1.00	28.66
AAAA								
ATOM	1439	CB	ASN A 199	-5.975	-5.724	-10.066	1.00	27.71
AAAA								
ATOM	1440	CG	ASN A 199	-5.641	-6.069	-8.632	1.00	26.12
AAAA								
ATOM	1441	OD1	ASN A 199	-4.501	-5.904	-8.200	1.00	24.15
AAAA								
ATOM	1442	ND2	ASN A 199	-6.631	-6.553	-7.884	1.00	24.90
AAAA								
ATOM	1443	C	ASN A 199	-5.144	-4.841	-12.248	1.00	29.87
AAAA								
ATOM	1444	O	ASN A 199	-4.834	-5.747	-13.024	1.00	30.26
AAAA								

ATOM	1445	N	GLN A 200	-5.746	-3.725	-12.644	1.00	31.15
AAAA								
ATOM	1446	CA	GLN A 200	-6.085	-3.498	-14.044	1.00	33.06
AAAA								
ATOM	1447	CB	GLN A 200	-7.396	-2.706	-14.145	1.00	34.24
AAAA								
ATOM	1448	CG	GLN A 200	-8.590	-3.368	-13.471	1.00	38.64
AAAA								
ATOM	1449	CD	GLN A 200	-8.923	-4.734	-14.050	1.00	41.05
AAAA								
ATOM	1450	OE1	GLN A 200	-9.131	-4.879	-15.256	1.00	43.10
AAAA								
ATOM	1451	NE2	GLN A 200	-8.983	-5.745	-13.185	1.00	43.12
AAAA								
ATOM	1452	C	GLN A 200	-4.989	-2.753	-14.812	1.00	32.52
AAAA								
ATOM	1453	O	GLN A 200	-4.809	-2.970	-16.008	1.00	34.23
AAAA								
ATOM	1454	N	THR A 201	-4.247	-1.895	-14.120	1.00	31.87
AAAA								
ATOM	1455	CA	THR A 201	-3.207	-1.092	-14.756	1.00	31.72
AAAA								
ATOM	1456	CB	THR A 201	-3.046	0.245	-13.999	1.00	32.41
AAAA								
ATOM	1457	OG1	THR A 201	-4.307	0.931	-13.976	1.00	32.19
AAAA								
ATOM	1458	CG2	THR A 201	-2.003	1.131	-14.668	1.00	32.29
AAAA								
ATOM	1459	C	THR A 201	-1.817	-1.728	-14.925	1.00	32.02
AAAA								
ATOM	1460	O	THR A 201	-1.206	-1.626	-15.991	1.00	31.47
AAAA								
ATOM	1461	N	MET A 202	-1.320	-2.394	-13.892	1.00	30.61
AAAA								
ATOM	1462	CA	MET A 202	0.019	-2.975	-13.963	1.00	30.10
AAAA								
ATOM	1463	CB	MET A 202	0.430	-3.507	-12.592	1.00	29.71
AAAA								
ATOM	1464	CG	MET A 202	0.564	-2.406	-11.548	1.00	28.99
AAAA								
ATOM	1465	SD	MET A 202	1.518	-0.961	-12.098	1.00	31.46
AAAA								
ATOM	1466	CE	MET A 202	3.184	-1.633	-12.184	1.00	29.20
AAAA								
ATOM	1467	C	MET A 202	0.286	-4.022	-15.042	1.00	29.48
AAAA								
ATOM	1468	O	MET A 202	1.389	-4.088	-15.568	1.00	29.15
AAAA								
ATOM	1469	N	PRO A 203	-0.703	-4.863	-15.379	1.00	30.34
AAAA								
ATOM	1470	CD	PRO A 203	-1.957	-5.186	-14.677	1.00	30.05
AAAA								
ATOM	1471	CA	PRO A 203	-0.415	-5.849	-16.426	1.00	31.11
AAAA								
ATOM	1472	CB	PRO A 203	-1.703	-6.654	-16.500	1.00	31.89
AAAA								
ATOM	1473	CG	PRO A 203	-2.188	-6.623	-15.072	1.00	31.09
AAAA								
ATOM	1474	C	PRO A 203	-0.103	-5.139	-17.746	1.00	33.02
AAAA								
ATOM	1475	O	PRO A 203	0.800	-5.530	-18.490	1.00	33.16
AAAA								
ATOM	1476	N	GLN A 204	-0.855	-4.081	-18.020	1.00	33.88
AAAA								
ATOM	1477	CA	GLN A 204	-0.666	-3.314	-19.242	1.00	34.99
AAAA								

ATOM	1478	CB	GLN A 204	-1.836	-2.34	-19.431	1.00	37.12
AAAA								
ATOM	1479	CG	GLN A 204	-3.177	-3.067	-19.538	1.00	40.86
AAAA								
ATOM	1480	CD	GLN A 204	-4.354	-2.121	-19.700	1.00	43.77
AAAA								
ATOM	1481	OE1	GLN A 204	-4.406	-1.330	-20.647	1.00	45.55
AAAA								
ATOM	1482	NE2	GLN A 204	-5.310	-2.198	-18.776	1.00	44.11
AAAA								
ATOM	1483	C	GLN A 204	0.659	-2.573	-19.190	1.00	33.42
AAAA								
ATOM	1484	O	GLN A 204	1.331	-2.431	-20.206	1.00	34.40
AAAA								
ATOM	1485	N	VAL A 205	1.045	-2.114	-18.002	1.00	32.44
AAAA								
ATOM	1486	CA	VAL A 205	2.313	-1.417	-17.836	1.00	30.42
AAAA								
ATOM	1487	CB	VAL A 205	2.466	-0.834	-16.408	1.00	31.72
AAAA								
ATOM	1488	CG1	VAL A 205	3.907	-0.406	-16.169	1.00	28.58
AAAA								
ATOM	1489	CG2	VAL A 205	1.544	0.356	-16.231	1.00	29.91
AAAA								
ATOM	1490	C	VAL A 205	3.446	-2.407	-18.086	1.00	30.65
AAAA								
ATOM	1491	O	VAL A 205	4.473	-2.062	-18.686	1.00	29.65
AAAA								
ATOM	1492	N	ALA A 206	3.255	-3.638	-17.616	1.00	29.08
AAAA								
ATOM	1493	CA	ALA A 206	4.253	-4.688	-17.796	1.00	30.43
AAAA								
ATOM	1494	CB	ALA A 206	3.763	-6.002	-17.169	1.00	27.77
AAAA								
ATOM	1495	C	ALA A 206	4.519	-4.886	-19.288	1.00	30.65
AAAA								
ATOM	1496	O	ALA A 206	5.668	-5.040	-19.709	1.00	30.70
AAAA								
ATOM	1497	N	ALA A 207	3.450	-4.879	-20.080	1.00	31.56
AAAA								
ATOM	1498	CA	ALA A 207	3.565	-5.053	-21.527	1.00	32.70
AAAA								
ATOM	1499	CB	ALA A 207	2.188	-4.997	-22.167	1.00	32.49
AAAA								
ATOM	1500	C	ALA A 207	4.470	-3.990	-22.145	1.00	32.72
AAAA								
ATOM	1501	O	ALA A 207	5.295	-4.284	-23.007	1.00	33.64
AAAA								
ATOM	1502	N	LYS A 208	4.321	-2.754	-21.692	1.00	33.07
AAAA								
ATOM	1503	CA	LYS A 208	5.112	-1.651	-22.216	1.00	33.20
AAAA								
ATOM	1504	CB	LYS A 208	4.477	-0.313	-21.814	1.00	35.14
AAAA								
ATOM	1505	CG	LYS A 208	3.199	0.044	-22.578	1.00	38.07
AAAA								
ATOM	1506	CD	LYS A 208	2.166	-1.062	-22.482	1.00	40.27
AAAA								
ATOM	1507	CE	LYS A 208	0.892	-0.731	-23.233	1.00	41.02
AAAA								
ATOM	1508	NZ	LYS A 208	-0.076	-1.857	-23.126	1.00	42.41
AAAA								
ATOM	1509	C	LYS A 208	6.571	-1.668	-21.779	1.00	32.58
AAAA								
ATOM	1510	O	LYS A 208	7.456	-1.274	-22.544	1.00	31.82
AAAA								

ATOM	1511	N	LEU A 209	6.829	-2.121	-20.556	1.00	30.72
AAAA								
ATOM	1512	CA	LEU A 209	8.193	-2.143	-20.042	1.00	30.48
AAAA								
ATOM	1513	CB	LEU A 209	8.191	-1.848	-18.535	1.00	29.34
AAAA								
ATOM	1514	CG	LEU A 209	7.596	-0.498	-18.107	1.00	31.02
AAAA								
ATOM	1515	CD1	LEU A 209	7.779	-0.318	-16.605	1.00	29.42
AAAA								
ATOM	1516	CD2	LEU A 209	8.273	0.641	-18.859	1.00	31.39
AAAA								
ATOM	1517	C	LEU A 209	8.970	-3.432	-20.315	1.00	29.73
AAAA								
ATOM	1518	O	LEU A 209	10.191	-3.455	-20.174	1.00	31.33
AAAA								
ATOM	1519	N	GLY A 210	8.269	-4.494	-20.698	1.00	29.76
AAAA								
ATOM	1520	CA	GLY A 210	8.924	-5.762	-20.986	1.00	29.99
AAAA								
ATOM	1521	C	GLY A 210	10.007	-6.188	-20.003	1.00	30.99
AAAA								
ATOM	1522	O	GLY A 210	9.788	-6.183	-18.789	1.00	30.80
AAAA								
ATOM	1523	N	ASP A 211	11.181	-6.536	-20.535	1.00	30.05
AAAA								
ATOM	1524	CA	ASP A 211	12.332	-6.999	-19.749	1.00	29.42
AAAA								
ATOM	1525	CB	ASP A 211	13.466	-7.479	-20.676	1.00	30.83
AAAA								
ATOM	1526	CG	ASP A 211	13.119	-8.735	-21.449	1.00	32.09
AAAA								
ATOM	1527	OD1	ASP A 211	13.977	-9.193	-22.235	1.00	34.13
AAAA								
ATOM	1528	OD2	ASP A 211	12.005	-9.269	-21.283	1.00	32.72
AAAA								
ATOM	1529	C	ASP A 211	12.960	-6.011	-18.776	1.00	29.03
AAAA								
ATOM	1530	O	ASP A 211	13.781	-6.417	-17.945	1.00	27.69
AAAA								
ATOM	1531	N	SER A 212	12.613	-4.730	-18.876	1.00	28.54
AAAA								
ATOM	1532	CA	SER A 212	13.204	-3.719	-18.002	1.00	27.61
AAAA								
ATOM	1533	CB	SER A 212	12.927	-2.308	-18.538	1.00	28.62
AAAA								
ATOM	1534	OG	SER A 212	11.546	-1.990	-18.498	1.00	30.84
AAAA								
ATOM	1535	C	SER A 212	12.759	-3.805	-16.542	1.00	26.31
AAAA								
ATOM	1536	O	SER A 212	13.395	-3.219	-15.666	1.00	25.39
AAAA								
ATOM	1537	N	VAL A 213	11.675	-4.528	-16.284	1.00	25.65
AAAA								
ATOM	1538	CA	VAL A 213	11.187	-4.671	-14.914	1.00	24.52
AAAA								
ATOM	1539	CB	VAL A 213	9.967	-3.747	-14.621	1.00	25.58
AAAA								
ATOM	1540	CG1	VAL A 213	10.296	-2.298	-14.953	1.00	26.31
AAAA								
ATOM	1541	CG2	VAL A 213	8.758	-4.225	-15.394	1.00	25.15
AAAA								
ATOM	1542	C	VAL A 213	10.751	-6.095	-14.607	1.00	23.77
AAAA								
ATOM	1543	O	VAL A 213	10.427	-6.874	-15.506	1.00	23.79
AAAA								

ATOM	1544	N	THR	A	214	10.770	-6.432	-13.323	1.00	23.49
AAAA										
ATOM	1545	CA	THR	A	214	10.326	-7.735	-12.861	1.00	21.50
AAAA										
ATOM	1546	CB	THR	A	214	11.499	-8.600	-12.325	1.00	21.99
AAAA										
ATOM	1547	OG1	THR	A	214	10.987	-9.870	-11.909	1.00	23.56
AAAA										
ATOM	1548	CG2	THR	A	214	12.220	-7.921	-11.174	1.00	20.60
AAAA										
ATOM	1549	C	THR	A	214	9.342	-7.362	-11.760	1.00	21.46
AAAA										
ATOM	1550	O	THR	A	214	9.657	-6.567	-10.880	1.00	21.12
AAAA										
ATOM	1551	N	ILE	A	215	8.150	-7.938	-11.827	1.00	21.73
AAAA										
ATOM	1552	CA	ILE	A	215	7.083	-7.601	-10.894	1.00	22.01
AAAA										
ATOM	1553	CB	ILE	A	215	5.831	-7.139	-11.688	1.00	22.41
AAAA										
ATOM	1554	CG2	ILE	A	215	4.707	-6.738	-10.734	1.00	22.94
AAAA										
ATOM	1555	CG1	ILE	A	215	6.198	-5.964	-12.599	1.00	22.71
AAAA										
ATOM	1556	CD1	ILE	A	215	5.078	-5.560	-13.545	1.00	21.71
AAAA										
ATOM	1557	C	ILE	A	215	6.617	-8.685	-9.929	1.00	21.67
AAAA										
ATOM	1558	O	ILE	A	215	6.600	-9.868	-10.257	1.00	20.14
AAAA										
ATOM	1559	N	TRP	A	216	6.248	-8.247	-8.728	1.00	21.03
AAAA										
ATOM	1560	CA	TRP	A	216	5.677	-9.121	-7.708	1.00	21.08
AAAA										
ATOM	1561	CB	TRP	A	216	6.541	-9.186	-6.455	1.00	21.14
AAAA										
ATOM	1562	CG	TRP	A	216	5.941	-10.063	-5.370	1.00	21.49
AAAA										
ATOM	1563	CD2	TRP	A	216	6.624	-10.588	-4.226	1.00	21.97
AAAA										
ATOM	1564	CE2	TRP	A	216	5.674	-11.309	-3.461	1.00	22.67
AAAA										
ATOM	1565	CE3	TRP	A	216	7.947	-10.521	-3.773	1.00	22.25
AAAA										
ATOM	1566	CD1	TRP	A	216	4.639	-10.478	-5.262	1.00	21.72
AAAA										
ATOM	1567	NE1	TRP	A	216	4.472	-11.231	-4.112	1.00	22.34
AAAA										
ATOM	1568	CZ2	TRP	A	216	6.011	-11.955	-2.265	1.00	24.81
AAAA										
ATOM	1569	CZ3	TRP	A	216	8.283	-11.166	-2.582	1.00	23.37
AAAA										
ATOM	1570	CH2	TRP	A	216	7.316	-11.872	-1.843	1.00	23.19
AAAA										
ATOM	1571	C	TRP	A	216	4.401	-8.352	-7.396	1.00	21.75
AAAA										
ATOM	1572	O	TRP	A	216	4.442	-7.330	-6.719	1.00	22.71
AAAA										
ATOM	1573	N	HIS	A	217	3.280	-8.844	-7.909	1.00	23.00
AAAA										
ATOM	1574	CA	HIS	A	217	1.987	-8.185	-7.751	1.00	24.05
AAAA										
ATOM	1575	CB	HIS	A	217	1.301	-8.167	-9.127	1.00	25.31
AAAA										
ATOM	1576	CG	HIS	A	217	0.075	-7.312	-9.201	1.00	27.29
AAAA										

ATOM	1577	CD2	HIS	A	217	-1.008	-7.226	-8.391	1.00	27.56
AAAA										
ATOM	1578	ND1	HIS	A	217	-0.146	-6.424	-10.233	1.00	28.22
AAAA										
ATOM	1579	CE1	HIS	A	217	-1.311	-5.828	-10.057	1.00	28.76
AAAA										
ATOM	1580	NE2	HIS	A	217	-1.856	-6.296	-8.947	1.00	27.39
AAAA										
ATOM	1581	C	HIS	A	217	1.095	-8.880	-6.714	1.00	22.49
AAAA										
ATOM	1582	O	HIS	A	217	0.785	-10.059	-6.851	1.00	24.60
AAAA										
ATOM	1583	N	GLN	A	218	0.696	-8.144	-5.679	1.00	24.33
AAAA										
ATOM	1584	CA	GLN	A	218	-0.184	-8.676	-4.629	1.00	24.84
AAAA										
ATOM	1585	CB	GLN	A	218	0.271	-8.181	-3.250	1.00	25.16
AAAA										
ATOM	1586	CG	GLN	A	218	-0.572	-8.709	-2.084	1.00	26.40
AAAA										
ATOM	1587	CD	GLN	A	218	-1.629	-7.722	-1.608	1.00	27.63
AAAA										
ATOM	1588	OE1	GLN	A	218	-2.762	-8.107	-1.297	1.00	29.31
AAAA										
ATOM	1589	NE2	GLN	A	218	-1.260	-6.455	-1.525	1.00	24.88
AAAA										
ATOM	1590	C	GLN	A	218	-1.573	-8.134	-4.983	1.00	24.83
AAAA										
ATOM	1591	O	GLN	A	218	-1.859	-6.960	-4.767	1.00	24.21
AAAA										
ATOM	1592	N	SER	A	219	-2.413	-9.008	-5.531	1.00	25.76
AAAA										
ATOM	1593	CA	SER	A	219	-3.745	-8.658	-6.022	1.00	27.99
AAAA										
ATOM	1594	CB	SER	A	219	-4.189	-9.704	-7.035	1.00	28.46
AAAA										
ATOM	1595	OG	SER	A	219	-4.394	-10.949	-6.387	1.00	29.92
AAAA										
ATOM	1596	C	SER	A	219	-4.887	-8.470	-5.034	1.00	29.52
AAAA										
ATOM	1597	O	SER	A	219	-5.842	-7.745	-5.321	1.00	29.47
AAAA										
ATOM	1598	N	GLY	A	220	-4.806	-9.135	-3.890	1.00	30.25
AAAA										
ATOM	1599	CA	GLY	A	220	-5.874	-9.031	-2.919	1.00	31.33
AAAA										
ATOM	1600	C	GLY	A	220	-6.696	-10.302	-2.952	1.00	32.52
AAAA										
ATOM	1601	O	GLY	A	220	-6.554	-11.126	-3.862	1.00	31.13
AAAA										
ATOM	1602	N	LYS	A	221	-7.563	-10.452	-1.956	1.00	33.12
AAAA										
ATOM	1603	CA	LYS	A	221	-8.423	-11.619	-1.815	1.00	34.69
AAAA										
ATOM	1604	CB	LYS	A	221	-9.340	-11.421	-0.601	1.00	35.93
AAAA										
ATOM	1605	CG	LYS	A	221	-10.257	-12.593	-0.285	1.00	38.70
AAAA										
ATOM	1606	CD	LYS	A	221	-11.079	-12.292	0.966	1.00	40.53
AAAA										
ATOM	1607	CE	LYS	A	221	-11.955	-13.465	1.368	1.00	41.74
AAAA										
ATOM	1608	NZ	LYS	A	221	-12.724	-13.160	2.614	1.00	43.70
AAAA										
ATOM	1609	C	LYS	A	221	-9.269	-11.932	-3.046	1.00	34.22
AAAA										

ATOM	1610	O	LYS A 221	-9.979	-11.078	-3.561	1.00	34.62
AAAA								
ATOM	1611	N	GLY A 222	-9.189	-13.180	-3.500	1.00	34.61
AAAA								
ATOM	1612	CA	GLY A 222	-9.956	-13.622	-4.651	1.00	34.89
AAAA								
ATOM	1613	C	GLY A 222	-9.598	-13.027	-6.000	1.00	35.07
AAAA								
ATOM	1614	O	GLY A 222	-10.325	-13.231	-6.974	1.00	35.62
AAAA								
ATOM	1615	N	SER A 223	-8.482	-12.309	-6.083	1.00	35.16
AAAA								
ATOM	1616	CA	SER A 223	-8.083	-11.691	-7.349	1.00	35.04
AAAA								
ATOM	1617	CB	SER A 223	-7.959	-10.175	-7.173	1.00	35.18
AAAA								
ATOM	1618	OG	SER A 223	-9.222	-9.593	-6.913	1.00	36.67
AAAA								
ATOM	1619	C	SER A 223	-6.783	-12.226	-7.949	1.00	34.73
AAAA								
ATOM	1620	O	SER A 223	-6.343	-11.758	-9.002	1.00	33.65
AAAA								
ATOM	1621	N	GLN A 224	-6.176	-13.202	-7.285	1.00	34.35
AAAA								
ATOM	1622	CA	GLN A 224	-4.922	-13.779	-7.753	1.00	34.39
AAAA								
ATOM	1623	CB	GLN A 224	-4.493	-14.910	-6.810	1.00	35.22
AAAA								
ATOM	1624	CG	GLN A 224	-3.016	-15.304	-6.895	1.00	34.71
AAAA								
ATOM	1625	CD	GLN A 224	-2.656	-15.983	-8.199	1.00	35.46
AAAA								
ATOM	1626	OE1	GLN A 224	-3.386	-16.844	-8.680	1.00	35.81
AAAA								
ATOM	1627	NE2	GLN A 224	-1.512	-15.610	-8.772	1.00	36.28
AAAA								
ATOM	1628	C	GLN A 224	-5.033	-14.301	-9.188	1.00	35.00
AAAA								
ATOM	1629	O	GLN A 224	-4.256	-13.915	-10.062	1.00	33.23
AAAA								
ATOM	1630	N	GLN A 225	-6.018	-15.160	-9.432	1.00	35.33
AAAA								
ATOM	1631	CA	GLN A 225	-6.208	-15.747	-10.752	1.00	36.18
AAAA								
ATOM	1632	CB	GLN A 225	-7.251	-16.871	-10.675	1.00	38.35
AAAA								
ATOM	1633	CG	GLN A 225	-6.692	-18.174	-10.103	1.00	40.67
AAAA								
ATOM	1634	CD	GLN A 225	-7.732	-19.274	-9.983	1.00	43.02
AAAA								
ATOM	1635	OE1	GLN A 225	-8.418	-19.609	-10.952	1.00	44.03
AAAA								
ATOM	1636	NE2	GLN A 225	-7.846	-19.850	-8.789	1.00	43.72
AAAA								
ATOM	1637	C	GLN A 225	-6.554	-14.790	-11.893	1.00	35.81
AAAA								
ATOM	1638	O	GLN A 225	-6.113	-15.001	-13.023	1.00	35.91
AAAA								
ATOM	1639	N	SER A 226	-7.325	-13.741	-11.619	1.00	34.00
AAAA								
ATOM	1640	CA	SER A 226	-7.689	-12.804	-12.683	1.00	34.21
AAAA								
ATOM	1641	CB	SER A 226	-8.865	-11.920	-12.251	1.00	34.12
AAAA								
ATOM	1642	OG	SER A 226	-8.460	-10.954	-11.300	1.00	36.16
AAAA								

ATOM	1643	C	SER A 226	-6.502	-11.926	-13.090	1.00	32.76
AAAA								
ATOM	1644	O	SER A 226	-6.343	-11.580	-14.260	1.00	32.64
AAAA								
ATOM	1645	N	VAL A 227	-5.669	-11.566	-12.121	1.00	31.82
AAAA								
ATOM	1646	CA	VAL A 227	-4.498	-10.737	-12.400	1.00	30.69
AAAA								
ATOM	1647	CB	VAL A 227	-3.942	-10.117	-11.102	1.00	29.27
AAAA								
ATOM	1648	CG1	VAL A 227	-2.619	-9.413	-11.370	1.00	29.04
AAAA								
ATOM	1649	CG2	VAL A 227	-4.951	-9.117	-10.546	1.00	29.09
AAAA								
ATOM	1650	C	VAL A 227	-3.418	-11.577	-13.082	1.00	30.43
AAAA								
ATOM	1651	O	VAL A 227	-2.716	-11.103	-13.973	1.00	29.50
AAAA								
ATOM	1652	N	GLU A 228	-3.297	-12.824	-12.644	1.00	30.82
AAAA								
ATOM	1653	CA	GLU A 228	-2.333	-13.766	-13.198	1.00	31.98
AAAA								
ATOM	1654	CB	GLU A 228	-2.456	-15.108	-12.464	1.00	31.67
AAAA								
ATOM	1655	CG	GLU A 228	-1.607	-16.231	-13.020	1.00	33.79
AAAA								
ATOM	1656	CD	GLU A 228	-0.159	-16.176	-12.559	1.00	34.94
AAAA								
ATOM	1657	OE1	GLU A 228	0.631	-17.041	-12.998	1.00	36.44
AAAA								
ATOM	1658	OE2	GLU A 228	0.190	-15.280	-11.761	1.00	35.02
AAAA								
ATOM	1659	C	GLU A 228	-2.658	-13.944	-14.685	1.00	32.05
AAAA								
ATOM	1660	O	GLU A 228	-1.770	-13.942	-15.539	1.00	32.57
AAAA								
ATOM	1661	N	GLN A 229	-3.945	-14.082	-14.981	1.00	31.94
AAAA								
ATOM	1662	CA	GLN A 229	-4.405	-14.255	-16.351	1.00	32.98
AAAA								
ATOM	1663	CB	GLN A 229	-5.896	-14.616	-16.359	1.00	35.59
AAAA								
ATOM	1664	CG	GLN A 229	-6.375	-15.211	-17.674	1.00	39.28
AAAA								
ATOM	1665	CD	GLN A 229	-7.825	-15.665	-17.623	1.00	41.31
AAAA								
ATOM	1666	OE1	GLN A 229	-8.317	-16.307	-18.553	1.00	43.67
AAAA								
ATOM	1667	NE2	GLN A 229	-8.516	-15.332	-16.538	1.00	43.19
AAAA								
ATOM	1668	C	GLN A 229	-4.171	-12.982	-17.154	1.00	31.60
AAAA								
ATOM	1669	O	GLN A 229	-3.878	-13.037	-18.348	1.00	32.04
AAAA								
ATOM	1670	N	ALA A 230	-4.296	-11.836	-16.490	1.00	30.96
AAAA								
ATOM	1671	CA	ALA A 230	-4.092	-10.542	-17.131	1.00	30.04
AAAA								
ATOM	1672	CB	ALA A 230	-4.453	-9.423	-16.165	1.00	30.37
AAAA								
ATOM	1673	C	ALA A 230	-2.649	-10.379	-17.598	1.00	29.65
AAAA								
ATOM	1674	O	ALA A 230	-2.392	-9.869	-18.689	1.00	29.50
AAAA								
ATOM	1675	N	TYR A 231	-1.706	-10.802	-16.762	1.00	27.99
AAAA								

ATOM	1676	CA	TYR A 231	-0.295	-10.707	-17.111	1.00	27.27
AAAA								
ATOM	1677	CB	TYR A 231	0.571	-11.065	-15.898	1.00	26.63
AAAA								
ATOM	1678	CG	TYR A 231	0.829	-9.898	-14.975	1.00	24.33
AAAA								
ATOM	1679	CD1	TYR A 231	1.687	-8.866	-15.354	1.00	22.96
AAAA								
ATOM	1680	CE1	TYR A 231	1.926	-7.786	-14.520	1.00	22.17
AAAA								
ATOM	1681	CD2	TYR A 231	0.210	-9.817	-13.725	1.00	24.32
AAAA								
ATOM	1682	CE2	TYR A 231	0.442	-8.737	-12.879	1.00	21.70
AAAA								
ATOM	1683	CZ	TYR A 231	1.298	-7.729	-13.281	1.00	21.49
AAAA								
ATOM	1684	OH	TYR A 231	1.532	-6.662	-12.466	1.00	18.68
AAAA								
ATOM	1685	C	TYR A 231	0.047	-11.618	-18.285	1.00	28.10
AAAA								
ATOM	1686	O	TYR A 231	0.834	-11.249	-19.163	1.00	27.39
AAAA								
ATOM	1687	N	ALA A 232	-0.547	-12.808	-18.297	1.00	28.86
AAAA								
ATOM	1688	CA	ALA A 232	-0.310	-13.775	-19.364	1.00	29.80
AAAA								
ATOM	1689	CB	ALA A 232	-1.013	-15.091	-19.046	1.00	30.32
AAAA								
ATOM	1690	C	ALA A 232	-0.814	-13.218	-20.694	1.00	30.76
AAAA								
ATOM	1691	O	ALA A 232	-0.147	-13.336	-21.725	1.00	30.92
AAAA								
ATOM	1692	N	GLU A 233	-1.996	-12.614	-20.662	1.00	31.01
AAAA								
ATOM	1693	CA	GLU A 233	-2.592	-12.034	-21.857	1.00	32.12
AAAA								
ATOM	1694	CB	GLU A 233	-4.051	-11.658	-21.579	1.00	33.81
AAAA								
ATOM	1695	CG	GLU A 233	-4.975	-12.871	-21.514	1.00	35.08
AAAA								
ATOM	1696	CD	GLU A 233	-6.402	-12.523	-21.117	1.00	37.70
AAAA								
ATOM	1697	OE1	GLU A 233	-6.875	-11.419	-21.473	1.00	37.78
AAAA								
ATOM	1698	OE2	GLU A 233	-7.056	-13.364	-20.461	1.00	37.69
AAAA								
ATOM	1699	C	GLU A 233	-1.800	-10.820	-22.325	1.00	32.01
AAAA								
ATOM	1700	O	GLU A 233	-1.825	-10.463	-23.508	1.00	32.48
AAAA								
ATOM	1701	N	ALA A 234	-1.093	-10.185	-21.398	1.00	30.89
AAAA								
ATOM	1702	CA	ALA A 234	-0.283	-9.022	-21.736	1.00	29.79
AAAA								
ATOM	1703	CB	ALA A 234	-0.089	-8.141	-20.505	1.00	30.39
AAAA								
ATOM	1704	C	ALA A 234	1.070	-9.501	-22.265	1.00	28.79
AAAA								
ATOM	1705	O	ALA A 234	1.934	-8.697	-22.604	1.00	28.46
AAAA								
ATOM	1706	N	GLY A 235	1.243	-10.818	-22.314	1.00	27.19
AAAA								
ATOM	1707	CA	GLY A 235	2.484	-11.388	-22.807	1.00	26.98
AAAA								
ATOM	1708	C	GLY A 235	3.650	-11.387	-21.832	1.00	25.89
AAAA								

ATOM	1709	O	GLY A 235	4.798	-11.527	-22.253	1.00	25.26
AAAA								
ATOM	1710	N	GLN A 236	3.370	-11.226	-20.540	1.00	24.71
AAAA								
ATOM	1711	CA	GLN A 236	4.419	-11.223	-19.518	1.00	24.12
AAAA								
ATOM	1712	CB	GLN A 236	4.652	-9.806	-18.977	1.00	24.66
AAAA								
ATOM	1713	CG	GLN A 236	5.116	-8.760	-20.003	1.00	25.88
AAAA								
ATOM	1714	CD	GLN A 236	6.454	-9.088	-20.647	1.00	26.71
AAAA								
ATOM	1715	OE1	GLN A 236	7.410	-9.488	-19.976	1.00	24.90
AAAA								
ATOM	1716	NE2	GLN A 236	6.533	-8.899	-21.960	1.00	26.33
AAAA								
ATOM	1717	C	GLN A 236	3.959	-12.132	-18.379	1.00	22.79
AAAA								
ATOM	1718	O	GLN A 236	3.823	-11.696	-17.233	1.00	22.19
AAAA								
ATOM	1719	N	PRO A 237	3.740	-13.419	-18.679	1.00	22.50
AAAA								
ATOM	1720	CD	PRO A 237	4.087	-14.093	-19.945	1.00	21.90
AAAA								
ATOM	1721	CA	PRO A 237	3.282	-14.395	-17.684	1.00	22.78
AAAA								
ATOM	1722	CB	PRO A 237	2.998	-15.626	-18.531	1.00	22.52
AAAA								
ATOM	1723	CG	PRO A 237	4.105	-15.558	-19.543	1.00	23.54
AAAA								
ATOM	1724	C	PRO A 237	4.252	-14.695	-16.550	1.00	22.53
AAAA								
ATOM	1725	O	PRO A 237	3.845	-15.217	-15.512	1.00	23.09
AAAA								
ATOM	1726	N	GLN A 238	5.521	-14.346	-16.735	1.00	22.30
AAAA								
ATOM	1727	CA	GLN A 238	6.539	-14.633	-15.726	1.00	22.49
AAAA								
ATOM	1728	CB	GLN A 238	7.947	-14.437	-16.304	1.00	22.24
AAAA								
ATOM	1729	CG	GLN A 238	8.376	-12.991	-16.520	1.00	21.45
AAAA								
ATOM	1730	CD	GLN A 238	7.727	-12.356	-17.736	1.00	22.77
AAAA								
ATOM	1731	OE1	GLN A 238	7.109	-13.038	-18.548	1.00	22.82
AAAA								
ATOM	1732	NE2	GLN A 238	7.881	-11.046	-17.870	1.00	22.96
AAAA								
ATOM	1733	C	GLN A 238	6.453	-13.856	-14.426	1.00	21.84
AAAA								
ATOM	1734	O	GLN A 238	7.059	-14.253	-13.427	1.00	21.75
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ATOM	1735	N	HIS A 239	5.724	-12.748	-14.420	1.00	22.21
AAAA								
ATOM	1736	CA	HIS A 239	5.632	-11.963	-13.202	1.00	22.02
AAAA								
ATOM	1737	CB	HIS A 239	4.919	-10.638	-13.479	1.00	22.03
AAAA								
ATOM	1738	CG	HIS A 239	5.688	-9.734	-14.392	1.00	22.30
AAAA								
ATOM	1739	CD2	HIS A 239	5.315	-9.057	-15.505	1.00	22.95
AAAA								
ATOM	1740	ND1	HIS A 239	7.021	-9.445	-14.197	1.00	21.95
AAAA								
ATOM	1741	CE1	HIS A 239	7.437	-8.628	-15.149	1.00	23.56
AAAA								

ATOM	1742	NE2	HIS	A	239	6.421	-8.378	-15.956	1.00	21.89
AAAA										
ATOM	1743	C	HIS	A	239	4.937	-12.739	-12.092	1.00	20.83
AAAA										
ATOM	1744	O	HIS	A	239	4.036	-13.538	-12.352	1.00	21.43
AAAA										
ATOM	1745	N	LYS	A	240	5.381	-12.506	-10.858	1.00	21.17
AAAA										
ATOM	1746	CA	LYS	A	240	4.819	-13.183	-9.687	1.00	22.02
AAAA										
ATOM	1747	CB	LYS	A	240	5.840	-13.175	-8.543	1.00	21.72
AAAA										
ATOM	1748	CG	LYS	A	240	5.420	-13.918	-7.257	1.00	22.71
AAAA										
ATOM	1749	CD	LYS	A	240	6.462	-13.691	-6.163	1.00	23.02
AAAA										
ATOM	1750	CE	LYS	A	240	6.155	-14.439	-4.855	1.00	22.89
AAAA										
ATOM	1751	NZ	LYS	A	240	6.359	-15.920	-4.960	1.00	23.41
AAAA										
ATOM	1752	C	LYS	A	240	3.545	-12.500	-9.214	1.00	21.50
AAAA										
ATOM	1753	O	LYS	A	240	3.527	-11.288	-9.022	1.00	22.79
AAAA										
ATOM	1754	N	VAL	A	241	2.490	-13.282	-9.012	1.00	23.27
AAAA										
ATOM	1755	CA	VAL	A	241	1.219	-12.751	-8.527	1.00	23.82
AAAA										
ATOM	1756	CB	VAL	A	241	0.111	-12.821	-9.598	1.00	23.97
AAAA										
ATOM	1757	CG1	VAL	A	241	-1.170	-12.185	-9.057	1.00	24.26
AAAA										
ATOM	1758	CG2	VAL	A	241	0.563	-12.105	-10.862	1.00	22.10
AAAA										
ATOM	1759	C	VAL	A	241	0.751	-13.565	-7.323	1.00	23.52
AAAA										
ATOM	1760	O	VAL	A	241	0.593	-14.781	-7.415	1.00	25.10
AAAA										
ATOM	1761	N	THR	A	242	0.547	-12.896	-6.195	1.00	24.29
AAAA										
ATOM	1762	CA	THR	A	242	0.083	-13.578	-4.991	1.00	25.34
AAAA										
ATOM	1763	CB	THR	A	242	1.176	-13.635	-3.892	1.00	23.46
AAAA										
ATOM	1764	OG1	THR	A	242	1.633	-12.312	-3.590	1.00	24.62
AAAA										
ATOM	1765	CG2	THR	A	242	2.354	-14.482	-4.351	1.00	25.33
AAAA										
ATOM	1766	C	THR	A	242	-1.144	-12.870	-4.435	1.00	26.25
AAAA										
ATOM	1767	O	THR	A	242	-1.278	-11.645	-4.534	1.00	25.29
AAAA										
ATOM	1768	N	GLU	A	243	-2.051	-13.647	-3.860	1.00	26.45
AAAA										
ATOM	1769	CA	GLU	A	243	-3.256	-13.070	-3.293	1.00	28.18
AAAA										
ATOM	1770	CB	GLU	A	243	-4.152	-14.184	-2.746	1.00	28.90
AAAA										
ATOM	1771	CG	GLU	A	243	-5.463	-13.705	-2.156	1.00	32.51
AAAA										
ATOM	1772	CD	GLU	A	243	-6.448	-14.845	-1.957	1.00	33.27
AAAA										
ATOM	1773	OE1	GLU	A	243	-6.002	-15.969	-1.646	1.00	33.05
AAAA										
ATOM	1774	OE2	GLU	A	243	-7.665	-14.612	-2.107	1.00	34.89
AAAA										

ATOM	1775	C	GLU A 243	-2.863	-12.089	-2.194	1.00	27.96
AAAA								
ATOM	1776	O	GLU A 243	-3.331	-10.951	-2.164	1.00	28.25
AAAA								
ATOM	1777	N	PHE A 244	-1.976	-12.528	-1.308	1.00	28.29
AAAA								
ATOM	1778	CA	PHE A 244	-1.509	-11.696	-0.208	1.00	29.32
AAAA								
ATOM	1779	CB	PHE A 244	-2.079	-12.202	1.122	1.00	31.34
AAAA								
ATOM	1780	CG	PHE A 244	-3.571	-12.360	1.139	1.00	32.25
AAAA								
ATOM	1781	CD1	PHE A 244	-4.406	-11.249	1.103	1.00	34.11
AAAA								
ATOM	1782	CD2	PHE A 244	-4.141	-13.623	1.246	1.00	33.07
AAAA								
ATOM	1783	CE1	PHE A 244	-5.794	-11.393	1.179	1.00	34.27
AAAA								
ATOM	1784	CE2	PHE A 244	-5.525	-13.780	1.323	1.00	34.74
AAAA								
ATOM	1785	CZ	PHE A 244	-6.353	-12.660	1.291	1.00	34.28
AAAA								
ATOM	1786	C	PHE A 244	0.010	-11.759	-0.103	1.00	29.21
AAAA								
ATOM	1787	O	PHE A 244	0.660	-12.503	-0.836	1.00	28.44
AAAA								
ATOM	1788	N	ILE A 245	0.560	-10.962	0.813	1.00	29.58
AAAA								
ATOM	1789	CA	ILE A 245	1.993	-10.956	1.116	1.00	30.22
AAAA								
ATOM	1790	CB	ILE A 245	2.764	-9.766	0.503	1.00	29.45
AAAA								
ATOM	1791	CG2	ILE A 245	4.190	-9.741	1.060	1.00	27.25
AAAA								
ATOM	1792	CG1	ILE A 245	2.824	-9.887	-1.020	1.00	26.11
AAAA								
ATOM	1793	CD1	ILE A 245	3.609	-8.774	-1.661	1.00	27.15
AAAA								
ATOM	1794	C	ILE A 245	2.086	-10.822	2.631	1.00	32.52
AAAA								
ATOM	1795	O	ILE A 245	1.987	-9.720	3.176	1.00	32.53
AAAA								
ATOM	1796	N	ASP A 246	2.271	-11.944	3.311	1.00	34.55
AAAA								
ATOM	1797	CA	ASP A 246	2.357	-11.926	4.763	1.00	36.92
AAAA								
ATOM	1798	CB	ASP A 246	2.222	-13.350	5.304	1.00	40.29
AAAA								
ATOM	1799	CG	ASP A 246	0.831	-13.926	5.075	1.00	43.98
AAAA								
ATOM	1800	OD1	ASP A 246	0.659	-15.159	5.218	1.00	46.68
AAAA								
ATOM	1801	OD2	ASP A 246	-0.093	-13.143	4.760	1.00	45.65
AAAA								
ATOM	1802	C	ASP A 246	3.650	-11.286	5.247	1.00	36.42
AAAA								
ATOM	1803	O	ASP A 246	3.631	-10.384	6.092	1.00	37.48
AAAA								
ATOM	1804	N	ASP A 247	4.771	-11.733	4.694	1.00	35.16
AAAA								
ATOM	1805	CA	ASP A 247	6.069	-11.200	5.085	1.00	34.25
AAAA								
ATOM	1806	CB	ASP A 247	7.145	-12.268	4.887	1.00	33.07
AAAA								
ATOM	1807	CG	ASP A 247	8.461	-11.901	5.543	1.00	33.19
AAAA								

ATOM	1808	OD1	ASP	A	247	8.689	-10.700	5.802	1.00	31.85
AAAA										
ATOM	1809	OD2	ASP	A	247	9.277	-12.816	5.791	1.00	32.31
AAAA										
ATOM	1810	C	ASP	A	247	6.422	-9.949	4.275	1.00	34.18
AAAA										
ATOM	1811	O	ASP	A	247	7.241	-10.003	3.354	1.00	33.62
AAAA										
ATOM	1812	N	MET	A	248	5.801	-8.825	4.617	1.00	33.66
AAAA										
ATOM	1813	CA	MET	A	248	6.069	-7.577	3.916	1.00	33.29
AAAA										
ATOM	1814	CB	MET	A	248	5.192	-6.448	4.461	1.00	34.30
AAAA										
ATOM	1815	CG	MET	A	248	3.852	-6.314	3.757	1.00	36.70
AAAA										
ATOM	1816	SD	MET	A	248	4.042	-5.940	1.987	1.00	40.22
AAAA										
ATOM	1817	CE	MET	A	248	2.590	-6.667	1.361	1.00	39.66
AAAA										
ATOM	1818	C	MET	A	248	7.533	-7.180	4.017	1.00	32.64
AAAA										
ATOM	1819	O	MET	A	248	8.082	-6.587	3.088	1.00	32.59
AAAA										
ATOM	1820	N	ALA	A	249	8.166	-7.500	5.142	1.00	30.31
AAAA										
ATOM	1821	CA	ALA	A	249	9.573	-7.163	5.316	1.00	29.81
AAAA										
ATOM	1822	CB	ALA	A	249	10.061	-7.597	6.706	1.00	28.83
AAAA										
ATOM	1823	C	ALA	A	249	10.406	-7.837	4.223	1.00	27.72
AAAA										
ATOM	1824	O	ALA	A	249	11.277	-7.208	3.622	1.00	27.98
AAAA										
ATOM	1825	N	ALA	A	250	10.127	-9.112	3.960	1.00	27.22
AAAA										
ATOM	1826	CA	ALA	A	250	10.858	-9.847	2.937	1.00	26.24
AAAA										
ATOM	1827	CB	ALA	A	250	10.449	-11.305	2.946	1.00	26.77
AAAA										
ATOM	1828	C	ALA	A	250	10.624	-9.250	1.553	1.00	26.35
AAAA										
ATOM	1829	O	ALA	A	250	11.543	-9.192	0.739	1.00	26.73
AAAA										
ATOM	1830	N	ALA	A	251	9.400	-8.807	1.279	1.00	25.03
AAAA										
ATOM	1831	CA	ALA	A	251	9.101	-8.225	-0.033	1.00	25.36
AAAA										
ATOM	1832	CB	ALA	A	251	7.597	-8.044	-0.205	1.00	24.69
AAAA										
ATOM	1833	C	ALA	A	251	9.816	-6.891	-0.209	1.00	24.97
AAAA										
ATOM	1834	O	ALA	A	251	10.342	-6.586	-1.287	1.00	24.32
AAAA										
ATOM	1835	N	TYR	A	252	9.832	-6.097	0.855	1.00	24.41
AAAA										
ATOM	1836	CA	TYR	A	252	10.488	-4.801	0.838	1.00	24.62
AAAA										
ATOM	1837	CB	TYR	A	252	10.191	-4.033	2.131	1.00	26.30
AAAA										
ATOM	1838	CG	TYR	A	252	8.815	-3.399	2.214	1.00	28.84
AAAA										
ATOM	1839	CD1	TYR	A	252	8.282	-3.027	3.450	1.00	29.34
AAAA										
ATOM	1840	CE1	TYR	A	252	7.048	-2.395	3.547	1.00	30.51
AAAA										

ATOM	1841	CD2	TYR	A	252	8.066	-3.123	1.064	1.00	28.35
AAAA										
ATOM	1842	CE2	TYR	A	252	6.821	-2.485	1.153	1.00	29.76
AAAA										
ATOM	1843	CZ	TYR	A	252	6.322	-2.125	2.401	1.00	30.32
AAAA										
ATOM	1844	OH	TYR	A	252	5.103	-1.492	2.515	1.00	29.75
AAAA										
ATOM	1845	C	TYR	A	252	11.998	-4.972	0.694	1.00	25.22
AAAA										
ATOM	1846	O	TYR	A	252	12.668	-4.106	0.139	1.00	24.57
AAAA										
ATOM	1847	N	ALA	A	253	12.527	-6.084	1.204	1.00	23.97
AAAA										
ATOM	1848	CA	ALA	A	253	13.961	-6.355	1.118	1.00	24.84
AAAA										
ATOM	1849	CB	ALA	A	253	14.311	-7.606	1.906	1.00	23.83
AAAA										
ATOM	1850	C	ALA	A	253	14.319	-6.560	-0.347	1.00	24.16
AAAA										
ATOM	1851	O	ALA	A	253	15.325	-6.045	-0.831	1.00	26.29
AAAA										
ATOM	1852	N	TRP	A	254	13.469	-7.315	-1.032	1.00	23.19
AAAA										
ATOM	1853	CA	TRP	A	254	13.640	-7.635	-2.447	1.00	22.89
AAAA										
ATOM	1854	CB	TRP	A	254	12.672	-8.753	-2.827	1.00	21.01
AAAA										
ATOM	1855	CG	TRP	A	254	12.534	-8.968	-4.304	1.00	21.21
AAAA										
ATOM	1856	CD2	TRP	A	254	11.508	-8.437	-5.155	1.00	20.22
AAAA										
ATOM	1857	CE2	TRP	A	254	11.766	-8.905	-6.463	1.00	20.36
AAAA										
ATOM	1858	CE3	TRP	A	254	10.397	-7.610	-4.939	1.00	20.38
AAAA										
ATOM	1859	CD1	TRP	A	254	13.353	-9.708	-5.105	1.00	20.80
AAAA										
ATOM	1860	NE1	TRP	A	254	12.895	-9.678	-6.404	1.00	22.48
AAAA										
ATOM	1861	CZ2	TRP	A	254	10.948	-8.573	-7.559	1.00	21.36
AAAA										
ATOM	1862	CZ3	TRP	A	254	9.582	-7.276	-6.030	1.00	21.09
AAAA										
ATOM	1863	CH2	TRP	A	254	9.867	-7.761	-7.323	1.00	20.78
AAAA										
ATOM	1864	C	TRP	A	254	13.433	-6.468	-3.414	1.00	22.65
AAAA										
ATOM	1865	O	TRP	A	254	14.218	-6.280	-4.345	1.00	23.19
AAAA										
ATOM	1866	N	ALA	A	255	12.376	-5.692	-3.194	1.00	21.49
AAAA										
ATOM	1867	CA	ALA	A	255	12.024	-4.586	-4.086	1.00	21.80
AAAA										
ATOM	1868	CB	ALA	A	255	10.652	-4.030	-3.677	1.00	22.15
AAAA										
ATOM	1869	C	ALA	A	255	12.988	-3.420	-4.299	1.00	21.27
AAAA										
ATOM	1870	O	ALA	A	255	13.844	-3.110	-3.469	1.00	21.35
AAAA										
ATOM	1871	N	ASP	A	256	12.820	-2.771	-5.447	1.00	21.80
AAAA										
ATOM	1872	CA	ASP	A	256	13.600	-1.590	-5.807	1.00	21.58
AAAA										
ATOM	1873	CB	ASP	A	256	14.082	-1.686	-7.263	1.00	23.50
AAAA										

ATOM	1874	CG	ASP	A	256	15.329	-2.542	-7.415	1.00	23.21
AAAA										
ATOM	1875	OD1	ASP	A	256	15.354	-3.417	-8.306	1.00	24.63
AAAA										
ATOM	1876	OD2	ASP	A	256	16.289	-2.328	-6.648	1.00	25.60
AAAA										
ATOM	1877	C	ASP	A	256	12.651	-0.397	-5.670	1.00	22.26
AAAA										
ATOM	1878	O	ASP	A	256	13.053	0.703	-5.300	1.00	22.77
AAAA										
ATOM	1879	N	VAL	A	257	11.379	-0.637	-5.968	1.00	23.20
AAAA										
ATOM	1880	CA	VAL	A	257	10.366	0.411	-5.914	1.00	23.31
AAAA										
ATOM	1881	CB	VAL	A	257	10.313	1.167	-7.267	1.00	23.63
AAAA										
ATOM	1882	CG1	VAL	A	257	9.950	0.206	-8.373	1.00	21.70
AAAA										
ATOM	1883	CG2	VAL	A	257	9.312	2.315	-7.205	1.00	23.86
AAAA										
ATOM	1884	C	VAL	A	257	8.997	-0.197	-5.607	1.00	23.39
AAAA										
ATOM	1885	O	VAL	A	257	8.735	-1.351	-5.933	1.00	22.20
AAAA										
ATOM	1886	N	VAL	A	258	8.127	0.587	-4.978	1.00	24.57
AAAA										
ATOM	1887	CA	VAL	A	258	6.792	0.114	-4.627	1.00	24.32
AAAA										
ATOM	1888	CB	VAL	A	258	6.590	0.100	-3.085	1.00	25.07
AAAA										
ATOM	1889	CG1	VAL	A	258	5.275	-0.596	-2.731	1.00	25.09
AAAA										
ATOM	1890	CG2	VAL	A	258	7.755	-0.599	-2.406	1.00	25.19
AAAA										
ATOM	1891	C	VAL	A	258	5.695	0.993	-5.228	1.00	24.77
AAAA										
ATOM	1892	O	VAL	A	258	5.806	2.220	-5.241	1.00	25.72
AAAA										
ATOM	1893	N	VAL	A	259	4.650	0.352	-5.738	1.00	24.90
AAAA										
ATOM	1894	CA	VAL	A	259	3.495	1.056	-6.291	1.00	24.40
AAAA										
ATOM	1895	CB	VAL	A	259	3.152	0.593	-7.713	1.00	24.26
AAAA										
ATOM	1896	CG1	VAL	A	259	1.928	1.371	-8.226	1.00	22.17
AAAA										
ATOM	1897	CG2	VAL	A	259	4.344	0.801	-8.628	1.00	21.85
AAAA										
ATOM	1898	C	VAL	A	259	2.351	0.653	-5.368	1.00	25.42
AAAA										
ATOM	1899	O	VAL	A	259	2.018	-0.528	-5.274	1.00	25.59
AAAA										
ATOM	1900	N	CYS	A	260	1.752	1.623	-4.685	1.00	25.57
AAAA										
ATOM	1901	CA	CYS	A	260	0.680	1.308	-3.750	1.00	26.61
AAAA										
ATOM	1902	CB	CYS	A	260	1.286	0.675	-2.495	1.00	25.90
AAAA										
ATOM	1903	SG	CYS	A	260	2.509	1.742	-1.683	1.00	29.42
AAAA										
ATOM	1904	C	CYS	A	260	-0.113	2.538	-3.330	1.00	27.15
AAAA										
ATOM	1905	O	CYS	A	260	0.221	3.664	-3.702	1.00	27.13
AAAA										
ATOM	1906	N	ARG	A	261	-1.164	2.306	-2.547	1.00	28.36
AAAA										

ATOM	1907	CA	ARG A 261	-1.986	3.391	-2.023	1.00	29.99
AAAA								
ATOM	1908	CB	ARG A 261	-3.244	2.848	-1.340	1.00	31.35
AAAA								
ATOM	1909	CG	ARG A 261	-4.237	2.168	-2.258	1.00	33.82
AAAA								
ATOM	1910	CD	ARG A 261	-4.829	3.143	-3.253	1.00	35.21
AAAA								
ATOM	1911	NE	ARG A 261	-5.949	2.547	-3.975	1.00	36.21
AAAA								
ATOM	1912	CZ	ARG A 261	-6.550	3.107	-5.017	1.00	36.46
AAAA								
ATOM	1913	NH1	ARG A 261	-6.138	4.283	-5.470	1.00	36.95
AAAA								
ATOM	1914	NH2	ARG A 261	-7.571	2.493	-5.599	1.00	37.72
AAAA								
ATOM	1915	C	ARG A 261	-1.118	4.076	-0.979	1.00	30.75
AAAA								
ATOM	1916	O	ARG A 261	-0.041	3.575	-0.641	1.00	29.94
AAAA								
ATOM	1917	N	SER A 262	-1.583	5.206	-0.453	1.00	30.70
AAAA								
ATOM	1918	CA	SER A 262	-0.807	5.924	0.544	1.00	31.00
AAAA								
ATOM	1919	CB	SER A 262	-0.290	7.245	-0.034	1.00	31.31
AAAA								
ATOM	1920	OG	SER A 262	-1.344	8.016	-0.581	1.00	32.21
AAAA								
ATOM	1921	C	SER A 262	-1.526	6.182	1.868	1.00	30.92
AAAA								
ATOM	1922	O	SER A 262	-1.624	7.322	2.317	1.00	31.37
AAAA								
ATOM	1923	N	GLY A 263	-2.040	5.121	2.483	1.00	30.70
AAAA								
ATOM	1924	CA	GLY A 263	-2.669	5.277	3.779	1.00	29.85
AAAA								
ATOM	1925	C	GLY A 263	-1.510	5.663	4.680	1.00	29.40
AAAA								
ATOM	1926	O	GLY A 263	-0.367	5.287	4.394	1.00	28.65
AAAA								
ATOM	1927	N	ALA A 264	-1.787	6.404	5.751	1.00	28.11
AAAA								
ATOM	1928	CA	ALA A 264	-0.752	6.872	6.674	1.00	28.19
AAAA								
ATOM	1929	CB	ALA A 264	-1.399	7.563	7.879	1.00	27.89
AAAA								
ATOM	1930	C	ALA A 264	0.249	5.826	7.166	1.00	27.95
AAAA								
ATOM	1931	O	ALA A 264	1.454	6.056	7.117	1.00	28.65
AAAA								
ATOM	1932	N	LEU A 265	-0.239	4.693	7.656	1.00	27.93
AAAA								
ATOM	1933	CA	LEU A 265	0.662	3.659	8.158	1.00	27.76
AAAA								
ATOM	1934	CB	LEU A 265	-0.141	2.524	8.798	1.00	28.60
AAAA								
ATOM	1935	CG	LEU A 265	-1.049	2.984	9.947	1.00	29.56
AAAA								
ATOM	1936	CD1	LEU A 265	-1.680	1.775	10.615	1.00	28.94
AAAA								
ATOM	1937	CD2	LEU A 265	-0.245	3.797	10.957	1.00	29.94
AAAA								
ATOM	1938	C	LEU A 265	1.566	3.116	7.053	1.00	27.53
AAAA								
ATOM	1939	O	LEU A 265	2.731	2.779	7.297	1.00	25.35
AAAA								

ATOM	1940	N	THR A 266	1.026	3.043	5.841	1.00	27.19
AAAA								
ATOM	1941	CA	THR A 266	1.778	2.553	4.689	1.00	27.20
AAAA								
ATOM	1942	CB	THR A 266	0.859	2.383	3.455	1.00	27.48
AAAA								
ATOM	1943	OG1	THR A 266	-0.066	1.315	3.697	1.00	27.63
AAAA								
ATOM	1944	CG2	THR A 266	1.683	2.059	2.202	1.00	27.00
AAAA								
ATOM	1945	C	THR A 266	2.916	3.507	4.341	1.00	27.11
AAAA								
ATOM	1946	O	THR A 266	4.036	3.072	4.070	1.00	26.97
AAAA								
ATOM	1947	N	VAL A 267	2.631	4.806	4.352	1.00	26.63
AAAA								
ATOM	1948	CA	VAL A 267	3.649	5.806	4.048	1.00	27.06
AAAA								
ATOM	1949	CB	VAL A 267	3.044	7.236	4.052	1.00	26.30
AAAA								
ATOM	1950	CG1	VAL A 267	4.146	8.289	4.011	1.00	26.39
AAAA								
ATOM	1951	CG2	VAL A 267	2.118	7.398	2.851	1.00	25.02
AAAA								
ATOM	1952	C	VAL A 267	4.809	5.730	5.044	1.00	28.55
AAAA								
ATOM	1953	O	VAL A 267	5.973	5.806	4.653	1.00	28.56
AAAA								
ATOM	1954	N	SER A 268	4.495	5.581	6.329	1.00	28.38
AAAA								
ATOM	1955	CA	SER A 268	5.537	5.492	7.351	1.00	29.48
AAAA								
ATOM	1956	CB	SER A 268	4.915	5.522	8.753	1.00	29.48
AAAA								
ATOM	1957	OG	SER A 268	4.291	6.768	9.003	1.00	30.64
AAAA								
ATOM	1958	C	SER A 268	6.348	4.208	7.179	1.00	28.97
AAAA								
ATOM	1959	O	SER A 268	7.557	4.181	7.399	1.00	30.06
AAAA								
ATOM	1960	N	GLU A 269	5.663	3.146	6.785	1.00	28.87
AAAA								
ATOM	1961	CA	GLU A 269	6.286	1.850	6.576	1.00	29.54
AAAA								
ATOM	1962	CB	GLU A 269	5.189	0.821	6.328	1.00	29.82
AAAA								
ATOM	1963	CG	GLU A 269	5.662	-0.594	6.185	1.00	31.86
AAAA								
ATOM	1964	CD	GLU A 269	4.508	-1.562	6.155	1.00	31.85
AAAA								
ATOM	1965	OE1	GLU A 269	3.996	-1.917	7.239	1.00	32.48
AAAA								
ATOM	1966	OE2	GLU A 269	4.100	-1.956	5.048	1.00	30.84
AAAA								
ATOM	1967	C	GLU A 269	7.263	1.910	5.394	1.00	29.59
AAAA								
ATOM	1968	O	GLU A 269	8.355	1.332	5.441	1.00	29.11
AAAA								
ATOM	1969	N	ILE A 270	6.867	2.616	4.340	1.00	27.88
AAAA								
ATOM	1970	CA	ILE A 270	7.711	2.763	3.158	1.00	28.64
AAAA								
ATOM	1971	CB	ILE A 270	6.968	3.520	2.028	1.00	28.20
AAAA								
ATOM	1972	CG2	ILE A 270	7.948	3.931	0.940	1.00	28.68
AAAA								

ATOM	1973	CG1	ILE A 270	5.845	2.646	1.461	1.00	28.04
AAAA								
ATOM	1974	CD1	ILE A 270	6.318	1.366	0.805	1.00	30.11
AAAA								
ATOM	1975	C	ILE A 270	8.978	3.532	3.522	1.00	28.84
AAAA								
ATOM	1976	O	ILE A 270	10.076	3.194	3.075	1.00	28.96
AAAA								
ATOM	1977	N	ALA A 271	8.818	4.568	4.340	1.00	28.51
AAAA								
ATOM	1978	CA	ALA A 271	9.952	5.374	4.768	1.00	28.79
AAAA								
ATOM	1979	CB	ALA A 271	9.462	6.576	5.572	1.00	28.12
AAAA								
ATOM	1980	C	ALA A 271	10.918	4.530	5.603	1.00	29.26
AAAA								
ATOM	1981	O	ALA A 271	12.136	4.575	5.394	1.00	29.35
AAAA								
ATOM	1982	N	ALA A 272	10.370	3.755	6.534	1.00	28.79
AAAA								
ATOM	1983	CA	ALA A 272	11.187	2.904	7.397	1.00	29.79
AAAA								
ATOM	1984	CB	ALA A 272	10.301	2.207	8.430	1.00	29.28
AAAA								
ATOM	1985	C	ALA A 272	11.957	1.872	6.566	1.00	30.22
AAAA								
ATOM	1986	O	ALA A 272	13.102	1.539	6.876	1.00	29.36
AAAA								
ATOM	1987	N	ALA A 273	11.327	1.377	5.503	1.00	30.03
AAAA								
ATOM	1988	CA	ALA A 273	11.961	0.394	4.628	1.00	30.65
AAAA								
ATOM	1989	CB	ALA A 273	10.914	-0.306	3.782	1.00	29.48
AAAA								
ATOM	1990	C	ALA A 273	13.005	1.041	3.720	1.00	31.45
AAAA								
ATOM	1991	O	ALA A 273	13.803	0.346	3.090	1.00	31.87
AAAA								
ATOM	1992	N	GLY A 274	12.998	2.368	3.662	1.00	31.20
AAAA								
ATOM	1993	CA	GLY A 274	13.937	3.078	2.814	1.00	32.26
AAAA								
ATOM	1994	C	GLY A 274	13.725	2.683	1.362	1.00	32.80
AAAA								
ATOM	1995	O	GLY A 274	14.652	2.226	0.692	1.00	33.38
AAAA								
ATOM	1996	N	LEU A 275	12.501	2.862	0.873	1.00	32.88
AAAA								
ATOM	1997	CA	LEU A 275	12.169	2.494	-0.497	1.00	32.70
AAAA								
ATOM	1998	CB	LEU A 275	11.266	1.262	-0.502	1.00	32.79
AAAA								
ATOM	1999	CG	LEU A 275	11.869	-0.138	-0.431	1.00	33.70
AAAA								
ATOM	2000	CD1	LEU A 275	10.762	-1.133	-0.114	1.00	33.69
AAAA								
ATOM	2001	CD2	LEU A 275	12.538	-0.484	-1.762	1.00	32.25
AAAA								
ATOM	2002	C	LEU A 275	11.479	3.568	-1.324	1.00	33.39
AAAA								
ATOM	2003	O	LEU A 275	10.638	4.320	-0.819	1.00	32.48
AAAA								
ATOM	2004	N	PRO A 276	11.835	3.654	-2.617	1.00	32.76
AAAA								
ATOM	2005	CD	PRO A 276	13.022	3.048	-3.244	1.00	32.59
AAAA								

ATOM	2006	CA	PRO A 276	11.221	4.636	-3.513	1.00	32.07
AAAA								
ATOM	2007	CB	PRO A 276	12.049	4.510	-4.791	1.00	32.16
AAAA								
ATOM	2008	CG	PRO A 276	13.383	4.072	-4.296	1.00	33.28
AAAA								
ATOM	2009	C	PRO A 276	9.794	4.143	-3.722	1.00	31.63
AAAA								
ATOM	2010	O	PRO A 276	9.531	2.936	-3.651	1.00	30.32
AAAA								
ATOM	2011	N	ALA A 277	8.864	5.049	-3.976	1.00	31.27
AAAA								
ATOM	2012	CA	ALA A 277	7.504	4.604	-4.180	1.00	30.99
AAAA								
ATOM	2013	CB	ALA A 277	6.764	4.558	-2.842	1.00	30.75
AAAA								
ATOM	2014	C	ALA A 277	6.722	5.450	-5.163	1.00	30.92
AAAA								
ATOM	2015	O	ALA A 277	6.948	6.652	-5.295	1.00	32.61
AAAA								
ATOM	2016	N	LEU A 278	5.809	4.796	-5.865	1.00	31.01
AAAA								
ATOM	2017	CA	LEU A 278	4.928	5.476	-6.796	1.00	31.08
AAAA								
ATOM	2018	CB	LEU A 278	4.884	4.758	-8.146	1.00	31.98
AAAA								
ATOM	2019	CG	LEU A 278	4.135	5.526	-9.241	1.00	32.77
AAAA								
ATOM	2020	CD1	LEU A 278	4.770	6.895	-9.412	1.00	34.58
AAAA								
ATOM	2021	CD2	LEU A 278	4.181	4.756	-10.543	1.00	31.93
AAAA								
ATOM	2022	C	LEU A 278	3.576	5.375	-6.101	1.00	30.98
AAAA								
ATOM	2023	O	LEU A 278	2.887	4.357	-6.197	1.00	31.03
AAAA								
ATOM	2024	N	PHE A 279	3.218	6.424	-5.369	1.00	30.84
AAAA								
ATOM	2025	CA	PHE A 279	1.964	6.447	-4.633	1.00	29.87
AAAA								
ATOM	2026	CB	PHE A 279	2.051	7.460	-3.489	1.00	29.31
AAAA								
ATOM	2027	CG	PHE A 279	2.948	7.033	-2.353	1.00	26.86
AAAA								
ATOM	2028	CD1	PHE A 279	3.961	7.870	-1.902	1.00	27.25
AAAA								
ATOM	2029	CD2	PHE A 279	2.751	5.817	-1.710	1.00	26.40
AAAA								
ATOM	2030	CE1	PHE A 279	4.765	7.506	-0.821	1.00	27.90
AAAA								
ATOM	2031	CE2	PHE A 279	3.549	5.439	-0.630	1.00	25.57
AAAA								
ATOM	2032	CZ	PHE A 279	4.555	6.286	-0.186	1.00	25.90
AAAA								
ATOM	2033	C	PHE A 279	0.765	6.773	-5.508	1.00	30.70
AAAA								
ATOM	2034	O	PHE A 279	0.790	7.719	-6.294	1.00	30.85
AAAA								
ATOM	2035	N	VAL A 280	-0.281	5.968	-5.367	1.00	31.23
AAAA								
ATOM	2036	CA	VAL A 280	-1.523	6.161	-6.101	1.00	32.57
AAAA								
ATOM	2037	CB	VAL A 280	-1.867	4.924	-6.954	1.00	33.12
AAAA								
ATOM	2038	CG1	VAL A 280	-3.196	5.122	-7.661	1.00	32.63
AAAA								

ATOM	2039	CG2	VAL	A	280	-0.768	4.688	-7.979	1.00	33.54
AAAA										
ATOM	2040	C	VAL	A	280	-2.598	6.394	-5.036	1.00	33.46
AAAA										
ATOM	2041	O	VAL	A	280	-3.320	5.478	-4.643	1.00	32.49
AAAA										
ATOM	2042	N	PRO	A	281	-2.695	7.640	-4.546	1.00	34.67
AAAA										
ATOM	2043	CD	PRO	A	281	-1.917	8.789	-5.036	1.00	34.47
AAAA										
ATOM	2044	CA	PRO	A	281	-3.652	8.061	-3.518	1.00	36.79
AAAA										
ATOM	2045	CB	PRO	A	281	-3.475	9.578	-3.478	1.00	36.20
AAAA										
ATOM	2046	CG	PRO	A	281	-2.060	9.772	-3.909	1.00	36.53
AAAA										
ATOM	2047	C	PRO	A	281	-5.097	7.676	-3.801	1.00	38.44
AAAA										
ATOM	2048	O	PRO	A	281	-5.564	7.763	-4.936	1.00	38.62
AAAA										
ATOM	2049	N	PHE	A	282	-5.800	7.237	-2.763	1.00	41.21
AAAA										
ATOM	2050	CA	PHE	A	282	-7.206	6.887	-2.910	1.00	44.31
AAAA										
ATOM	2051	CB	PHE	A	282	-7.722	6.169	-1.664	1.00	45.63
AAAA										
ATOM	2052	CG	PHE	A	282	-9.142	5.697	-1.785	1.00	47.68
AAAA										
ATOM	2053	CD1	PHE	A	282	-9.452	4.570	-2.542	1.00	48.21
AAAA										
ATOM	2054	CD2	PHE	A	282	-10.176	6.387	-1.156	1.00	48.55
AAAA										
ATOM	2055	CE1	PHE	A	282	-10.772	4.136	-2.673	1.00	49.11
AAAA										
ATOM	2056	CE2	PHE	A	282	-11.501	5.963	-1.280	1.00	49.07
AAAA										
ATOM	2057	CZ	PHE	A	282	-11.799	4.833	-2.041	1.00	48.80
AAAA										
ATOM	2058	C	PHE	A	282	-7.908	8.233	-3.052	1.00	45.26
AAAA										
ATOM	2059	O	PHE	A	282	-7.720	9.121	-2.224	1.00	45.48
AAAA										
ATOM	2060	N	GLN	A	283	-8.706	8.387	-4.101	1.00	47.00
AAAA										
ATOM	2061	CA	GLN	A	283	-9.399	9.648	-4.339	1.00	48.78
AAAA										
ATOM	2062	CB	GLN	A	283	-9.958	9.677	-5.768	1.00	48.98
AAAA										
ATOM	2063	CG	GLN	A	283	-10.606	11.000	-6.170	1.00	50.07
AAAA										
ATOM	2064	CD	GLN	A	283	-9.649	12.179	-6.082	1.00	50.05
AAAA										
ATOM	2065	OE1	GLN	A	283	-9.206	12.556	-4.997	1.00	50.12
AAAA										
ATOM	2066	NE2	GLN	A	283	-9.321	12.762	-7.230	1.00	50.62
AAAA										
ATOM	2067	C	GLN	A	283	-10.519	9.918	-3.335	1.00	49.60
AAAA										
ATOM	2068	O	GLN	A	283	-11.317	9.035	-3.018	1.00	49.68
AAAA										
ATOM	2069	N	HIS	A	284	-10.558	11.151	-2.838	1.00	50.76
AAAA										
ATOM	2070	CA	HIS	A	284	-11.570	11.579	-1.875	1.00	51.60
AAAA										
ATOM	2071	CB	HIS	A	284	-11.329	10.918	-0.515	1.00	52.12
AAAA										

ATOM	2072	CG	HIS A 284	-12.436	11.140	0.469	1.00	52.63
AAAA								
ATOM	2073	CD2	HIS A 284	-13.327	10.280	1.017	1.00	52.98
AAAA								
ATOM	2074	ND1	HIS A 284	-12.733	12.381	0.991	1.00	52.98
AAAA								
ATOM	2075	CE1	HIS A 284	-13.758	12.276	1.817	1.00	52.69
AAAA								
ATOM	2076	NE2	HIS A 284	-14.138	11.011	1.851	1.00	52.96
AAAA								
ATOM	2077	C	HIS A 284	-11.497	13.098	-1.745	1.00	52.04
AAAA								
ATOM	2078	O	HIS A 284	-10.451	13.697	-2.000	1.00	52.03
AAAA								
ATOM	2079	N	LYS A 285	-12.604	13.719	-1.347	1.00	52.27
AAAA								
ATOM	2080	CA	LYS A 285	-12.653	15.171	-1.210	1.00	52.70
AAAA								
ATOM	2081	CB	LYS A 285	-14.018	15.604	-0.669	1.00	53.61
AAAA								
ATOM	2082	CG	LYS A 285	-14.256	17.111	-0.701	1.00	55.17
AAAA								
ATOM	2083	CD	LYS A 285	-14.503	17.634	-2.122	1.00	56.00
AAAA								
ATOM	2084	CE	LYS A 285	-13.244	17.625	-2.984	1.00	56.62
AAAA								
ATOM	2085	NZ	LYS A 285	-13.513	18.075	-4.383	1.00	56.60
AAAA								
ATOM	2086	C	LYS A 285	-11.552	15.746	-0.319	1.00	52.35
AAAA								
ATOM	2087	O	LYS A 285	-10.988	16.800	-0.619	1.00	51.96
AAAA								
ATOM	2088	N	ASP A 286	-11.246	15.054	0.773	1.00	51.71
AAAA								
ATOM	2089	CA	ASP A 286	-10.218	15.521	1.693	1.00	51.34
AAAA								
ATOM	2090	CB	ASP A 286	-10.405	14.869	3.067	1.00	53.33
AAAA								
ATOM	2091	CG	ASP A 286	-10.003	13.403	3.083	1.00	55.00
AAAA								
ATOM	2092	OD1	ASP A 286	-10.412	12.648	2.174	1.00	56.57
AAAA								
ATOM	2093	OD2	ASP A 286	-9.280	13.004	4.018	1.00	56.62
AAAA								
ATOM	2094	C	ASP A 286	-8.817	15.230	1.164	1.00	49.69
AAAA								
ATOM	2095	O	ASP A 286	-7.840	15.829	1.616	1.00	49.71
AAAA								
ATOM	2096	N	ARG A 287	-8.724	14.315	0.203	1.00	47.93
AAAA								
ATOM	2097	CA	ARG A 287	-7.436	13.944	-0.380	1.00	45.79
AAAA								
ATOM	2098	CB	ARG A 287	-6.848	15.121	-1.156	1.00	45.56
AAAA								
ATOM	2099	CG	ARG A 287	-7.744	15.660	-2.251	1.00	45.87
AAAA								
ATOM	2100	CD	ARG A 287	-7.172	16.949	-2.801	1.00	45.75
AAAA								
ATOM	2101	NE	ARG A 287	-5.999	16.724	-3.637	1.00	46.20
AAAA								
ATOM	2102	CZ	ARG A 287	-4.981	17.573	-3.733	1.00	46.22
AAAA								
ATOM	2103	NH1	ARG A 287	-4.986	18.702	-3.037	1.00	46.26
AAAA								
ATOM	2104	NH2	ARG A 287	-3.962	17.297	-4.533	1.00	46.42
AAAA								

ATOM	2105	C	ARG A 287	-6.464	13.533	0.722	1.00	44.13
AAAA								
ATOM	2106	O	ARG A 287	-5.279	13.870	0.685	1.00	43.87
AAAA								
ATOM	2107	N	GLN A 288	-6.975	12.804	1.704	1.00	42.92
AAAA								
ATOM	2108	CA	GLN A 288	-6.157	12.359	2.824	1.00	42.41
AAAA								
ATOM	2109	CB	GLN A 288	-6.955	11.395	3.704	1.00	42.02
AAAA								
ATOM	2110	CG	GLN A 288	-6.226	10.947	4.958	1.00	41.95
AAAA								
ATOM	2111	CD	GLN A 288	-7.033	9.951	5.766	1.00	42.04
AAAA								
ATOM	2112	OE1	GLN A 288	-7.356	8.860	5.288	1.00	41.14
AAAA								
ATOM	2113	NE2	GLN A 288	-7.369	10.322	6.997	1.00	41.32
AAAA								
ATOM	2114	C	GLN A 288	-4.867	11.682	2.372	1.00	41.36
AAAA								
ATOM	2115	O	GLN A 288	-3.772	12.113	2.734	1.00	41.61
AAAA								
ATOM	2116	N	GLN A 289	-4.999	10.626	1.575	1.00	41.32
AAAA								
ATOM	2117	CA	GLN A 289	-3.835	9.886	1.105	1.00	40.21
AAAA								
ATOM	2118	CB	GLN A 289	-4.267	8.678	0.280	1.00	39.57
AAAA								
ATOM	2119	CG	GLN A 289	-5.126	7.703	1.068	1.00	37.69
AAAA								
ATOM	2120	CD	GLN A 289	-4.976	6.274	0.595	1.00	37.80
AAAA								
ATOM	2121	OE1	GLN A 289	-4.422	6.014	-0.475	1.00	35.48
AAAA								
ATOM	2122	NE2	GLN A 289	-5.478	5.337	1.388	1.00	36.57
AAAA								
ATOM	2123	C	GLN A 289	-2.862	10.744	0.318	1.00	40.38
AAAA								
ATOM	2124	O	GLN A 289	-1.661	10.469	0.301	1.00	40.11
AAAA								
ATOM	2125	N	TYR A 290	-3.373	11.782	-0.335	1.00	40.27
AAAA								
ATOM	2126	CA	TYR A 290	-2.504	12.678	-1.081	1.00	39.93
AAAA								
ATOM	2127	CB	TYR A 290	-3.316	13.715	-1.860	1.00	41.72
AAAA								
ATOM	2128	CG	TYR A 290	-2.473	14.873	-2.352	1.00	43.41
AAAA								
ATOM	2129	CD1	TYR A 290	-1.590	14.716	-3.421	1.00	44.44
AAAA								
ATOM	2130	CE1	TYR A 290	-0.764	15.763	-3.836	1.00	45.65
AAAA								
ATOM	2131	CD2	TYR A 290	-2.513	16.109	-1.709	1.00	43.91
AAAA								
ATOM	2132	CE2	TYR A 290	-1.695	17.161	-2.111	1.00	45.19
AAAA								
ATOM	2133	CZ	TYR A 290	-0.821	16.981	-3.174	1.00	46.54
AAAA								
ATOM	2134	OH	TYR A 290	0.003	18.014	-3.566	1.00	47.98
AAAA								
ATOM	2135	C	TYR A 290	-1.604	13.399	-0.085	1.00	39.33
AAAA								
ATOM	2136	O	TYR A 290	-0.396	13.529	-0.296	1.00	39.19
AAAA								
ATOM	2137	N	TRP A 291	-2.202	13.871	1.005	1.00	38.32
AAAA								

ATOM	2138	CA	TRP A 291	-1.451	14.585	2.025	1.00	37.84
AAAA								
ATOM	2139	CB	TRP A 291	-2.409	15.307	2.979	1.00	37.98
AAAA								
ATOM	2140	CG	TRP A 291	-3.211	16.366	2.286	1.00	39.40
AAAA								
ATOM	2141	CD2	TRP A 291	-2.721	17.612	1.778	1.00	39.83
AAAA								
ATOM	2142	CE2	TRP A 291	-3.810	18.270	1.162	1.00	40.18
AAAA								
ATOM	2143	CE3	TRP A 291	-1.467	18.238	1.781	1.00	40.07
AAAA								
ATOM	2144	CD1	TRP A 291	-4.540	16.319	1.969	1.00	38.96
AAAA								
ATOM	2145	NE1	TRP A 291	-4.908	17.459	1.294	1.00	39.51
AAAA								
ATOM	2146	CZ2	TRP A 291	-3.684	19.525	0.554	1.00	40.53
AAAA								
ATOM	2147	CZ3	TRP A 291	-1.340	19.488	1.177	1.00	41.40
AAAA								
ATOM	2148	CH2	TRP A 291	-2.446	20.116	0.572	1.00	40.92
AAAA								
ATOM	2149	C	TRP A 291	-0.506	13.680	2.803	1.00	36.79
AAAA								
ATOM	2150	O	TRP A 291	0.515	14.141	3.306	1.00	36.64
AAAA								
ATOM	2151	N	ASN A 292	-0.841	12.397	2.907	1.00	36.82
AAAA								
ATOM	2152	CA	ASN A 292	0.030	11.467	3.619	1.00	37.08
AAAA								
ATOM	2153	CB	ASN A 292	-0.658	10.116	3.842	1.00	36.47
AAAA								
ATOM	2154	CG	ASN A 292	-1.841	10.203	4.783	1.00	36.02
AAAA								
ATOM	2155	OD1	ASN A 292	-1.924	11.104	5.618	1.00	35.88
AAAA								
ATOM	2156	ND2	ASN A 292	-2.757	9.248	4.667	1.00	35.26
AAAA								
ATOM	2157	C	ASN A 292	1.302	11.246	2.803	1.00	37.41
AAAA								
ATOM	2158	O	ASN A 292	2.402	11.170	3.353	1.00	36.90
AAAA								
ATOM	2159	N	ALA A 293	1.138	11.166	1.485	1.00	38.20
AAAA								
ATOM	2160	CA	ALA A 293	2.253	10.936	0.567	1.00	38.64
AAAA								
ATOM	2161	CB	ALA A 293	1.729	10.343	-0.737	1.00	37.83
AAAA								
ATOM	2162	C	ALA A 293	3.085	12.176	0.267	1.00	39.51
AAAA								
ATOM	2163	O	ALA A 293	4.311	12.094	0.158	1.00	39.51
AAAA								
ATOM	2164	N	LEU A 294	2.422	13.321	0.137	1.00	40.40
AAAA								
ATOM	2165	CA	LEU A 294	3.101	14.575	-0.169	1.00	40.96
AAAA								
ATOM	2166	CB	LEU A 294	2.166	15.757	0.101	1.00	41.41
AAAA								
ATOM	2167	CG	LEU A 294	2.666	17.155	-0.272	1.00	41.36
AAAA								
ATOM	2168	CD1	LEU A 294	3.231	17.168	-1.688	1.00	41.61
AAAA								
ATOM	2169	CD2	LEU A 294	1.510	18.136	-0.147	1.00	41.60
AAAA								
ATOM	2170	C	LEU A 294	4.419	14.762	0.585	1.00	42.04
AAAA								

ATOM	2171	O	LEU A 294	5.404	15.228	0.013	1.00	42.14
AAAA								
ATOM	2172	N	PRO A 295	4.459	14.401	1.877	1.00	42.80
AAAA								
ATOM	2173	CD	PRO A 295	3.351	14.022	2.772	1.00	42.95
AAAA								
ATOM	2174	CA	PRO A 295	5.706	14.560	2.634	1.00	43.42
AAAA								
ATOM	2175	CB	PRO A 295	5.336	14.032	4.015	1.00	43.51
AAAA								
ATOM	2176	CG	PRO A 295	3.889	14.406	4.128	1.00	43.40
AAAA								
ATOM	2177	C	PRO A 295	6.900	13.813	2.022	1.00	44.05
AAAA								
ATOM	2178	O	PRO A 295	8.007	14.349	1.957	1.00	44.17
AAAA								
ATOM	2179	N	LEU A 296	6.682	12.577	1.581	1.00	44.41
AAAA								
ATOM	2180	CA	LEU A 296	7.766	11.800	0.980	1.00	45.13
AAAA								
ATOM	2181	CB	LEU A 296	7.373	10.324	0.852	1.00	44.54
AAAA								
ATOM	2182	CG	LEU A 296	7.424	9.484	2.130	1.00	44.46
AAAA								
ATOM	2183	CD1	LEU A 296	6.951	8.069	1.840	1.00	43.91
AAAA								
ATOM	2184	CD2	LEU A 296	8.844	9.469	2.667	1.00	44.76
AAAA								
ATOM	2185	C	LEU A 296	8.151	12.346	-0.391	1.00	45.53
AAAA								
ATOM	2186	O	LEU A 296	9.333	12.406	-0.732	1.00	45.28
AAAA								
ATOM	2187	N	GLU A 297	7.155	12.747	-1.174	1.00	46.35
AAAA								
ATOM	2188	CA	GLU A 297	7.421	13.291	-2.502	1.00	47.94
AAAA								
ATOM	2189	CB	GLU A 297	6.113	13.563	-3.251	1.00	48.43
AAAA								
ATOM	2190	CG	GLU A 297	6.306	14.349	-4.544	1.00	49.91
AAAA								
ATOM	2191	CD	GLU A 297	5.014	14.543	-5.318	1.00	51.34
AAAA								
ATOM	2192	OE1	GLU A 297	4.562	13.586	-5.981	1.00	51.89
AAAA								
ATOM	2193	OE2	GLU A 297	4.446	15.655	-5.257	1.00	52.41
AAAA								
ATOM	2194	C	GLU A 297	8.225	14.579	-2.393	1.00	48.46
AAAA								
ATOM	2195	O	GLU A 297	9.155	14.806	-3.165	1.00	48.78
AAAA								
ATOM	2196	N	LYS A 298	7.860	15.421	-1.431	1.00	49.07
AAAA								
ATOM	2197	CA	LYS A 298	8.556	16.685	-1.226	1.00	49.76
AAAA								
ATOM	2198	CB	LYS A 298	7.914	17.468	-0.077	1.00	50.85
AAAA								
ATOM	2199	CG	LYS A 298	8.644	18.753	0.277	1.00	52.14
AAAA								
ATOM	2200	CD	LYS A 298	8.032	19.429	1.492	1.00	53.44
AAAA								
ATOM	2201	CE	LYS A 298	8.820	20.675	1.882	1.00	53.80
AAAA								
ATOM	2202	NZ	LYS A 298	8.281	21.309	3.116	1.00	54.32
AAAA								
ATOM	2203	C	LYS A 298	10.022	16.420	-0.908	1.00	49.36
AAAA								

ATOM	2204	O	LYS A 298	10.904	17.180	-1.305	1.00	50.01
AAAA								
ATOM	2205	N	ALA A 299	10.275	15.335	-0.188	1.00	48.67
AAAA								
ATOM	2206	CA	ALA A 299	11.635	14.975	0.182	1.00	47.48
AAAA								
ATOM	2207	CB	ALA A 299	11.615	14.001	1.353	1.00	47.29
AAAA								
ATOM	2208	C	ALA A 299	12.354	14.356	-1.009	1.00	46.69
AAAA								
ATOM	2209	O	ALA A 299	13.554	14.098	-0.953	1.00	46.67
AAAA								
ATOM	2210	N	GLY A 300	11.613	14.133	-2.090	1.00	45.80
AAAA								
ATOM	2211	CA	GLY A 300	12.197	13.538	-3.278	1.00	44.79
AAAA								
ATOM	2212	C	GLY A 300	12.399	12.042	-3.119	1.00	44.04
AAAA								
ATOM	2213	O	GLY A 300	13.343	11.472	-3.665	1.00	44.02
AAAA								
ATOM	2214	N	ALA A 301	11.505	11.404	-2.370	1.00	43.01
AAAA								
ATOM	2215	CA	ALA A 301	11.589	9.967	-2.131	1.00	42.10
AAAA								
ATOM	2216	CB	ALA A 301	11.514	9.684	-0.632	1.00	42.10
AAAA								
ATOM	2217	C	ALA A 301	10.484	9.209	-2.858	1.00	41.88
AAAA								
ATOM	2218	O	ALA A 301	10.480	7.976	-2.882	1.00	41.48
AAAA								
ATOM	2219	N	ALA A 302	9.549	9.941	-3.453	1.00	40.88
AAAA								
ATOM	2220	CA	ALA A 302	8.451	9.303	-4.156	1.00	40.59
AAAA								
ATOM	2221	CB	ALA A 302	7.411	8.819	-3.153	1.00	39.61
AAAA								
ATOM	2222	C	ALA A 302	7.786	10.197	-5.191	1.00	40.72
AAAA								
ATOM	2223	O	ALA A 302	8.123	11.372	-5.340	1.00	40.90
AAAA								
ATOM	2224	N	LYS A 303	6.837	9.610	-5.910	1.00	41.39
AAAA								
ATOM	2225	CA	LYS A 303	6.073	10.309	-6.930	1.00	41.79
AAAA								
ATOM	2226	CB	LYS A 303	6.455	9.807	-8.325	1.00	41.86
AAAA								
ATOM	2227	CG	LYS A 303	5.540	10.295	-9.442	1.00	43.46
AAAA								
ATOM	2228	CD	LYS A 303	5.608	11.807	-9.614	1.00	44.98
AAAA								
ATOM	2229	CE	LYS A 303	4.676	12.284	-10.729	1.00	46.33
AAAA								
ATOM	2230	NZ	LYS A 303	4.767	13.759	-10.957	1.00	46.15
AAAA								
ATOM	2231	C	LYS A 303	4.603	10.022	-6.671	1.00	41.86
AAAA								
ATOM	2232	O	LYS A 303	4.219	8.873	-6.441	1.00	41.54
AAAA								
ATOM	2233	N	ILE A 304	3.782	11.065	-6.702	1.00	41.98
AAAA								
ATOM	2234	CA	ILE A 304	2.354	10.905	-6.475	1.00	42.52
AAAA								
ATOM	2235	CB	ILE A 304	1.808	11.961	-5.492	1.00	42.27
AAAA								
ATOM	2236	CG2	ILE A 304	0.321	11.738	-5.278	1.00	41.77
AAAA								

ATOM	2237	CG1	ILE	A	304	2.554	11.889	-4.159	1.00	42.76
AAAA										
ATOM	2238	CD1	ILE	A	304	2.094	12.921	-3.140	1.00	41.84
AAAA										
ATOM	2239	C	ILE	A	304	1.580	11.047	-7.777	1.00	43.43
AAAA										
ATOM	2240	O	ILE	A	304	1.818	11.969	-8.555	1.00	43.89
AAAA										
ATOM	2241	N	ILE	A	305	0.649	10.129	-8.006	1.00	44.38
AAAA										
ATOM	2242	CA	ILE	A	305	-0.177	10.164	-9.199	1.00	45.28
AAAA										
ATOM	2243	CB	ILE	A	305	0.287	9.124	-10.247	1.00	44.81
AAAA										
ATOM	2244	CG2	ILE	A	305	-0.610	9.188	-11.478	1.00	43.86
AAAA										
ATOM	2245	CG1	ILE	A	305	1.738	9.400	-10.647	1.00	44.38
AAAA										
ATOM	2246	CD1	ILE	A	305	2.305	8.405	-11.647	1.00	45.12
AAAA										
ATOM	2247	C	ILE	A	305	-1.620	9.870	-8.807	1.00	47.13
AAAA										
ATOM	2248	O	ILE	A	305	-1.985	8.724	-8.550	1.00	46.47
AAAA										
ATOM	2249	N	GLU	A	306	-2.435	10.918	-8.745	1.00	49.50
AAAA										
ATOM	2250	CA	GLU	A	306	-3.839	10.761	-8.396	1.00	51.69
AAAA										
ATOM	2251	CB	GLU	A	306	-4.430	12.110	-7.987	1.00	51.85
AAAA										
ATOM	2252	CG	GLU	A	306	-3.603	12.818	-6.927	1.00	51.67
AAAA										
ATOM	2253	CD	GLU	A	306	-4.324	13.990	-6.296	1.00	52.25
AAAA										
ATOM	2254	OE1	GLU	A	306	-5.351	13.763	-5.621	1.00	52.52
AAAAATOM	2255	OE2	GLU	A	306	-3.861	15.135	-6.472	1.00	52.12
AAAAATOM	2256	C	GLU	A	306	-4.552	10.202	-9.619	1.00	53.21
AAAAATOM	2257	O	GLU	A	306	-4.180	10.515	-10.749	1.00	53.53
AAAAATOM	2258	N	GLN	A	307	-5.570	9.376	-9.393	1.00	55.39
AAAAATOM	2259	CA	GLN	A	307	-6.313	8.750	-10.483	1.00	57.63
AAAAATOM	2260	CB	GLN	A	307	-7.553	8.035	-9.934	1.00	58.22
AAAAATOM	2261	CG	GLN	A	307	-7.213	6.925	-8.937	1.00	59.17
AAAAATOM	2262	CD	GLN	A	307	-8.196	5.766	-8.970	1.00	59.83
AAAAATOM	2263	OE1	GLN	A	307	-8.110	4.840	-8.160	1.00	60.26
AAAAATOM	2264	NE2	GLN	A	307	-9.131	5.807	-9.912	1.00	60.69
AAAAATOM	2265	C	GLN	A	307	-6.703	9.663	-11.648	1.00	58.47
AAAAATOM	2266	O	GLN	A	307	-6.774	9.208	-12.791	1.00	58.81
AAAAATOM	2267	N	PRO	A	308	-6.968	10.956	-11.385	1.00	59.24
AAAAATOM	2268	CD	PRO	A	308	-7.113	11.674	-10.105	1.00	59.76
AAAAATOM	2269	CA	PRO	A	308	-7.334	11.825	-12.507	1.00	59.72
AAAAATOM	2270	CB	PRO	A	308	-7.360	13.209	-11.870	1.00	59.96
AAAAATOM	2271	CG	PRO	A	308	-7.896	12.914	-10.510	1.00	60.00
AAAAATOM	2272	C	PRO	A	308	-6.318	11.723	-13.641	1.00	59.84
AAAAATOM	2273	O	PRO	A	308	-6.685	11.496	-14.795	1.00	60.34
AAAAATOM	2274	N	GLN	A	309	-5.042	11.881	-13.305	1.00	59.45
AAAAATOM	2275	CA	GLN	A	309	-3.985	11.794	-14.303	1.00	58.69
AAAAATOM	2276	CB	GLN	A	309	-2.992	12.947	-14.135	1.00	59.92
AAAAATOM	2277	CG	GLN	A	309	-2.082	12.838	-12.920	1.00	60.97
AAAAATOM	2278	CD	GLN	A	309	-1.077	13.975	-12.843	1.00	61.96
AAAAATOM	2279	OE1	GLN	A	309	-0.180	13.974	-11.997	1.00	62.79
AAAAATOM	2280	NE2	GLN	A	309	-1.226	14.956	-13.728	1.00	62.49
AAAAATOM	2281	C	GLN	A	309	-3.250	10.459	-14.204	1.00	57.53
AAAAATOM	2282	O	GLN	A	309	-2.078	10.358	-14.567	1.00	57.67
AAAAATOM	2283	N	LEU	A	310	-3.947	9.437	-13.711	1.00	55.75
AAAAATOM	2284	CA	LEU	A	310	-3.364	8.107	-13.570	1.00	53.92
AAAAATOM	2285	CB	LEU	A	310	-3.799	7.473	-12.241	1.00	53.77

AAAAATOM	2286	CG	LEU	A	310	-3.242	6.108	-11.804	1.00	53.75
AAAAATOM	2287	CD1	LEU	A	310	-3.810	4.998	-12.669	1.00	54.14
AAAAATOM	2288	CD2	LEU	A	310	-1.727	6.123	-11.876	1.00	52.88
AAAAATOM	2289	C	LEU	A	310	-3.813	7.243	-14.740	1.00	52.48
AAAAATOM	2290	O	LEU	A	310	-5.003	7.162	-15.044	1.00	53.10
AAAAATOM	2291	N	SER	A	311	-2.852	6.603	-15.395	1.00	49.96
AAAAATOM	2292	CA	SER	A	311	-3.136	5.748	-16.540	1.00	47.96
AAAAATOM	2293	CB	SER	A	311	-3.409	6.599	-17.778	1.00	47.62
AAAAATOM	2294	OG	SER	A	311	-2.232	7.287	-18.168	1.00	46.72
AAAAATOM	2295	C	SER	A	311	-1.936	4.849	-16.815	1.00	46.16
AAAAATOM	2296	O	SER	A	311	-0.873	5.018	-16.212	1.00	45.34
AAAAATOM	2297	N	VAL	A	312	-2.113	3.907	-17.736	1.00	44.77
AAAAATOM	2298	CA	VAL	A	312	-1.056	2.972	-18.103	1.00	43.52
AAAAATOM	2299	CB	VAL	A	312	-1.496	2.066	-19.278	1.00	43.96
AAAAATOM	2300	CG1	VAL	A	312	-0.373	1.112	-19.656	1.00	43.81
AAAAATOM	2301	CG2	VAL	A	312	-2.740	1.285	-18.892	1.00	43.95
AAAAATOM	2302	C	VAL	A	312	0.215	3.712	-18.498	1.00	42.79
AAAAATOM	2303	O	VAL	A	312	1.284	3.488	-17.922	1.00	41.92
AAAAATOM	2304	N	ASP	A	313	0.096	4.610	-19.470	1.00	42.00
AAAAATOM	2305	CA	ASP	A	313	1.252	5.364	-19.939	1.00	41.37
AAAAATOM	2306	CB	ASP	A	313	0.877	6.203	-21.163	1.00	43.96
AAAAATOM	2307	CG	ASP	A	313	0.506	5.345	-22.357	1.00	46.32
AAAAATOM	2308	OD1	ASP	A	313	1.334	4.496	-22.755	1.00	47.81
AAAAATOM	2309	OD2	ASP	A	313	-0.610	5.514	-22.896	1.00	48.38
AAAAATOM	2310	C	ASP	A	313	1.856	6.249	-18.864	1.00	39.53
AAAAATOM	2311	O	ASP	A	313	3.069	6.452	-18.832	1.00	39.95
AAAAATOM	2312	N	ALA	A	314	1.015	6.768	-17.978	1.00	38.08
AAAAATOM	2313	CA	ALA	A	314	1.492	7.629	-16.905	1.00	36.44
AAAAATOM	2314	CB	ALA	A	314	0.306	8.233	-16.156	1.00	36.79
AAAAATOM	2315	C	ALA	A	314	2.382	6.844	-15.939	1.00	35.41
AAAAATOM	2316	O	ALA	A	314	3.448	7.313	-15.535	1.00	35.44
AAAAATOM	2317	N	VAL	A	315	1.940	5.648	-15.569	1.00	34.29
AAAAATOM	2318	CA	VAL	A	315	2.708	4.809	-14.652	1.00	33.44
AAAAATOM	2319	CB	VAL	A	315	1.886	3.592	-14.169	1.00	33.40
AAAAATOM	2320	CG1	VAL	A	315	2.707	2.775	-13.180	1.00	33.12
AAAAATOM	2321	CG2	VAL	A	315	0.588	4.059	-13.521	1.00	32.76
AAAAATOM	2322	C	VAL	A	315	3.970	4.295	-15.328	1.00	32.88
AAAAATOM	2323	O	VAL	A	315	5.071	4.426	-14.792	1.00	32.35
AAAAATOM	2324	N	ALA	A	316	3.805	3.708	-16.508	1.00	33.02
AAAAATOM	2325	CA	ALA	A	316	4.940	3.172	-17.250	1.00	34.17
AAAAATOM	2326	CB	ALA	A	316	4.469	2.616	-18.593	1.00	33.68
AAAAATOM	2327	C	ALA	A	316	6.002	4.252	-17.456	1.00	34.75
AAAAATOM	2328	O	ALA	A	316	7.190	4.026	-17.211	1.00	34.70
AAAAATOM	2329	N	ASN	A	317	5.578	5.434	-17.889	1.00	35.49
AAAAATOM	2330	CA	ASN	A	317	6.524	6.518	-18.108	1.00	35.27
AAAAATOM	2331	CB	ASN	A	317	5.815	7.738	-18.694	1.00	37.74
AAAAATOM	2332	CG	ASN	A	317	5.395	7.518	-20.128	1.00	38.86
AAAAATOM	2333	OD1	ASN	A	317	6.099	6.855	-20.889	1.00	39.80
AAAAATOM	2334	ND2	ASN	A	317	4.252	8.077	-20.511	1.00	40.96
AAAAATOM	2335	C	ASN	A	317	7.272	6.916	-16.347	1.00	35.18
AAAAATOM	2336	O	ASN	A	317	8.458	7.239	-16.904	1.00	34.36
AAAAATOM	2337	N	THR	A	318	6.592	6.891	-15.704	1.00	34.31
AAAAATOM	2338	CA	THR	A	318	7.251	7.262	-14.456	1.00	34.35
AAAAATOM	2339	CB	THR	A	318	6.245	7.358	-13.282	1.00	34.55
AAAAATOM	2340	OG1	THR	A	318	5.353	8.460	-13.498	1.00	34.46
AAAAATOM	2341	CG2	THR	A	318	6.984	7.563	-11.969	1.00	34.42
AAAAATOM	2342	C	THR	A	318	8.335	6.252	-14.093	1.00	34.52
AAAAATOM	2343	O	THR	A	318	9.464	6.624	-13.783	1.00	34.11
AAAAATOM	2344	N	LEU	A	319	7.987	4.971	-14.139	1.00	35.35
AAAAATOM	2345	CA	LEU	A	319	8.937	3.918	-13.801	1.00	35.23
AAAAATOM	2346	CB	LEU	A	319	8.233	2.556	-13.804	1.00	34.91
AAAAATOM	2347	CG	LEU	A	319	7.142	2.362	-12.743	1.00	34.50
AAAAATOM	2348	CD1	LEU	A	319	6.445	1.031	-12.956	1.00	34.48
AAAAATOM	2349	CD2	LEU	A	319	7.761	2.432	-11.351	1.00	35.13
AAAAATOM	2350	C	LEU	A	319	10.107	3.907	-14.777	1.00	35.72
AAAAATOM	2351	O	LEU	A	319	11.264	3.830	-14.370	1.00	34.85

AAAAATOM	2352	N	ALA	A	320	9.801	3.997	-16.067	1.00	36.49
AAAAATOM	2353	CA	ALA	A	320	10.832	3.989	-17.096	1.00	38.10
AAAAATOM	2354	CB	ALA	A	320	10.192	4.051	-18.472	1.00	37.58
AAAAATOM	2355	C	ALA	A	320	11.809	5.144	-16.924	1.00	38.94
AAAAATOM	2356	O	ALA	A	320	12.939	5.087	-17.410	1.00	39.51
AAAAATOM	2357	N	GLY	A	321	11.375	6.186	-16.219	1.00	38.88
AAAAATOM	2358	CA	GLY	A	321	12.224	7.347	-16.013	1.00	38.68
AAAAATOM	2359	C	GLY	A	321	13.117	7.303	-14.788	1.00	38.70
AAAAATOM	2360	O	GLY	A	321	13.881	8.235	-14.542	1.00	38.64
AAAAATOM	2361	N	TRP	A	322	13.028	6.230	-14.010	1.00	38.46
AAAAATOM	2362	CA	TRP	A	322	13.855	6.108	-12.820	1.00	38.53
AAAAATOM	2363	CB	TRP	A	322	13.008	5.688	-11.611	1.00	39.41
AAAAATOM	2364	CG	TRP	A	322	12.047	6.748	-11.146	1.00	40.01
AAAAATOM	2365	CD2	TRP	A	322	10.898	6.558	-10.307	1.00	40.49
AAAAATOM	2366	CE2	TRP	A	322	10.330	7.833	-10.081	1.00	41.27
AAAAATOM	2367	CE3	TRP	A	322	10.295	5.436	-9.722	1.00	40.54
AAAAATOM	2368	CD1	TRP	A	322	12.126	8.091	-11.389	1.00	39.97
AAAAATOM	2369	NE1	TRP	A	322	11.098	8.749	-10.752	1.00	40.69
AAAAATOM	2370	CZ2	TRP	A	322	9.186	8.018	-9.293	1.00	41.67
AAAAATOM	2371	CZ3	TRP	A	322	9.155	5.619	-8.938	1.00	41.40
AAAAATOM	2372	CH2	TRP	A	322	8.615	6.903	-8.732	1.00	41.69
AAAAATOM	2373	C	TRP	A	322	14.984	5.109	-13.027	1.00	38.48
AAAAATOM	2374	O	TRP	A	322	14.743	3.929	-13.271	1.00	38.22
AAAAATOM	2375	N	SER	A	323	16.217	5.596	-12.935	1.00	38.13
AAAAATOM	2376	CA	SER	A	323	17.395	4.753	-13.101	1.00	38.51
AAAAATOM	2377	CB	SER	A	323	18.573	5.590	-13.591	1.00	38.51
AAAAATOM	2378	OG	SER	A	323	18.994	6.489	-12.582	1.00	39.52
AAAAATOM	2379	C	SER	A	323	17.739	4.150	-11.744	1.00	38.37
AAAAATOM	2380	O	SER	A	323	17.188	4.566	-10.725	1.00	37.29
AAAAATOM	2381	N	ARG	A	324	18.647	3.178	-11.723	1.00	37.86
AAAAATOM	2382	CA	ARG	A	324	19.030	2.563	-10.461	1.00	37.82
AAAAATOM	2383	CB	ARG	A	324	19.924	1.341	-10.688	1.00	36.36
AAAAATOM	2384	CG	ARG	A	324	19.130	0.077	-10.959	1.00	34.77
AAAAATOM	2385	CD	ARG	A	324	19.978	-1.176	-10.849	1.00	33.04
AAAAATOM	2386	NE	ARG	A	324	19.143	-2.372	-10.888	1.00	31.23
AAAAATOM	2387	CZ	ARG	A	324	18.318	-2.738	-9.908	1.00	29.95
AAAAATOM	2388	NH1	ARG	A	324	18.228	-2.006	-8.808	1.00	28.46
AAAAATOM	2389	NH2	ARG	A	324	17.562	-3.815	-10.041	1.00	28.17
AAAAATOM	2390	C	ARG	A	324	19.731	3.571	-9.569	1.00	38.78
AAAAATOM	2391	O	ARG	A	324	19.532	3.578	-8.354	1.00	38.12
AAAAATOM	2392	N	GLU	A	325	20.551	4.428	-10.169	1.00	39.55
AAAAATOM	2393	CA	GLU	A	325	21.251	5.447	-9.401	1.00	40.60
AAAAATOM	2394	CB	GLU	A	325	22.208	6.236	-10.304	1.00	42.74
AAAAATOM	2395	CG	GLU	A	325	22.642	7.589	-9.745	1.00	46.19
AAAAATOM	2396	CD	GLU	A	325	23.197	7.517	-8.327	1.00	48.10
AAAAATOM	2397	OE1	GLU	A	325	23.535	8.586	-7.770	1.00	49.61
AAAAATOM	2398	OE2	GLU	A	325	23.297	6.403	-7.768	1.00	49.87
AAAAATOM	2399	C	GLU	A	325	20.214	6.380	-8.784	1.00	39.88
AAAAATOM	2400	O	GLU	A	325	20.324	6.771	-7.623	1.00	39.45
AAAAATOM	2401	N	THR	A	326	19.202	6.725	-9.572	1.00	39.89
AAAAATOM	2402	CA	THR	A	326	18.130	7.591	-9.102	1.00	40.25
AAAAATOM	2403	CB	THR	A	326	17.139	7.912	-10.240	1.00	40.72
AAAAATOM	2404	OG1	THR	A	326	17.828	8.593	-11.298	1.00	42.28
AAAAATOM	2405	CG2	THR	A	326	16.006	8.795	-9.730	1.00	41.64
AAAAATOM	2406	C	THR	A	326	17.371	6.897	-7.968	1.00	39.76
AAAAATOM	2407	O	THR	A	326	17.108	7.497	-6.925	1.00	39.87
AAAAATOM	2408	N	LEU	A	327	17.027	5.628	-8.175	1.00	38.46
AAAAATOM	2409	CA	LEU	A	327	16.294	4.867	-7.169	1.00	37.41
AAAAATOM	2410	CB	LEU	A	327	15.968	3.466	-7.697	1.00	36.19
AAAAATOM	2411	CG	LEU	A	327	14.952	3.426	-8.843	1.00	35.32
AAAAATOM	2412	CD1	LEU	A	327	14.802	2.002	-9.370	1.00	35.07
AAAAATOM	2413	CD2	LEU	A	327	13.614	3.961	-8.354	1.00	34.69
AAAAATOM	2414	C	LEU	A	327	17.050	4.774	-5.845	1.00	37.39
AAAAATOM	2415	O	LEU	A	327	16.437	4.807	-4.778	1.00	36.80
AAAAATOM	2416	N	LEU	A	328	18.375	4.665	-5.909	1.00	37.58
AAAAATOM	2417	CA	LEU	A	328	19.184	4.593	-4.693	1.00	38.35

AAAAATOM	2418	CB	LEU	A	328	20.662	4.368	-5.030	1.00	38.95
AAAAATOM	2419	CG	LEU	A	328	21.636	4.544	-3.854	1.00	40.10
AAAAATOM	2420	CD1	LEU	A	328	21.303	3.551	-2.752	1.00	39.51
AAAAATOM	2421	CD2	LEU	A	328	23.068	4.349	-4.330	1.00	40.30
AAAAATOM	2422	C	LEU	A	328	19.039	5.899	-3.926	1.00	38.68
AAAAATOM	2423	O	LEU	A	328	18.929	5.906	-2.697	1.00	38.65
AAAAATOM	2424	N	THR	A	329	19.048	7.004	-4.664	1.00	39.35
AAAAATOM	2425	CA	THR	A	329	18.908	8.326	-4.068	1.00	39.98
AAAAATOM	2426	CB	THR	A	329	19.002	9.433	-5.136	1.00	40.05
AAAAATOM	2427	OG1	THR	A	329	20.280	9.364	-5.782	1.00	41.54
AAAAATOM	2428	CG2	THR	A	329	18.841	10.808	-4.497	1.00	40.35
AAAAATOM	2429	C	THR	A	329	17.557	8.425	-3.367	1.00	39.68
AAAAATOM	2430	O	THR	A	329	17.485	8.743	-2.179	1.00	39.91
AAAAATOM	2431	N	MET	A	330	16.492	8.147	-4.111	1.00	39.51
AAAAATOM	2432	CA	MET	A	330	15.143	8.190	-3.564	1.00	38.79
AAAAATOM	2433	CB	MET	A	330	14.141	7.718	-4.617	1.00	38.09
AAAAATOM	2434	CG	MET	A	330	14.011	8.657	-5.804	1.00	36.84
AAAAATOM	2435	SD	MET	A	330	12.977	7.980	-7.108	1.00	37.95
AAAAATOM	2436	CE	MET	A	330	11.332	8.342	-6.478	1.00	37.58
AAAAATOM	2437	C	MET	A	330	15.037	7.315	-2.319	1.00	39.71
AAAAATOM	2438	O	MET	A	330	14.418	7.703	-1.326	1.00	39.60
AAAAATOM	2439	N	ALA	A	331	15.646	6.135	-2.381	1.00	39.50
AAAAATOM	2440	CA	ALA	A	331	15.625	5.202	-1.266	1.00	40.36
AAAAATOM	2441	CB	ALA	A	331	16.378	3.928	-1.634	1.00	39.91
AAAAATOM	2442	C	ALA	A	331	16.243	5.843	-0.032	1.00	40.98
AAAAATOM	2443	O	ALA	A	331	15.662	5.805	1.052	1.00	40.34
AAAAATOM	2444	N	GLU	A	332	17.422	6.435	-0.201	1.00	41.85
AAAAATOM	2445	CA	GLU	A	332	18.102	7.087	0.911	1.00	42.77
AAAAATOM	2446	CB	GLU	A	332	19.470	7.607	0.465	1.00	44.04
AAAAATOM	2447	CG	GLU	A	332	20.414	6.500	0.016	1.00	46.55
AAAAATOM	2448	CD	GLU	A	332	21.822	6.994	-0.248	1.00	48.04
AAAAATOM	2449	OE1	GLU	A	332	21.981	7.923	-1.065	1.00	49.87
AAAAATOM	2450	OE2	GLU	A	332	22.770	6.449	0.359	1.00	49.38
AAAAATOM	2451	C	GLU	A	332	17.246	8.228	1.445	1.00	42.38
AAAAATOM	2452	O	GLU	A	332	17.156	8.435	2.653	1.00	42.66
AAAAATOM	2453	N	ARG	A	333	16.619	8.969	0.540	1.00	41.80
AAAAATOM	2454	CA	ARG	A	333	15.752	10.067	0.937	1.00	42.25
AAAAATOM	2455	CB	ARG	A	333	15.212	10.784	-0.306	1.00	43.43
AAAAATOM	2456	CG	ARG	A	333	16.184	11.793	-0.926	1.00	45.99
AAAAATOM	2457	CD	ARG	A	333	15.844	12.060	-2.389	1.00	48.51
AAAAATOM	2458	NE	ARG	A	333	16.415	13.301	-2.913	1.00	50.45
AAAAATOM	2459	CZ	ARG	A	333	17.703	13.631	-2.859	1.00	52.07
AAAAATOM	2460	NH1	ARG	A	333	18.585	12.814	-2.297	1.00	52.45
AAAAATOM	2461	NH2	ARG	A	333	18.112	14.784	-3.377	1.00	51.94
AAAAATOM	2462	C	ARG	A	333	14.594	9.519	1.777	1.00	41.39
AAAAATOM	2463	O	ARG	A	333	14.275	10.060	2.834	1.00	40.21
AAAAATOM	2464	N	ALA	A	334	13.981	8.435	1.308	1.00	40.03
AAAAATOM	2465	CA	ALA	A	334	12.859	7.825	2.014	1.00	39.84
AAAAATOM	2466	CB	ALA	A	334	12.356	6.612	1.241	1.00	38.43
AAAAATOM	2467	C	ALA	A	334	13.239	7.417	3.435	1.00	40.05
AAAAATOM	2468	O	ALA	A	334	12.493	7.665	4.386	1.00	40.41
AAAAATOM	2469	N	ARG	A	335	14.404	6.797	3.577	1.00	39.11
AAAAATOM	2470	CA	ARG	A	335	14.874	6.351	4.881	1.00	40.00
AAAAATOM	2471	CB	ARG	A	335	16.137	5.506	4.719	1.00	39.98
AAAAATOM	2472	CG	ARG	A	335	16.631	4.865	6.000	1.00	40.54
AAAAATOM	2473	CD	ARG	A	335	15.653	3.814	6.501	1.00	42.08
AAAAATOM	2474	NE	ARG	A	335	16.263	2.949	7.507	1.00	42.95
AAAAATOM	2475	CZ	ARG	A	335	16.403	1.634	7.373	1.00	43.43
AAAAATOM	2476	NH1	ARG	A	335	15.972	1.024	6.274	1.00	43.17
AAAAATOM	2477	NH2	ARG	A	335	16.983	0.927	8.335	1.00	43.96
AAAAATOM	2478	C	ARG	A	335	15.167	7.527	5.802	1.00	40.09
AAAAATOM	2479	O	ARG	A	335	14.877	7.479	6.997	1.00	39.35
AAAAATOM	2480	N	ALA	A	336	15.745	8.581	5.237	1.00	40.52
AAAAATOM	2481	CA	ALA	A	336	16.089	9.774	6.001	1.00	41.50
AAAAATOM	2482	CB	ALA	A	336	16.850	10.754	5.116	1.00	41.05
AAAAATOM	2483	C	ALA	A	336	14.847	10.447	6.573	1.00	42.00

AAAAATOM	2484	O	ALA	A	336	14.905	11.087	7.621	1.00	42.49
AAAAATOM	2485	N	ALA	A	337	13.725	10.300	5.879	1.00	42.58
AAAAATOM	2486	CA	ALA	A	337	12.475	10.903	6.320	1.00	42.55
AAAAATOM	2487	CB	ALA	A	337	11.656	11.338	5.111	1.00	42.34
AAAAATOM	2488	C	ALA	A	337	11.670	9.932	7.174	1.00	42.43
AAAAATOM	2489	O	ALA	A	337	10.444	10.000	7.209	1.00	44.01
AAAAATOM	2490	N	SER	A	338	12.360	9.035	7.868	1.00	41.93
AAAAATOM	2491	CA	SER	A	338	11.686	8.053	8.708	1.00	41.12
AAAAATOM	2492	CB	SER	A	338	12.097	6.641	8.293	1.00	40.73
AAAAATOM	2493	OG	SER	A	338	11.504	5.671	9.139	1.00	40.32
AAAAATOM	2494	C	SER	A	338	11.964	8.235	10.198	1.00	40.88
AAAAATOM	2495	O	SER	A	338	13.042	8.674	10.594	1.00	41.46
AAAAATOM	2496	N	ILE	A	339	10.971	7.898	11.013	1.00	40.11
AAAAATOM	2497	CA	ILE	A	339	11.080	7.985	12.461	1.00	39.66
AAAAATOM	2498	CB	ILE	A	339	10.061	8.992	13.038	1.00	39.74
AAAAATOM	2499	CG2	ILE	A	339	10.249	9.118	14.544	1.00	38.88
AAAAATOM	2500	CG1	ILE	A	339	10.249	10.354	12.361	1.00	39.75
AAAAATOM	2501	CD1	ILE	A	339	9.263	11.423	12.804	1.00	40.42
AAAAATOM	2502	C	ILE	A	339	10.788	6.576	12.978	1.00	40.19
AAAAATOM	2503	O	ILE	A	339	9.653	6.102	12.923	1.00	39.97
AAAAATOM	2504	N	PRO	A	340	11.821	5.886	13.484	1.00	40.75
AAAAATOM	2505	CD	PRO	A	340	13.225	6.336	13.448	1.00	40.95
AAAAATOM	2506	CA	PRO	A	340	11.728	4.520	14.012	1.00	40.57
AAAAATOM	2507	CB	PRO	A	340	13.161	4.021	13.877	1.00	41.22
AAAAATOM	2508	CG	PRO	A	340	13.944	5.244	14.222	1.00	41.12
AAAAATOM	2509	C	PRO	A	340	11.180	4.294	15.424	1.00	40.38
AAAAATOM	2510	O	PRO	A	340	10.841	3.163	15.776	1.00	40.48
AAAAATOM	2511	N	ASP	A	341	11.080	5.345	16.232	1.00	39.43
AAAAATOM	2512	CA	ASP	A	341	10.603	5.174	17.603	1.00	38.32
AAAAATOM	2513	CB	ASP	A	341	11.668	5.696	18.578	1.00	38.62
AAAAATOM	2514	CG	ASP	A	341	12.044	7.146	18.317	1.00	39.54
AAAAATOM	2515	OD1	ASP	A	341	11.727	7.658	17.221	1.00	38.30
AAAAATOM	2516	OD2	ASP	A	341	12.668	7.771	19.209	1.00	40.07
AAAAATOM	2517	C	ASP	A	341	9.241	5.789	17.939	1.00	37.27
AAAAATOM	2518	O	ASP	A	341	9.014	6.235	19.066	1.00	35.88
AAAAATOM	2519	N	ALA	A	342	8.329	5.789	16.971	1.00	36.20
AAAAATOM	2520	CA	ALA	A	342	6.996	6.349	17.181	1.00	34.98
AAAAATOM	2521	CB	ALA	A	342	6.150	6.156	15.927	1.00	35.84
AAAAATOM	2522	C	ALA	A	342	6.280	5.744	18.389	1.00	34.17
AAAAATOM	2523	O	ALA	A	342	5.843	6.465	19.289	1.00	33.36
AAAAATOM	2524	N	THR	A	343	6.159	4.421	18.410	1.00	33.49
AAAAATOM	2525	CA	THR	A	343	5.481	3.747	19.512	1.00	33.39
AAAAATOM	2526	CB	THR	A	343	5.567	2.211	19.362	1.00	33.34
AAAAATOM	2527	OG1	THR	A	343	4.951	1.818	18.128	1.00	34.05
AAAAATOM	2528	CG2	THR	A	343	4.851	1.519	20.516	1.00	33.82
AAAAATOM	2529	C	THR	A	343	6.067	4.155	20.865	1.00	33.89
AAAAATOM	2530	O	THR	A	343	5.340	4.591	21.756	1.00	32.15
AAAAATOM	2531	N	GLU	A	344	7.383	4.027	21.007	1.00	34.87
AAAAATOM	2532	CA	GLU	A	344	8.055	4.379	22.257	1.00	35.80
AAAAATOM	2533	CB	GLU	A	344	9.553	4.054	22.177	1.00	37.79
AAAAATOM	2534	CG	GLU	A	344	9.892	2.570	22.029	1.00	41.45
AAAAATOM	2535	CD	GLU	A	344	9.963	2.101	20.581	1.00	44.16
AAAAATOM	2536	OE1	GLU	A	344	10.311	0.917	20.357	1.00	45.57
AAAAATOM	2537	OE2	GLU	A	344	9.676	2.910	19.668	1.00	45.28
AAAAATOM	2538	C	GLU	A	344	7.886	5.856	22.590	1.00	35.95
AAAAATOM	2539	O	GLU	A	344	7.751	6.233	23.754	1.00	35.12
AAAAATOM	2540	N	ARG	A	345	7.896	6.689	21.559	1.00	35.83
AAAAATOM	2541	CA	ARG	A	345	7.759	8.127	21.731	1.00	36.32
AAAAATOM	2542	CB	ARG	A	345	7.999	8.803	20.386	1.00	38.26
AAAAATOM	2543	CG	ARG	A	345	8.268	10.280	20.448	1.00	41.85
AAAAATOM	2544	CD	ARG	A	345	9.006	10.686	19.194	1.00	44.45
AAAAATOM	2545	NE	ARG	A	345	9.194	12.128	19.098	1.00	47.27
AAAAATOM	2546	CZ	ARG	A	345	9.855	12.721	18.111	1.00	47.66
AAAAATOM	2547	NH1	ARG	A	345	10.390	11.988	17.144	1.00	48.37
AAAAATOM	2548	NH2	ARG	A	345	9.974	14.042	18.090	1.00	48.27
AAAAATOM	2549	C	ARG	A	345	6.384	8.510	22.289	1.00	35.99

AAAAATOM	2550	O	ARG	A	345	6.285	9.209	23.302	1.00	35.24
AAAAATOM	2551	N	VAL	A	346	5.324	8.052	21.630	1.00	34.14
AAAAATOM	2552	CA	VAL	A	346	3.975	8.355	22.092	1.00	33.40
AAAAATOM	2553	CB	VAL	A	346	2.909	7.816	21.110	1.00	33.26
AAAAATOM	2554	CG1	VAL	A	346	1.516	7.969	21.709	1.00	33.83
AAAAATOM	2555	CG2	VAL	A	346	3.005	8.565	19.793	1.00	32.47
AAAAATOM	2556	C	VAL	A	346	3.770	7.727	23.466	1.00	33.14
AAAAATOM	2557	O	VAL	A	346	3.172	8.336	24.352	1.00	32.24
AAAAATOM	2558	N	ALA	A	347	4.280	6.510	23.643	1.00	32.01
AAAAATOM	2559	CA	ALA	A	347	4.159	5.813	24.917	1.00	32.80
AAAAATOM	2560	CB	ALA	A	347	4.831	4.447	24.839	1.00	31.97
AAAAATOM	2561	C	ALA	A	347	4.788	6.639	26.031	1.00	33.01
AAAAATOM	2562	O	ALA	A	347	4.214	6.769	27.114	1.00	32.22
AAAAATOM	2563	N	ASN	A	348	5.968	7.193	25.758	1.00	33.65
AAAAATOM	2564	CA	ASN	A	348	6.681	8.009	26.738	1.00	35.77
AAAAATOM	2565	CB	ASN	A	348	8.078	8.382	26.228	1.00	37.45
AAAAATOM	2566	CG	ASN	A	348	8.996	7.183	26.119	1.00	40.90
AAAAATOM	2567	OD1	ASN	A	348	8.998	6.308	26.989	1.00	43.23
AAAAATOM	2568	ND2	ASN	A	348	9.795	7.140	25.057	1.00	42.50
AAAAATOM	2569	C	ASN	A	348	5.912	9.281	27.074	1.00	35.43
AAAAATOM	2570	O	ASN	A	348	5.824	9.662	28.240	1.00	34.83
AAAAATOM	2571	N	GLU	A	349	5.372	9.943	26.051	1.00	35.34
AAAAATOM	2572	CA	GLU	A	349	4.600	11.164	26.264	1.00	34.80
AAAAATOM	2573	CB	GLU	A	349	4.203	11.802	24.932	1.00	36.04
AAAAATOM	2574	CG	GLU	A	349	5.277	12.681	24.323	1.00	38.86
AAAAATOM	2575	CD	GLU	A	349	5.713	13.801	25.257	1.00	40.72
AAAAATOM	2576	OE1	GLU	A	349	4.836	14.458	25.860	1.00	41.85
AAAAATOM	2577	OE2	GLU	A	349	6.933	14.033	25.385	1.00	42.23
AAAAATOM	2578	C	GLU	A	349	3.357	10.863	27.084	1.00	32.75
AAAAATOM	2579	O	GLU	A	349	2.962	11.658	27.932	1.00	32.53
AAAAATOM	2580	N	VAL	A	350	2.737	9.716	26.827	1.00	31.83
AAAAATOM	2581	CA	VAL	A	350	1.556	9.323	27.583	1.00	31.06
AAAAATOM	2582	CB	VAL	A	350	0.952	8.000	27.049	1.00	31.68
AAAAATOM	2583	CG1	VAL	A	350	0.006	7.406	28.081	1.00	31.12
AAAAATOM	2584	CG2	VAL	A	350	0.205	8.260	25.753	1.00	31.66
AAAAATOM	2585	C	VAL	A	350	1.949	9.135	29.048	1.00	30.82
AAAAATOM	2586	O	VAL	A	350	1.239	9.579	29.953	1.00	30.31
AAAAATOM	2587	N	SER	A	351	3.087	8.486	29.276	1.00	29.94
AAAAATOM	2588	CA	SER	A	351	3.569	8.248	30.635	1.00	31.15
AAAAATOM	2589	CB	SER	A	351	4.830	7.378	30.610	1.00	31.12
AAAAATOM	2590	OG	SER	A	351	5.292	7.138	31.926	1.00	32.12
AAAAATOM	2591	C	SER	A	351	3.880	9.558	31.351	1.00	30.90
AAAAATOM	2592	O	SER	A	351	3.556	9.731	32.527	1.00	30.97
AAAAATOM	2593	N	ARG	A	352	4.511	10.478	30.633	1.00	31.65
AAAAATOM	2594	CA	ARG	A	352	4.873	11.771	31.193	1.00	33.50
AAAAATOM	2595	CB	ARG	A	352	5.681	12.572	30.172	1.00	35.69
AAAAATOM	2596	CG	ARG	A	352	6.406	13.776	30.753	1.00	40.36
AAAAATOM	2597	CD	ARG	A	352	6.877	14.713	29.652	1.00	43.61
AAAAATOM	2598	NE	ARG	A	352	5.742	15.305	28.947	1.00	47.26
AAAAATOM	2599	CZ	ARG	A	352	5.846	16.181	27.952	1.00	49.17
AAAAATOM	2600	NH1	ARG	A	352	7.043	16.575	27.532	1.00	50.34
AAAAATOM	2601	NH2	ARG	A	352	4.751	16.670	27.381	1.00	49.80
AAAAATOM	2602	C	ARG	A	352	3.623	12.558	31.588	1.00	33.09
AAAAATOM	2603	O	ARG	A	352	3.570	13.159	32.660	1.00	33.61
AAAAATOM	2604	N	VAL	A	353	2.622	12.554	30.713	1.00	32.09
AAAAATOM	2605	CA	VAL	A	353	1.380	13.272	30.975	1.00	32.29
AAAAATOM	2606	CB	VAL	A	353	0.490	13.307	29.714	1.00	31.98
AAAAATOM	2607	CG1	VAL	A	353	-0.897	13.828	30.062	1.00	30.21
AAAAATOM	2608	CG2	VAL	A	353	1.129	14.200	28.665	1.00	30.41
AAAAATOM	2609	C	VAL	A	353	0.596	12.660	32.131	1.00	32.54
AAAAATOM	2610	O	VAL	A	353	0.075	13.379	32.985	1.00	32.79
AAAAATOM	2611	N	ALA	A	354	0.513	11.335	32.159	1.00	32.97
AAAAATOM	2612	CA	ALA	A	354	-0.206	10.650	33.224	1.00	34.65
AAAAATOM	2613	CB	ALA	A	354	-0.157	9.145	33.007	1.00	33.53
AAAAATOM	2614	C	ALA	A	354	0.391	11.002	34.583	1.00	35.84
AAAAATOM	2615	O	ALA	A	354	-0.316	11.026	35.588	1.00	36.31

AAAAATOM	2616	N	ARG	A	355	1.694	11.271	34.609	1.00	38.21
AAAAATOM	2617	CA	ARG	A	355	2.382	11.619	35.852	1.00	41.12
AAAAATOM	2618	CB	ARG	A	355	3.837	11.141	35.802	1.00	42.43
AAAAATOM	2619	CG	ARG	A	355	3.976	9.627	35.701	1.00	44.93
AAAAATOM	2620	CD	ARG	A	355	5.416	9.190	35.457	1.00	47.18
AAAAATOM	2621	NE	ARG	A	355	5.482	7.790	35.042	1.00	48.82
AAAAATOM	2622	CZ	ARG	A	355	5.248	6.754	35.842	1.00	50.06
AAAAATOM	2623	NH1	ARG	A	355	4.939	6.947	37.117	1.00	50.68
AAAAATOM	2624	NH2	ARG	A	355	5.302	5.519	35.360	1.00	50.06
AAAAATOM	2625	C	ARG	A	355	2.333	13.125	36.103	1.00	42.42
AAAAATOM	2626	O	ARG	A	355	2.883	13.621	37.086	1.00	42.30
AAAAATOM	2627	N	ALA	A	356	1.660	13.840	35.203	1.00	43.60
AAAAATOM	2628	CA	ALA	A	356	1.504	15.289	35.294	1.00	44.67
AAAAATOM	2629	CB	ALA	A	356	0.702	15.651	36.547	1.00	45.12
AAAAATOM	2630	C	ALA	A	356	2.830	16.042	35.288	1.00	45.36
AAAAATOM	2631	O	ALA	A	356	2.980	17.042	35.989	1.00	45.40
AAAAATOM	2632	N	LEU	A	357	3.779	15.569	34.487	1.00	46.31
AAAAATOM	2633	CA	LEU	A	357	5.093	16.201	34.392	1.00	47.87
AAAAATOM	2634	CB	LEU	A	357	6.122	15.212	33.843	1.00	47.62
AAAAATOM	2635	CG	LEU	A	357	6.465	14.017	34.734	1.00	47.58
AAAAATOM	2636	CD1	LEU	A	357	7.330	13.041	33.958	1.00	47.32
AAAAATOM	2637	CD2	LEU	A	357	7.187	14.497	35.985	1.00	47.50
AAAAATOM	2638	C	LEU	A	357	5.064	17.438	33.505	1.00	48.87
AAAAATOM	2639	OT1	LEU	A	357	5.458	18.518	33.993	1.00	50.17
AAAAATOM	2640	OT2	LEU	A	357	4.659	17.313	32.330	1.00	50.17
AAAA										
ATOM	2641	CB	LYS	B	7	-5.082	-44.913	-47.742	1.00	46.68
BBBB										
ATOM	2642	CG	LYS	B	7	-4.666	-44.949	-49.196	1.00	49.02
BBBB										
ATOM	2643	CD	LYS	B	7	-3.162	-44.896	-49.340	1.00	49.96
BBBB										
ATOM	2644	CE	LYS	B	7	-2.769	-45.054	-50.794	1.00	50.91
BBBB										
ATOM	2645	NZ	LYS	B	7	-1.300	-45.222	-50.954	1.00	52.39
BBBB										
ATOM	2646	C	LYS	B	7	-6.742	-45.658	-46.035	1.00	43.87
BBBB										
ATOM	2647	O	LYS	B	7	-7.135	-44.760	-45.287	1.00	43.90
BBBB										
ATOM	2648	N	LYS	B	7	-7.490	-44.434	-48.090	1.00	46.26
BBBB										
ATOM	2649	CA	LYS	B	7	-6.512	-45.403	-47.519	1.00	45.28
BBBB										
ATOM	2650	N	ARG	B	8	-6.486	-46.895	-45.620	1.00	41.24
BBBB										
ATOM	2651	CA	ARG	B	8	-6.682	-47.303	-44.240	1.00	38.63
BBBB										
ATOM	2652	CB	ARG	B	8	-7.493	-48.600	-44.201	1.00	40.59
BBBB										
ATOM	2653	CG	ARG	B	8	-8.927	-48.466	-44.677	1.00	43.69
BBBB										
ATOM	2654	CD	ARG	B	8	-9.417	-49.774	-45.269	1.00	46.42
BBBB										
ATOM	2655	NE	ARG	B	8	-10.866	-49.789	-45.425	1.00	50.16
BBBBATOM	2656	CZ	ARG	B	8	-11.722	-49.833	-44.408	1.00	51.89
BBBBATOM	2657	NH1	ARG	B	8	-11.268	-49.869	-43.165	1.00	52.20
BBBBATOM	2658	NH2	ARG	B	8	-13.031	-49.841	-44.631	1.00	53.20
BBBBATOM	2659	C	ARG	B	8	-5.371	-47.512	-43.495	1.00	35.87
BBBBATOM	2660	O	ARG	B	8	-4.474	-48.206	-43.973	1.00	34.76
BBBBATOM	2661	N	LEU	B	9	-5.272	-46.899	-42.321	1.00	32.91
BBBBATOM	2662	CA	LEU	B	9	-4.094	-47.039	-41.477	1.00	30.88
BBBBATOM	2663	CB	LEU	B	9	-3.390	-45.694	-41.278	1.00	30.40
BBBBATOM	2664	CG	LEU	B	9	-2.381	-45.626	-40.119	1.00	29.02
BBBBATOM	2665	CD1	LEU	B	9	-1.157	-46.466	-40.442	1.00	29.47
BBBBATOM	2666	CD2	LEU	B	9	-1.975	-44.178	-39.873	1.00	29.56

BBBBATOM	2667	C	LEU	B	9	-4.513	-47.562	-40.115	1.00	29.67
BBBBATOM	2668	O	LEU	B	9	-5.505	-47.101	-39.543	1.00	28.43
BBBBATOM	2669	N	MET	B	10	-3.772	-48.541	-39.604	1.00	27.75
BBBBATOM	2670	CA	MET	B	10	-4.048	-49.055	-38.275	1.00	26.66
BBBBATOM	2671	CB	MET	B	10	-4.268	-50.571	-38.274	1.00	27.09
BBBBATOM	2672	CG	MET	B	10	-4.496	-51.113	-36.869	1.00	28.55
BBBBATOM	2673	SD	MET	B	10	-5.474	-52.612	-36.799	1.00	29.60
BBBBATOM	2674	CE	MET	B	10	-7.126	-51.913	-36.618	1.00	29.41
BBBBATOM	2675	C	MET	B	10	-2.826	-48.691	-37.448	1.00	25.08
BBBBATOM	2676	O	MET	B	10	-1.690	-48.971	-37.839	1.00	24.38
BBBBATOM	2677	N	VAL	B	11	-3.062	-48.037	-36.317	1.00	23.45
BBBBATOM	2678	CA	VAL	B	11	-1.982	-47.605	-35.449	1.00	23.16
BBBBATOM	2679	CB	VAL	B	11	-2.159	-46.116	-35.029	1.00	23.01
BBBBATOM	2680	CG1	VAL	B	11	-0.971	-45.666	-34.184	1.00	20.91
BBBBATOM	2681	CG2	VAL	B	11	-2.305	-45.225	-36.276	1.00	23.82
BBBBATOM	2682	C	VAL	B	11	-1.935	-48.461	-34.184	1.00	23.59
BBBBATOM	2683	O	VAL	B	11	-2.962	-48.712	-33.567	1.00	23.24
BBBBATOM	2684	N	MET	B	12	-0.734	-48.902	-33.817	1.00	23.68
BBBBATOM	2685	CA	MET	B	12	-0.523	-49.707	-32.613	1.00	24.54
BBBBATOM	2686	CB	MET	B	12	0.192	-51.019	-32.971	1.00	24.28
BBBBATOM	2687	CG	MET	B	12	-0.402	-51.726	-34.188	1.00	25.19
BBBBATOM	2688	SD	MET	B	12	0.399	-53.284	-34.669	1.00	26.54
BBBBATOM	2689	CE	MET	B	12	1.990	-52.691	-35.289	1.00	22.99
BBBBATOM	2690	C	MET	B	12	0.361	-48.840	-31.720	1.00	25.31
BBBBATOM	2691	O	MET	B	12	1.546	-48.645	-32.006	1.00	23.88
BBBBATOM	2692	N	ALA	B	13	-0.224	-48.292	-30.657	1.00	27.08
BBBBATOM	2693	CA	ALA	B	13	0.508	-47.410	-29.752	1.00	29.43
BBBBATOM	2694	CB	ALA	B	13	0.747	-46.074	-30.429	1.00	28.82
BBBBATOM	2695	C	ALA	B	13	-0.239	-47.192	-28.436	1.00	31.80
BBBBATOM	2696	O	ALA	B	13	-1.143	-46.350	-28.352	1.00	32.16
BBBBATOM	2697	N	GLY	B	14	0.150	-47.934	-27.405	1.00	32.46
BBBBATOM	2698	CA	GLY	B	14	-0.513	-47.804	-26.120	1.00	33.82
BBBBATOM	2699	C	GLY	B	14	-0.107	-46.595	-25.299	1.00	34.82
BBBBATOM	2700	O	GLY	B	14	0.975	-46.040	-25.479	1.00	35.47
BBBBATOM	2701	N	GLY	B	15	-0.986	-46.188	-24.385	1.00	35.56
BBBBATOM	2702	CA	GLY	B	15	-0.700	-45.047	-23.536	1.00	36.08
BBBBATOM	2703	C	GLY	B	15	0.539	-45.254	-22.683	1.00	36.84
BBBBATOM	2704	O	GLY	B	15	1.293	-44.311	-22.426	1.00	36.03
BBBBATOM	2705	N	THR	B	16	0.755	-46.488	-22.240	1.00	36.65
BBBBATOM	2706	CA	THR	B	16	1.920	-46.787	-21.421	1.00	38.51
BBBBATOM	2707	CB	THR	B	16	1.926	-48.258	-20.974	1.00	38.51
BBBBATOM	2708	OG1	THR	B	16	0.686	-48.558	-20.321	1.00	38.39
BBBBATOM	2709	CG2	THR	B	16	3.075	-48.518	-20.005	1.00	39.11
BBBBATOM	2710	C	THR	B	16	3.158	-46.497	-22.264	1.00	38.35
BBBBATOM	2711	O	THR	B	16	3.191	-46.798	-23.460	1.00	39.90
BBBBATOM	2712	N	GLY	B	17	4.168	-45.897	-21.649	1.00	37.68
BBBBATOM	2713	CA	GLY	B	17	5.367	-45.567	-22.392	1.00	36.57
BBBBATOM	2714	C	GLY	B	17	5.161	-44.303	-23.211	1.00	35.56
BBBBATOM	2715	O	GLY	B	17	6.079	-43.843	-23.890	1.00	35.03
BBBBATOM	2716	N	GLY	B	18	3.949	-43.752	-23.150	1.00	33.83
BBBBATOM	2717	CA	GLY	B	18	3.631	-42.529	-23.872	1.00	33.49
BBBBATOM	2718	C	GLY	B	18	3.825	-42.593	-25.378	1.00	33.12
BBBBATOM	2719	O	GLY	B	18	4.345	-41.650	-25.984	1.00	35.38
BBBBATOM	2720	N	HIS	B	19	3.416	-43.699	-25.988	1.00	30.26
BBBBATOM	2721	CA	HIS	B	19	3.548	-43.865	-27.435	1.00	28.22
BBBBATOM	2722	CB	HIS	B	19	3.772	-45.349	-27.779	1.00	25.81
BBBBATOM	2723	CG	HIS	B	19	4.957	-45.966	-27.094	1.00	25.35
BBBBATOM	2724	CD2	HIS	B	19	6.281	-45.694	-27.184	1.00	24.18
BBBBATOM	2725	ND1	HIS	B	19	4.845	-47.025	-26.217	1.00	24.57
BBBBATOM	2726	CE1	HIS	B	19	6.046	-47.380	-25.798	1.00	23.08
BBBBATOM	2727	NE2	HIS	B	19	6.936	-46.589	-26.369	1.00	25.51
BBBBATOM	2728	C	HIS	B	19	2.280	-43.370	-28.144	1.00	27.91
BBBBATOM	2729	O	HIS	B	19	2.300	-43.049	-29.337	1.00	26.91
BBBBATOM	2730	N	VAL	B	20	1.180	-43.310	-27.402	1.00	27.65
BBBBATOM	2731	CA	VAL	B	20	-0.098	-42.894	-27.965	1.00	27.77
BBBBATOM	2732	CB	VAL	B	20	-1.248	-43.080	-26.942	1.00	28.57

BBBBATOM	2733	CG1	VAL	B	20	-1.082	-42.114	-25.787	1.00	30.03
BBBBATOM	2734	CG2	VAL	B	20	-2.602	-42.873	-27.631	1.00	26.82
BBBBATOM	2735	C	VAL	B	20	-0.140	-41.452	-28.470	1.00	27.57
BBBBATOM	2736	O	VAL	B	20	-0.771	-41.172	-29.486	1.00	27.12
BBBBATOM	2737	N	PHE	B	21	0.528	-40.543	-27.770	1.00	28.03
BBBBATOM	2738	CA	PHE	B	21	0.517	-39.136	-28.160	1.00	29.00
BBBBATOM	2739	CB	PHE	B	21	1.215	-38.289	-27.094	1.00	30.27
BBBBATOM	2740	CG	PHE	B	21	0.565	-38.383	-25.746	1.00	33.59
BBBBATOM	2741	CD1	PHE	B	21	-0.764	-37.999	-25.578	1.00	33.84
BBBBATOM	2742	CD2	PHE	B	21	1.256	-38.909	-24.659	1.00	35.22
BBBBATOM	2743	CE1	PHE	B	21	-1.397	-38.142	-24.350	1.00	35.17
BBBBATOM	2744	CE2	PHE	B	21	0.630	-39.057	-23.422	1.00	36.08
BBBBATOM	2745	CZ	PHE	B	21	-0.700	-38.673	-23.269	1.00	35.65
BBBBATOM	2746	C	PHE	B	21	1.129	-38.898	-29.535	1.00	28.53
BBBBATOM	2747	O	PHE	B	21	0.521	-38.236	-30.378	1.00	28.69
BBBBATOM	2748	N	PRO	B	22	2.336	-39.430	-29.781	1.00	27.41
BBBBATOM	2749	CD	PRO	B	22	3.251	-40.074	-28.819	1.00	27.82
BBBBATOM	2750	CA	PRO	B	22	2.986	-39.252	-31.086	1.00	26.12
BBBBATOM	2751	CB	PRO	B	22	4.362	-39.884	-30.883	1.00	27.48
BBBBATOM	2752	CG	PRO	B	22	4.594	-39.757	-29.403	1.00	28.99
BBBBATOM	2753	C	PRO	B	22	2.188	-39.972	-32.176	1.00	26.37
BBBBATOM	2754	O	PRO	B	22	2.129	-39.522	-33.321	1.00	24.40
BBBBATOM	2755	N	GLY	B	23	1.585	-41.102	-31.807	1.00	24.71
BBBBATOM	2756	CA	GLY	B	23	0.787	-41.864	-32.752	1.00	25.07
BBBBATOM	2757	C	GLY	B	23	-0.459	-41.088	-33.144	1.00	25.00
BBBBATOM	2758	O	GLY	B	23	-0.913	-41.144	-34.295	1.00	23.40
BBBBATOM	2759	N	LEU	B	24	-1.014	-40.366	-32.176	1.00	24.65
BBBBATOM	2760	CA	LEU	B	24	-2.201	-39.551	-32.401	1.00	25.32
BBBBATOM	2761	CB	LEU	B	24	-2.732	-39.017	-31.064	1.00	25.08
BBBBATOM	2762	CG	LEU	B	24	-3.594	-39.997	-30.264	1.00	23.58
BBBBATOM	2763	CD1	LEU	B	24	-3.823	-39.482	-28.828	1.00	25.41
BBBBATOM	2764	CD2	LEU	B	24	-4.919	-40.192	-30.998	1.00	24.78
BBBBATOM	2765	C	LEU	B	24	-1.843	-38.397	-33.336	1.00	25.69
BBBBATOM	2766	O	LEU	B	24	-2.634	-38.017	-34.204	1.00	25.99
BBBBATOM	2767	N	ALA	B	25	-0.644	-37.850	-33.164	1.00	24.89
BBBBATOM	2768	CA	ALA	B	25	-0.197	-36.754	-34.013	1.00	25.94
BBBBATOM	2769	CB	ALA	B	25	1.195	-36.278	-33.590	1.00	25.12
BBBBATOM	2770	C	ALA	B	25	-0.171	-37.207	-35.469	1.00	27.14
BBBBATOM	2771	O	ALA	B	25	-0.626	-36.483	-36.354	1.00	27.46
BBBBATOM	2772	N	VAL	B	26	0.368	-38.403	-35.709	1.00	26.50
BBBBATOM	2773	CA	VAL	B	26	0.466	-38.955	-37.056	1.00	25.70
BBBBATOM	2774	CB	VAL	B	26	1.373	-40.226	-37.081	1.00	26.22
BBBBATOM	2775	CG1	VAL	B	26	1.410	-40.833	-38.479	1.00	26.25
BBBBATOM	2776	CG2	VAL	B	26	2.778	-39.861	-36.631	1.00	24.56
BBBBATOM	2777	C	VAL	B	26	-0.908	-39.310	-37.612	1.00	26.20
BBBBATOM	2778	O	VAL	B	26	-1.178	-39.091	-38.796	1.00	25.87
BBBBATOM	2779	N	ALA	B	27	-1.777	-39.851	-36.764	1.00	24.68
BBBBATOM	2780	CA	ALA	B	27	-3.116	-40.222	-37.199	1.00	26.15
BBBBATOM	2781	CB	ALA	B	27	-3.868	-40.909	-36.066	1.00	26.23
BBBBATOM	2782	C	ALA	B	27	-3.888	-38.984	-37.661	1.00	27.60
BBBBATOM	2783	O	ALA	B	27	-4.492	-38.985	-38.736	1.00	27.05
BBBBATOM	2784	N	HIS	B	28	-3.864	-37.933	-36.847	1.00	27.68
BBBBATOM	2785	CA	HIS	B	28	-4.574	-36.702	-37.190	1.00	29.32
BBBBATOM	2786	CB	HIS	B	28	-4.498	-35.693	-36.039	1.00	27.05
BBBBATOM	2787	CG	HIS	B	28	-5.491	-35.957	-34.952	1.00	27.65
BBBBATOM	2788	CD2	HIS	B	28	-5.327	-36.213	-33.632	1.00	26.92
BBBBATOM	2789	ND1	HIS	B	28	-6.850	-36.010	-35.188	1.00	27.29
BBBBATOM	2790	CE1	HIS	B	28	-7.479	-36.290	-34.060	1.00	26.85
BBBBATOM	2791	NE2	HIS	B	28	-6.578	-36.417	-33.101	1.00	27.78
BBBBATOM	2792	C	HIS	B	28	-4.018	-36.095	-38.462	1.00	30.24
BBBBATOM	2793	O	HIS	B	28	-4.766	-35.589	-39.297	1.00	31.14
BBBBATOM	2794	N	HIS	B	29	-2.702	-36.164	-38.618	1.00	31.42
BBBBATOM	2795	CA	HIS	B	29	-2.070	-35.623	-39.806	1.00	32.38
BBBBATOM	2796	CB	HIS	B	29	-0.554	-35.764	-39.720	1.00	33.49
BBBBATOM	2797	CG	HIS	B	29	0.177	-34.957	-40.743	1.00	35.61
BBBBATOM	2798	CD2	HIS	B	29	0.667	-35.292	-41.960	1.00	36.38

BBBBATOM	2799	ND1	HIS	B	29	0.436	-33.612	-40.583	1.00	37.53
BBBBATOM	2800	CE1	HIS	B	29	1.055	-33.155	-41.657	1.00	37.93
BBBBATOM	2801	NE2	HIS	B	29	1.207	-34.154	-42.508	1.00	37.24
BBBBATOM	2802	C	HIS	B	29	-2.567	-36.324	-41.068	1.00	33.00
BBBBATOM	2803	O	HIS	B	29	-2.845	-35.674	-42.078	1.00	33.02
BBBBATOM	2804	N	LEU	B	30	-2.676	-37.650	-41.012	1.00	31.69
BBBBATOM	2805	CA	LEU	B	30	-3.136	-38.417	-42.162	1.00	32.00
BBBBATOM	2806	CB	LEU	B	30	-2.701	-39.883	-42.033	1.00	30.44
BBBBATOM	2807	CG	LEU	B	30	-1.191	-40.099	-42.203	1.00	29.95
BBBBATOM	2808	CD1	LEU	B	30	-0.823	-41.550	-41.898	1.00	28.64
BBBBATOM	2809	CD2	LEU	B	30	-0.785	-39.736	-43.621	1.00	28.97
BBBBATOM	2810	C	LEU	B	30	-4.641	-38.332	-42.375	1.00	32.37
BBBBATOM	2811	O	LEU	B	30	-5.109	-38.414	-43.507	1.00	33.16
BBBBATOM	2812	N	MET	B	31	-5.401	-38.168	-41.297	1.00	33.50
BBBBATOM	2813	CA	MET	B	31	-6.849	-38.064	-41.424	1.00	34.91
BBBBATOM	2814	CB	MET	B	31	-7.514	-38.061	-40.048	1.00	35.67
BBBBATOM	2815	CG	MET	B	31	-7.536	-39.424	-39.391	1.00	36.44
BBBBATOM	2816	SD	MET	B	31	-8.407	-39.436	-37.827	1.00	37.84
BBBBATOM	2817	CE	MET	B	31	-7.095	-39.039	-36.719	1.00	37.80
BBBBATOM	2818	C	MET	B	31	-7.197	-36.786	-42.173	1.00	35.99
BBBBATOM	2819	O	MET	B	31	-8.224	-36.710	-42.847	1.00	37.36
BBBBATOM	2820	N	ALA	B	32	-6.326	-35.791	-42.052	1.00	36.39
BBBBATOM	2821	CA	ALA	B	32	-6.510	-34.511	-42.722	1.00	37.55
BBBBATOM	2822	CB	ALA	B	32	-5.622	-33.458	-42.073	1.00	36.85
BBBBATOM	2823	C	ALA	B	32	-6.151	-34.663	-44.205	1.00	38.60
BBBBATOM	2824	O	ALA	B	32	-6.392	-33.760	-45.013	1.00	38.04
BBBBATOM	2825	N	GLN	B	33	-5.569	-35.809	-44.555	1.00	38.35
BBBBATOM	2826	CA	GLN	B	33	-5.182	-36.070	-45.938	1.00	38.24
BBBBATOM	2827	CB	GLN	B	33	-3.792	-36.706	-46.011	1.00	39.81
BBBBATOM	2828	CG	GLN	B	33	-2.771	-36.162	-45.028	1.00	41.67
BBBBATOM	2829	CD	GLN	B	33	-2.269	-34.781	-45.384	1.00	41.96
BBBBATOM	2830	OE1	GLN	B	33	-1.735	-34.559	-46.471	1.00	41.35
BBBBATOM	2831	NE2	GLN	B	33	-2.423	-33.843	-44.456	1.00	42.42
BBBBATOM	2832	C	GLN	B	33	-6.187	-37.027	-46.556	1.00	36.70
BBBBATOM	2833	O	GLN	B	33	-5.970	-37.541	-47.647	1.00	36.47
BBBBATOM	2834	N	GLY	B	34	-7.281	-37.274	-45.845	1.00	36.09
BBBBATOM	2835	CA	GLY	B	34	-8.305	-38.169	-46.353	1.00	35.75
BBBBATOM	2836	C	GLY	B	34	-8.219	-39.600	-45.837	1.00	35.33
BBBBATOM	2837	O	GLY	B	34	-9.075	-40.426	-46.146	1.00	34.43
BBBBATOM	2838	N	TRP	B	35	-7.196	-39.896	-45.042	1.00	35.23
BBBBATOM	2839	CA	TRP	B	35	-7.016	-41.246	-44.508	1.00	34.58
BBBBATOM	2840	CB	TRP	B	35	-5.618	-41.400	-43.908	1.00	35.03
BBBBATOM	2841	CG	TRP	B	35	-4.511	-41.558	-44.901	1.00	34.87
BBBBATOM	2842	CD2	TRP	B	35	-3.666	-42.704	-45.060	1.00	35.81
BBBBATOM	2843	CE2	TRP	B	35	-2.733	-42.399	-46.076	1.00	35.60
BBBBATOM	2844	CE3	TRP	B	35	-3.605	-43.961	-44.441	1.00	36.59
BBBBATOM	2845	CD1	TRP	B	35	-4.075	-40.633	-45.803	1.00	35.62
BBBBATOM	2846	NE1	TRP	B	35	-3.004	-41.129	-46.513	1.00	34.95
BBBBATOM	2847	CZ2	TRP	B	35	-1.746	-43.305	-46.488	1.00	37.19
BBBBATOM	2848	CZ3	TRP	B	35	-2.620	-44.865	-44.952	1.00	36.85
BBBBATOM	2849	CH2	TRP	B	35	-1.705	-44.528	-45.867	1.00	36.87
BBBBATOM	2850	C	TRP	B	35	-8.022	-41.670	-43.449	1.00	34.58
BBBBATOM	2851	O	TRP	B	35	-8.546	-40.850	-42.699	1.00	33.58
BBBBATOM	2852	N	GLN	B	36	-8.295	-42.969	-43.410	1.00	34.54
BBBBATOM	2853	CA	GLN	B	36	-9.175	-43.535	-42.402	1.00	35.40
BBBBATOM	2854	CB	GLN	B	36	-10.095	-44.596	-43.003	1.00	37.42
BBBBATOM	2855	CG	GLN	B	36	-11.219	-44.027	-43.862	1.00	41.66
BBBBATOM	2856	CD	GLN	B	36	-11.996	-45.103	-44.601	1.00	44.12
BBBBATOM	2857	OE1	GLN	B	36	-12.988	-44.816	-45.277	1.00	45.76
BBBBATOM	2858	NE2	GLN	B	36	-11.546	-46.350	-44.480	1.00	44.99
BBBBATOM	2859	C	GLN	B	36	-8.183	-44.186	-41.451	1.00	34.89
BBBBATOM	2860	O	GLN	B	36	-7.272	-44.885	-41.889	1.00	34.58
BBBBATOM	2861	N	VAL	B	37	-8.336	-43.941	-40.158	1.00	35.26
BBBBATOM	2862	CA	VAL	B	37	-7.417	-44.516	-39.184	1.00	34.16
BBBBATOM	2863	CB	VAL	B	37	-6.561	-43.417	-38.509	1.00	34.99
BBBBATOM	2864	CG1	VAL	B	37	-5.630	-44.032	-37.479	1.00	34.72

BBBBATOM	2865	CG2	VAL	B	37	-5.755	-42.668	-38.552	1.00	34.06
BBBBATOM	2866	C	VAL	B	37	-8.166	-45.288	-38.109	1.00	34.02
BBBBATOM	2867	O	VAL	B	37	-9.207	-44.849	-37.618	1.00	33.01
BBBBATOM	2868	N	ARG	B	38	-7.629	-46.451	-37.758	1.00	32.20
BBBBATOM	2869	CA	ARG	B	38	-8.219	-47.286	-36.730	1.00	31.56
BBBBATOM	2870	CB	ARG	B	38	-8.811	-48.554	-37.344	1.00	33.53
BBBBATOM	2871	CG	ARG	B	38	-9.706	-49.324	-36.397	1.00	36.77
BBBBATOM	2872	CD	ARG	B	38	-11.107	-49.511	-36.975	1.00	38.80
BBBBATOM	2873	NE	ARG	B	38	-12.000	-50.108	-35.989	1.00	41.24
BBBBATOM	2874	CZ	ARG	B	38	-13.304	-50.293	-36.161	1.00	43.18
BBBBATOM	2875	NH1	ARG	B	38	-13.892	-49.927	-37.294	1.00	43.21
BBBBATOM	2876	NH2	ARG	B	38	-14.026	-50.839	-35.189	1.00	44.37
BBBBATOM	2877	C	ARG	B	38	-7.097	-47.628	-35.751	1.00	30.48
BBBBATOM	2878	O	ARG	B	38	-5.936	-47.742	-36.134	1.00	29.62
BBBBATOM	2879	N	TRP	B	39	-7.447	-47.782	-34.484	1.00	28.40
BBBBATOM	2880	CA	TRP	B	39	-6.456	-48.070	-33.471	1.00	27.41
BBBBATOM	2881	CB	TRP	B	39	-6.696	-47.145	-32.291	1.00	27.98
BBBBATOM	2882	CG	TRP	B	39	-5.480	-46.788	-31.568	1.00	28.00
BBBBATOM	2883	CD2	TRP	B	39	-4.677	-45.627	-31.784	1.00	28.42
BBBBATOM	2884	CE2	TRP	B	39	-3.625	-45.673	-30.851	1.00	28.85
BBBBATOM	2885	CE3	TRP	B	39	-4.749	-44.549	-32.680	1.00	29.78
BBBBATOM	2886	CD1	TRP	B	39	-4.898	-47.476	-30.549	1.00	28.26
BBBBATOM	2887	NE1	TRP	B	39	-3.783	-46.812	-30.111	1.00	28.48
BBBBATOM	2888	CZ2	TRP	B	39	-2.648	-44.684	-30.778	1.00	30.55
BBBBATOM	2889	CZ3	TRP	B	39	-3.770	-43.561	-32.610	1.00	29.22
BBBBATOM	2890	CH2	TRP	B	39	-2.734	-43.639	-31.662	1.00	30.90
BBBBATOM	2891	C	TRP	B	39	-6.478	-49.517	-32.999	1.00	25.82
BBBBATOM	2892	O	TRP	B	39	-7.509	-50.176	-33.055	1.00	24.87
BBBBATOM	2893	N	LEU	B	40	-5.323	-50.004	-32.549	1.00	25.21
BBBBATOM	2894	CA	LEU	B	40	-5.200	-51.364	-32.026	1.00	24.71
BBBBATOM	2895	CB	LEU	B	40	-4.326	-52.221	-32.952	1.00	25.21
BBBBATOM	2896	CG	LEU	B	40	-4.416	-53.754	-32.868	1.00	26.95
BBBBATOM	2897	CD1	LEU	B	40	-3.037	-54.334	-32.571	1.00	27.63
BBBBATOM	2898	CD2	LEU	B	40	-5.421	-54.179	-31.817	1.00	26.69
BBBBATOM	2899	C	LEU	B	40	-4.535	-51.235	-30.655	1.00	23.33
BBBBATOM	2900	O	LEU	B	40	-3.387	-50.824	-30.563	1.00	23.43
BBBBATOM	2901	N	GLY	B	41	-5.260	-51.567	-29.591	1.00	24.01
BBBBATOM	2902	CA	GLY	B	41	-4.691	-51.450	-28.257	1.00	23.47
BBBBATOM	2903	C	GLY	B	41	-5.292	-52.479	-27.322	1.00	23.99
BBBBATOM	2904	O	GLY	B	41	-5.797	-53.498	-27.785	1.00	22.90
BBBBATOM	2905	N	THR	B	42	-5.225	-52.225	-26.017	1.00	26.62
BBBBATOM	2906	CA	THR	B	42	-5.787	-53.141	-25.027	1.00	29.84
BBBBATOM	2907	CB	THR	B	42	-4.693	-53.715	-24.092	1.00	30.17
BBBBATOM	2908	OG1	THR	B	42	-4.019	-52.647	-23.418	1.00	30.77
BBBBATOM	2909	CG2	THR	B	42	-3.683	-54.514	-24.900	1.00	31.30
BBBBATOM	2910	C	THR	B	42	-6.852	-52.420	-24.200	1.00	32.04
BBBBATOM	2911	O	THR	B	42	-6.737	-51.226	-23.924	1.00	31.27
BBBBATOM	2912	N	ALA	B	43	-7.881	-53.160	-23.801	1.00	35.37
BBBBATOM	2913	CA	ALA	B	43	-9.000	-52.595	-23.047	1.00	38.81
BBBBATOM	2914	CB	ALA	B	43	-10.063	-53.669	-22.835	1.00	38.49
BBBBATOM	2915	C	ALA	B	43	-8.671	-51.928	-21.713	1.00	41.06
BBBBATOM	2916	O	ALA	B	43	-9.224	-50.875	-21.391	1.00	42.22
BBBBATOM	2917	N	ASP	B	44	-7.777	-52.521	-20.931	1.00	43.18
BBBBATOM	2918	CA	ASP	B	44	-7.455	-51.942	-19.632	1.00	44.47
BBBBATOM	2919	CB	ASP	B	44	-7.311	-53.057	-18.586	1.00	46.93
BBBBATOM	2920	CG	ASP	B	44	-8.646	-53.724	-18.255	1.00	48.65
BBBBATOM	2921	OD1	ASP	B	44	-9.553	-53.026	-17.753	1.00	50.52
BBBBATOM	2922	OD2	ASP	B	44	-8.791	-54.943	-18.498	1.00	49.40
BBBBATOM	2923	C	ASP	B	44	-6.236	-51.025	-19.598	1.00	44.13
BBBBATOM	2924	O	ASP	B	44	-5.520	-50.968	-18.595	1.00	45.05
BBBBATOM	2925	N	ARG	B	45	-6.001	-50.307	-20.692	1.00	42.34
BBBBATOM	2926	CA	ARG	B	45	-4.887	-49.367	-20.763	1.00	40.44
BBBBATOM	2927	CB	ARG	B	45	-3.802	-49.869	-21.725	1.00	41.87
BBBBATOM	2928	CG	ARG	B	45	-2.935	-50.994	-21.149	1.00	43.86
BBBBATOM	2929	CD	ARG	B	45	-2.218	-50.541	-19.881	1.00	45.24
BBBBATOM	2930	NE	ARG	B	45	-1.385	-51.582	-19.277	1.00	46.96

BBBBBATOM	2931	CZ	ARG	B	45	-1.840	-52.753	-18.839	1.00	47.69
BBBBBATOM	2932	NH1	ARG	B	45	-3.130	-53.051	-18.937	1.00	48.59
BBBBBATOM	2933	NH2	ARG	B	45	-1.005	-53.626	-18.289	1.00	48.33
BBBBBATOM	2934	C	ARG	B	45	-5.390	-47.992	-21.195	1.00	38.74
BBBBBATOM	2935	O	ARG	B	45	-6.486	-47.866	-21.738	1.00	37.69
BBBBBATOM	2936	N	MET	B	46	-4.567	-46.977	-20.955	1.00	37.09
BBBBBATOM	2937	CA	MET	B	46	-4.881	-45.581	-21.249	1.00	36.33
BBBBBATOM	2938	CB	MET	B	46	-3.644	-44.725	-20.945	1.00	37.92
BBBBBATOM	2939	CG	MET	B	46	-3.873	-43.222	-20.952	1.00	40.65
BBBBBATOM	2940	SD	MET	B	46	-3.420	-42.436	-22.517	1.00	44.22
BBBBBATOM	2941	CE	MET	B	46	-1.720	-41.959	-22.168	1.00	41.80
BBBBBATOM	2942	C	MET	B	46	-5.430	-45.239	-22.643	1.00	34.96
BBBBBATOM	2943	O	MET	B	46	-6.264	-44.338	-22.774	1.00	33.21
BBBBBATOM	2944	N	GLU	B	47	-4.976	-45.941	-23.678	1.00	32.85
BBBBBATOM	2945	CA	GLU	B	47	-5.458	-45.655	-25.029	1.00	31.79
BBBBBATOM	2946	CB	GLU	B	47	-4.624	-46.402	-26.080	1.00	30.62
BBBBBATOM	2947	CG	GLU	B	47	-4.755	-47.922	-26.051	1.00	29.85
BBBBBATOM	2948	CD	GLU	B	47	-3.793	-48.597	-25.082	1.00	29.78
BBBBBATOM	2949	OE1	GLU	B	47	-3.188	-47.895	-24.247	1.00	28.76
BBBBBATOM	2950	OE2	GLU	B	47	-3.649	-49.840	-25.156	1.00	29.01
BBBBBATOM	2951	C	GLU	B	47	-6.938	-46.017	-25.191	1.00	31.81
BBBBBATOM	2952	O	GLU	B	47	-7.626	-45.476	-26.055	1.00	31.31
BBBBBATOM	2953	N	ALA	B	48	-7.428	-46.924	-24.352	1.00	31.55
BBBBBATOM	2954	CA	ALA	B	48	-8.821	-47.344	-24.414	1.00	32.58
BBBBBATOM	2955	CB	ALA	B	48	-9.085	-48.450	-23.384	1.00	33.19
BBBBBATOM	2956	C	ALA	B	48	-9.761	-46.168	-24.164	1.00	33.37
BBBBBATOM	2957	O	ALA	B	48	-10.860	-46.114	-24.716	1.00	33.81
BBBBBATOM	2958	N	ASP	B	49	-9.328	-45.232	-23.328	1.00	34.05
BBBBBATOM	2959	CA	ASP	B	49	-10.143	-44.065	-23.009	1.00	35.60
BBBBBATOM	2960	CB	ASP	B	49	-10.033	-43.736	-21.514	1.00	36.58
BBBBBATOM	2961	CG	ASP	B	49	-10.645	-44.812	-20.628	1.00	39.54
BBBBBATOM	2962	OD1	ASP	B	49	-11.835	-45.144	-20.825	1.00	40.82
BBBBBATOM	2963	OD2	ASP	B	49	-9.939	-45.323	-19.730	1.00	39.49
BBBBBATOM	2964	C	ASP	B	49	-9.768	-42.832	-23.831	1.00	34.79
BBBBBATOM	2965	O	ASP	B	49	-10.637	-42.064	-24.241	1.00	35.85
BBBBBATOM	2966	N	LEU	B	50	-8.478	-42.648	-24.088	1.00	34.06
BBBBBATOM	2967	CA	LEU	B	50	-8.026	-41.484	-24.840	1.00	33.49
BBBBBATOM	2968	CB	LEU	B	50	-6.526	-41.264	-24.635	1.00	33.25
BBBBBATOM	2969	CG	LEU	B	50	-6.001	-39.986	-25.299	1.00	33.36
BBBBBATOM	2970	CD1	LEU	B	50	-6.679	-38.771	-24.659	1.00	34.04
BBBBBATOM	2971	CD2	LEU	B	50	-4.496	-39.894	-25.157	1.00	33.08
BBBBBATOM	2972	C	LEU	B	50	-8.320	-41.486	-26.337	1.00	33.52
BBBBBATOM	2973	O	LEU	B	50	-8.769	-40.477	-26.882	1.00	32.52
BBBBBATOM	2974	N	VAL	B	51	-8.073	-42.605	-27.011	1.00	32.94
BBBBBATOM	2975	CA	VAL	B	51	-8.299	-42.641	-28.449	1.00	32.68
BBBBBATOM	2976	CB	VAL	B	51	-7.829	-43.982	-29.058	1.00	33.06
BBBBBATOM	2977	CG1	VAL	B	51	-8.115	-44.013	-30.565	1.00	31.54
BBBBBATOM	2978	CG2	VAL	B	51	-6.329	-44.145	-28.813	1.00	31.45
BBBBBATOM	2979	C	VAL	B	51	-9.747	-42.348	-28.829	1.00	33.08
BBBBBATOM	2980	O	VAL	B	51	-10.000	-41.623	-29.792	1.00	32.88
BBBBBATOM	2981	N	PRO	B	52	-10.721	-42.900	-28.085	1.00	33.67
BBBBBATOM	2982	CD	PRO	B	52	-10.667	-44.012	-27.119	1.00	33.29
BBBBBATOM	2983	CA	PRO	B	52	-12.111	-42.601	-28.453	1.00	34.43
BBBBBATOM	2984	CB	PRO	B	52	-12.915	-43.465	-27.489	1.00	34.36
BBBBBATOM	2985	CG	PRO	B	52	-12.021	-44.661	-27.307	1.00	33.77
BBBBBATOM	2986	C	PRO	B	52	-12.422	-41.111	-28.294	1.00	35.67
BBBBBATOM	2987	O	PRO	B	52	-13.219	-40.548	-29.048	1.00	36.65
BBBBBATOM	2988	N	LYS	B	53	-11.790	-40.478	-27.310	1.00	35.75
BBBBBATOM	2989	CA	LYS	B	53	-11.998	-39.054	-27.064	1.00	36.73
BBBBBATOM	2990	CB	LYS	B	53	-11.334	-38.633	-25.746	1.00	37.14
BBBBBATOM	2991	CG	LYS	B	53	-12.020	-39.207	-24.514	1.00	38.38
BBBBBATOM	2992	CD	LYS	B	53	-11.368	-38.746	-23.218	1.00	39.34
BBBBBATOM	2993	CE	LYS	B	53	-12.057	-39.379	-22.012	1.00	40.74
BBBBBATOM	2994	NZ	LYS	B	53	-11.352	-39.092	-20.725	1.00	40.94
BBBBBATOM	2995	C	LYS	B	53	-11.445	-38.231	-28.220	1.00	36.11
BBBBBATOM	2996	O	LYS	B	53	-11.703	-37.036	-28.323	1.00	36.71

BBBBATOM	2997	N	HIS	B	54	-10.688	-38.881	-29.096	1.00	35.60
BBBBATOM	2998	CA	HIS	B	54	-10.116	-38.212	-30.259	1.00	34.62
BBBBATOM	2999	CB	HIS	B	54	-8.666	-38.647	-30.464	1.00	34.78
BBBBATOM	3000	CG	HIS	B	54	-7.676	-37.810	-29.721	1.00	33.79
BBBBATOM	3001	CD2	HIS	B	54	-7.360	-37.760	-28.406	1.00	33.76
BBBBATOM	3002	ND1	HIS	B	54	-6.884	-36.869	-30.343	1.00	34.27
BBBBATOM	3003	CE1	HIS	B	54	-6.120	-36.277	-29.441	1.00	34.41
BBBBATOM	3004	NE2	HIS	B	54	-6.390	-36.799	-28.258	1.00	33.91
BBBBATOM	3005	C	HIS	B	54	-10.919	-38.524	-31.512	1.00	34.28
BBBBATOM	3006	O	HIS	B	54	-10.487	-38.224	-32.620	1.00	34.99
BBBBATOM	3007	N	GLY	B	55	-12.082	-39.140	-31.325	1.00	34.47
BBBBATOM	3008	CA	GLY	B	55	-12.938	-39.481	-32.447	1.00	35.34
BBBBATOM	3009	C	GLY	B	55	-12.427	-40.619	-33.310	1.00	36.18
BBBBATOM	3010	O	GLY	B	55	-12.883	-40.799	-34.442	1.00	35.99
BBBBATOM	3011	N	ILE	B	56	-11.490	-41.399	-32.776	1.00	35.32
BBBBATOM	3012	CA	ILE	B	56	-10.909	-42.517	-33.514	1.00	33.81
BBBBATOM	3013	CB	ILE	B	56	-9.374	-42.445	-33.462	1.00	33.36
BBBBATOM	3014	CG2	ILE	B	56	-8.761	-43.602	-34.245	1.00	32.87
BBBBATOM	3015	CG1	ILE	B	56	-8.916	-41.097	-34.029	1.00	32.05
BBBBATOM	3016	CD1	ILE	B	56	-7.461	-40.792	-33.818	1.00	30.35
BBBBATOM	3017	C	ILE	B	56	-11.375	-43.859	-32.956	1.00	34.45
BBBBATOM	3018	O	ILE	B	56	-11.394	-44.069	-31.738	1.00	34.26
BBBBATOM	3019	N	GLU	B	57	-11.764	-44.758	-33.855	1.00	33.40
BBBBATOM	3020	CA	GLU	B	57	-12.228	-46.083	-33.467	1.00	34.16
BBBBATOM	3021	CB	GLU	B	57	-12.905	-46.769	-34.651	1.00	37.41
BBBBATOM	3022	CG	GLU	B	57	-14.064	-45.982	-35.244	1.00	42.10
BBBBATOM	3023	CD	GLU	B	57	-14.653	-46.659	-36.465	1.00	45.50
BBBBATOM	3024	OE1	GLU	B	57	-13.903	-46.875	-37.448	1.00	46.39
BBBBATOM	3025	OE2	GLU	B	57	-15.866	-46.977	-36.441	1.00	48.36
BBBBATOM	3026	C	GLU	B	57	-11.044	-46.923	-33.005	1.00	33.01
BBBBATOM	3027	O	GLU	B	57	-9.931	-46.769	-33.504	1.00	31.58
BBBBATOM	3028	N	ILE	B	58	-11.287	-47.817	-32.056	1.00	31.85
BBBBATOM	3029	CA	ILE	B	58	-10.217	-48.658	-31.553	1.00	31.38
BBBBATOM	3030	CB	ILE	B	58	-9.651	-48.099	-30.223	1.00	30.95
BBBBATOM	3031	CG2	ILE	B	58	-10.769	-47.946	-29.205	1.00	31.48
BBBBATOM	3032	CG1	ILE	B	58	-8.553	-49.030	-29.690	1.00	31.13
BBBBATOM	3033	CD1	ILE	B	58	-7.736	-48.437	-28.572	1.00	29.87
BBBBATOM	3034	C	ILE	B	58	-10.647	-50.102	-31.357	1.00	31.67
BBBBATOM	3035	O	ILE	B	58	-11.716	-50.384	-30.801	1.00	30.68
BBBBATOM	3036	N	ASP	B	59	-9.807	-51.011	-31.844	1.00	30.76
BBBBATOM	3037	CA	ASP	B	59	-10.039	-52.442	-31.720	1.00	31.09
BBBBATOM	3038	CB	ASP	B	59	-9.732	-53.153	-33.037	1.00	31.37
BBBBATOM	3039	CG	ASP	B	59	-10.766	-52.863	-34.104	1.00	32.68
BBBBATOM	3040	OD1	ASP	B	59	-11.969	-53.037	-33.812	1.00	32.40
BBBBATOM	3041	OD2	ASP	B	59	-10.378	-52.468	-35.224	1.00	33.40
BBBBATOM	3042	C	ASP	B	59	-9.119	-52.950	-30.618	1.00	30.50
BBBBATOM	3043	O	ASP	B	59	-7.987	-52.491	-30.492	1.00	30.24
BBBBATOM	3044	N	PHE	B	60	-9.608	-53.888	-29.815	1.00	30.65
BBBBATOM	3045	CA	PHE	B	60	-8.809	-54.410	-28.713	1.00	30.32
BBBBATOM	3046	CB	PHE	B	60	-9.560	-54.239	-27.385	1.00	30.74
BBBBATOM	3047	CG	PHE	B	60	-9.925	-52.815	-27.058	1.00	32.14
BBBBATOM	3048	CD1	PHE	B	60	-11.250	-52.392	-27.129	1.00	33.15
BBBBATOM	3049	CD2	PHE	B	60	-8.955	-51.908	-26.649	1.00	31.57
BBBBATOM	3050	CE1	PHE	B	60	-11.605	-51.083	-26.791	1.00	34.05
BBBBATOM	3051	CE2	PHE	B	60	-9.294	-50.598	-26.310	1.00	33.00
BBBBATOM	3052	CZ	PHE	B	60	-10.626	-50.185	-26.380	1.00	33.82
BBBBATOM	3053	C	PHE	B	60	-8.430	-55.878	-28.846	1.00	29.86
BBBBATOM	3054	O	PHE	B	60	-9.154	-56.668	-29.445	1.00	29.93
BBBBATOM	3055	N	ILE	B	61	-7.271	-56.229	-28.295	1.00	29.38
BBBBATOM	3056	CA	ILE	B	61	-6.832	-57.616	-28.269	1.00	28.55
BBBBATOM	3057	CB	ILE	B	61	-5.674	-57.923	-29.258	1.00	28.48
BBBBATOM	3058	CG2	ILE	B	61	-6.123	-57.650	-30.694	1.00	27.65
BBBBATOM	3059	CG1	ILE	B	61	-4.422	-57.126	-28.892	1.00	26.70
BBBBATOM	3060	CD1	ILE	B	61	-3.177	-57.615	-29.638	1.00	27.03
BBBBATOM	3061	C	ILE	B	61	-6.344	-57.855	-26.848	1.00	29.13
BBBBATOM	3062	O	ILE	B	61	-6.124	-56.906	-26.091	1.00	28.80

BBBBBATOM	3063	N	ARG	B	62	-6.186	-59.116	-26.473	1.00	29.38
BBBBBATOM	3064	CA	ARG	B	62	-5.709	-59.416	-25.133	1.00	30.76
BBBBBATOM	3065	CB	ARG	B	62	-6.630	-60.447	-24.461	1.00	32.36
BBBBBATOM	3066	CG	ARG	B	62	-6.130	-60.955	-23.114	1.00	35.99
BBBBBATOM	3067	CD	ARG	B	62	-5.438	-59.859	-22.311	1.00	37.86
BBBBBATOM	3068	NE	ARG	B	62	-6.297	-58.718	-22.004	1.00	40.01
BBBBBATOM	3069	CZ	ARG	B	62	-5.840	-57.504	-21.711	1.00	39.09
BBBBBATOM	3070	NH1	ARG	B	62	-4.536	-57.275	-21.690	1.00	39.24
BBBBBATOM	3071	NH2	ARG	B	62	-6.686	-56.518	-21.439	1.00	40.03
BBBBBATOM	3072	C	ARG	B	62	-4.274	-59.923	-25.156	1.00	29.32
BBBBBATOM	3073	O	ARG	B	62	-3.933	-60.809	-25.934	1.00	28.65
BBBBBATOM	3074	N	ILE	B	63	-3.428	-59.342	-24.313	1.00	30.07
BBBBBATOM	3075	CA	ILE	B	63	-2.036	-59.770	-24.231	1.00	31.38
BBBBBATOM	3076	CB	ILE	B	63	-1.081	-58.745	-24.883	1.00	30.06
BBBBBATOM	3077	CG2	ILE	B	63	-1.442	-58.567	-26.353	1.00	30.41
BBBBBATOM	3078	CG1	ILE	B	63	-1.143	-57.411	-24.137	1.00	29.94
BBBBBATOM	3079	CD1	ILE	B	63	-0.128	-56.384	-24.632	1.00	29.62
BBBBBATOM	3080	C	ILE	B	63	-1.623	-59.981	-22.775	1.00	33.08
BBBBBATOM	3081	O	ILE	B	63	-0.444	-59.872	-22.430	1.00	33.21
BBBBBATOM	3082	N	SER	B	64	-2.603	-60.284	-21.927	1.00	35.38
BBBBBATOM	3083	CA	SER	B	64	-2.356	-60.520	-20.505	1.00	37.51
BBBBBATOM	3084	CB	SER	B	64	-3.652	-60.912	-19.792	1.00	38.82
BBBBBATOM	3085	OG	SER	B	64	-4.558	-59.823	-19.750	1.00	42.88
BBBBBATOM	3086	C	SER	B	64	-1.326	-61.622	-20.311	1.00	37.32
BBBBBATOM	3087	O	SER	B	64	-1.411	-62.682	-20.933	1.00	37.86
BBBBBATOM	3088	N	GLY	B	65	-0.356	-61.370	-19.441	1.00	37.81
BBBBBATOM	3089	CA	GLY	B	65	0.679	-62.355	-19.199	1.00	37.13
BBBBBATOM	3090	C	GLY	B	65	1.798	-62.283	-20.226	1.00	36.76
BBBBBATOM	3091	O	GLY	B	65	2.858	-62.889	-20.038	1.00	37.57
BBBBBATOM	3092	N	LEU	B	66	1.577	-61.539	-21.307	1.00	34.63
BBBBBATOM	3093	CA	LEU	B	66	2.591	-61.413	-22.355	1.00	33.17
BBBBBATOM	3094	CB	LEU	B	66	1.936	-61.470	-23.735	1.00	32.08
BBBBBATOM	3095	CG	LEU	B	66	1.162	-62.747	-24.061	1.00	32.52
BBBBBATOM	3096	CD1	LEU	B	66	0.563	-62.626	-25.445	1.00	31.38
BBBBBATOM	3097	CD2	LEU	B	66	2.093	-63.957	-23.984	1.00	31.67
BBBBBATOM	3098	C	LEU	B	66	3.414	-60.133	-22.246	1.00	32.72
BBBBBATOM	3099	O	LEU	B	66	4.451	-60.002	-22.893	1.00	33.13
BBBBBATOM	3100	N	ARG	B	67	2.953	-59.185	-21.440	1.00	31.54
BBBBBATOM	3101	CA	ARG	B	67	3.671	-57.928	-21.277	1.00	30.90
BBBBBATOM	3102	CB	ARG	B	67	2.888	-56.984	-20.363	1.00	32.28
BBBBBATOM	3103	CG	ARG	B	67	1.540	-56.576	-20.913	1.00	34.65
BBBBBATOM	3104	CD	ARG	B	67	0.926	-55.440	-20.097	1.00	36.69
BBBBBATOM	3105	NE	ARG	B	67	-0.259	-54.889	-20.748	1.00	38.28
BBBBBATOM	3106	CZ	ARG	B	67	-1.425	-55.519	-20.853	1.00	39.05
BBBBBATOM	3107	NH1	ARG	B	67	-1.583	-56.734	-20.341	1.00	39.61
BBBBBATOM	3108	NH2	ARG	B	67	-2.434	-54.935	-21.487	1.00	39.52
BBBBBATOM	3109	C	ARG	B	67	5.071	-58.142	-20.713	1.00	29.99
BBBBBATOM	3110	O	ARG	B	67	5.294	-59.034	-19.889	1.00	28.67
BBBBBATOM	3111	N	GLY	B	68	6.014	-57.321	-21.165	1.00	27.75
BBBBBATOM	3112	CA	GLY	B	68	7.380	-57.427	-20.685	1.00	26.79
BBBBBATOM	3113	C	GLY	B	68	8.166	-58.579	-21.280	1.00	25.41
BBBBBATOM	3114	O	GLY	B	68	9.326	-58.779	-20.943	1.00	26.04
BBBBBATOM	3115	N	LYS	B	69	7.546	-59.342	-22.170	1.00	24.55
BBBBBATOM	3116	CA	LYS	B	69	8.238	-60.463	-22.796	1.00	23.93
BBBBBATOM	3117	CB	LYS	B	69	7.284	-61.641	-23.033	1.00	24.12
BBBBBATOM	3118	CG	LYS	B	69	6.757	-62.360	-21.794	1.00	25.08
BBBBBATOM	3119	CD	LYS	B	69	5.887	-63.553	-22.224	1.00	25.44
BBBBBATOM	3120	CE	LYS	B	69	5.357	-64.358	-21.035	1.00	28.31
BBBBBATOM	3121	NZ	LYS	B	69	6.468	-64.877	-20.175	1.00	29.71
BBBBBATOM	3122	C	LYS	B	69	8.825	-60.062	-24.142	1.00	23.32
BBBBBATOM	3123	O	LYS	B	69	8.151	-59.404	-24.944	1.00	21.96
BBBBBATOM	3124	N	GLY	B	70	10.075	-60.470	-24.374	1.00	22.48
BBBBBATOM	3125	CA	GLY	B	70	10.755	-60.229	-25.636	1.00	22.26
BBBBBATOM	3126	C	GLY	B	70	10.308	-61.337	-26.388	1.00	22.17
BBBBBATOM	3127	O	GLY	B	70	9.512	-62.183	-26.195	1.00	21.62
BBBBBATOM	3128	N	ILE	B	71	10.819	-61.373	-27.814	1.00	21.85

BBBBATOM	3129	CA	ILE	B	71	10.357	-62.386	-28.762	1.00	23.55
BBBBATOM	3130	CB	ILE	B	71	10.926	-62.142	-30.181	1.00	23.52
BBBBATOM	3131	CG2	ILE	B	71	12.435	-62.375	-30.192	1.00	25.96
BBBBATOM	3132	CG1	ILE	B	71	10.264	-63.096	-31.182	1.00	24.18
BBBBATOM	3133	CD1	ILE	B	71	8.745	-62.981	-31.263	1.00	25.73
BBBBATOM	3134	C	ILE	B	71	10.616	-63.840	-28.359	1.00	23.88
BBBBATOM	3135	O	ILE	B	71	9.775	-64.707	-28.592	1.00	21.66
BBBBATOM	3136	N	LYS	B	72	11.764	-64.119	-27.751	1.00	23.82
BBBBATOM	3137	CA	LYS	B	72	12.038	-65.491	-27.343	1.00	24.92
BBBBATOM	3138	CB	LYS	B	72	13.491	-65.634	-26.875	1.00	26.86
BBBBATOM	3139	CG	LYS	B	72	14.496	-65.590	-28.019	1.00	31.29
BBBBATOM	3140	CD	LYS	B	72	15.925	-65.791	-27.518	1.00	36.00
BBBBATOM	3141	CE	LYS	B	72	16.926	-65.816	-28.671	1.00	38.82
BBBBATOM	3142	NZ	LYS	B	72	18.342	-65.957	-28.192	1.00	41.21
BBBBATOM	3143	C	LYS	B	72	11.068	-65.925	-26.245	1.00	23.73
BBBBATOM	3144	O	LYS	B	72	10.592	-67.062	-26.245	1.00	24.08
BBBBATOM	3145	N	ALA	B	73	10.765	-65.016	-25.322	1.00	21.62
BBBBATOM	3146	CA	ALA	B	73	9.839	-65.306	-24.233	1.00	21.18
BBBBATOM	3147	CB	ALA	B	73	9.895	-64.196	-23.187	1.00	22.25
BBBBATOM	3148	C	ALA	B	73	8.412	-65.454	-24.771	1.00	20.36
BBBBATOM	3149	O	ALA	B	73	7.619	-66.250	-24.267	1.00	18.97
BBBBATOM	3150	N	LEU	B	74	8.076	-64.673	-25.791	1.00	20.23
BBBBATOM	3151	CA	LEU	B	74	6.745	-64.762	-26.387	1.00	19.36
BBBBATOM	3152	CB	LEU	B	74	6.540	-63.643	-27.417	1.00	18.42
BBBBATOM	3153	CG	LEU	B	74	6.422	-62.208	-26.884	1.00	18.80
BBBBATOM	3154	CD1	LEU	B	74	6.473	-61.197	-28.039	1.00	19.86
BBBBATOM	3155	CD2	LEU	B	74	5.109	-62.071	-26.104	1.00	19.45
BBBBATOM	3156	C	LEU	B	74	6.549	-66.110	-27.069	1.00	19.37
BBBBATOM	3157	O	LEU	B	74	5.539	-66.779	-26.863	1.00	20.01
BBBBATOM	3158	N	ILE	B	75	7.520	-66.507	-27.883	1.00	20.59
BBBBATOM	3159	CA	ILE	B	75	7.434	-67.768	-28.601	1.00	21.18
BBBBATOM	3160	CB	ILE	B	75	8.571	-67.896	-29.641	1.00	22.95
BBBBATOM	3161	CG2	ILE	B	75	8.334	-69.108	-30.527	1.00	25.38
BBBBATOM	3162	CG1	ILE	B	75	8.598	-66.657	-30.540	1.00	26.82
BBBBATOM	3163	CD1	ILE	B	75	7.304	-66.442	-31.327	1.00	28.48
BBBBATOM	3164	C	ILE	B	75	7.488	-68.942	-27.624	1.00	21.20
BBBBATOM	3165	O	ILE	B	75	7.125	-70.063	-27.979	1.00	21.59
BBBBATOM	3166	N	ALA	B	76	7.940	-68.680	-26.399	1.00	20.49
BBBBATOM	3167	CA	ALA	B	76	7.996	-69.726	-25.374	1.00	21.72
BBBBATOM	3168	CB	ALA	B	76	9.026	-69.372	-24.305	1.00	21.92
BBBBATOM	3169	C	ALA	B	76	6.624	-69.904	-24.732	1.00	21.54
BBBBATOM	3170	O	ALA	B	76	6.441	-70.778	-23.875	1.00	20.75
BBBBATOM	3171	N	ALA	B	77	5.668	-69.066	-25.145	1.00	20.61
BBBBATOM	3172	CA	ALA	B	77	4.289	-69.121	-24.655	1.00	21.07
BBBBATOM	3173	CB	ALA	B	77	3.937	-67.830	-23.924	1.00	20.10
BBBBATOM	3174	C	ALA	B	77	3.383	-69.298	-25.881	1.00	21.69
BBBBATOM	3175	O	ALA	B	77	2.567	-68.430	-26.199	1.00	21.93
BBBBATOM	3176	N	PRO	B	78	3.507	-70.446	-26.564	1.00	22.38
BBBBATOM	3177	CD	PRO	B	78	4.211	-71.603	-25.976	1.00	21.89
BBBBATOM	3178	CA	PRO	B	78	2.772	-70.846	-27.771	1.00	20.95
BBBBATOM	3179	CB	PRO	B	78	3.027	-72.350	-27.861	1.00	22.21
BBBBATOM	3180	CG	PRO	B	78	4.288	-72.547	-27.117	1.00	24.07
BBBBATOM	3181	C	PRO	B	78	1.278	-70.535	-27.813	1.00	21.19
BBBBATOM	3182	O	PRO	B	78	0.789	-69.939	-28.776	1.00	19.68
BBBBATOM	3183	N	LEU	B	79	0.544	-70.961	-26.790	1.00	21.21
BBBBATOM	3184	CA	LEU	B	79	-0.896	-70.728	-26.783	1.00	21.32
BBBBATOM	3185	CB	LEU	B	79	-1.569	-71.476	-25.630	1.00	20.99
BBBBATOM	3186	CG	LEU	B	79	-1.397	-72.988	-25.617	1.00	22.40
BBBBATOM	3187	CD1	LEU	B	79	-2.504	-73.619	-24.772	1.00	22.01
BBBBATOM	3188	CD2	LEU	B	79	-1.438	-73.521	-27.021	1.00	23.82
BBBBATOM	3189	C	LEU	B	79	-1.275	-69.263	-26.707	1.00	21.17
BBBBATOM	3190	O	LEU	B	79	-2.125	-68.800	-27.481	1.00	20.44
BBBBATOM	3191	N	ARG	B	80	-0.656	-68.529	-25.788	1.00	20.91
BBBBATOM	3192	CA	ARG	B	80	-0.980	-67.115	-25.637	1.00	21.30
BBBBATOM	3193	CB	ARG	B	80	-0.444	-66.583	-24.312	1.00	22.12
BBBBATOM	3194	CG	ARG	B	80	-1.286	-67.051	-23.118	1.00	24.03

BBBBBATOM	3195	CD	ARG	B	80	-0.610	-66.738	-21.807	1.00	23.42
BBBBBATOM	3196	NE	ARG	B	80	0.581	-67.556	-21.610	1.00	24.59
BBBBBATOM	3197	CZ	ARG	B	80	1.466	-67.351	-20.642	1.00	26.08
BBBBBATOM	3198	NH1	ARG	B	80	1.290	-66.349	-19.787	1.00	26.92
BBBBBATOM	3199	NH2	ARG	B	80	2.514	-68.152	-20.519	1.00	27.22
BBBBBATOM	3200	C	ARG	B	80	-0.526	-66.233	-26.790	1.00	21.29
BBBBBATOM	3201	O	ARG	B	80	-1.278	-65.355	-27.223	1.00	21.47
BBBBBATOM	3202	N	ILE	B	81	0.683	-66.448	-27.303	1.00	19.29
BBBBBATOM	3203	CA	ILE	B	81	1.113	-65.621	-28.421	1.00	19.47
BBBBBATOM	3204	CB	ILE	B	81	2.639	-65.793	-28.730	1.00	17.92
BBBBBATOM	3205	CG2	ILE	B	81	2.949	-67.200	-29.206	1.00	17.33
BBBBBATOM	3206	CG1	ILE	B	81	3.067	-64.753	-29.769	1.00	18.63
BBBBBATOM	3207	CD1	ILE	B	81	2.746	-63.318	-29.346	1.00	17.46
BBBBBATOM	3208	C	ILE	B	81	0.256	-65.937	-29.654	1.00	18.99
BBBBBATOM	3209	O	ILE	B	81	-0.149	-65.028	-30.378	1.00	19.38
BBBBBATOM	3210	N	PHE	B	82	-0.056	-67.211	-29.880	1.00	19.39
BBBBBATOM	3211	CA	PHE	B	82	-0.875	-67.582	-31.038	1.00	19.15
BBBBBATOM	3212	CB	PHE	B	82	-1.057	-69.103	-31.136	1.00	19.27
BBBBBATOM	3213	CG	PHE	B	82	-1.811	-69.548	-32.368	1.00	19.87
BBBBBATOM	3214	CD1	PHE	B	82	-1.180	-69.602	-33.603	1.00	20.87
BBBBBATOM	3215	CD2	PHE	B	82	-3.154	-69.898	-32.289	1.00	21.11
BBBBBATOM	3216	CE1	PHE	B	82	-1.872	-70.002	-34.753	1.00	21.20
BBBBBATOM	3217	CE2	PHE	B	82	-3.857	-70.297	-33.429	1.00	22.26
BBBBBATOM	3218	CZ	PHE	B	82	-3.212	-70.349	-34.663	1.00	22.14
BBBBBATOM	3219	C	PHE	B	82	-2.250	-66.931	-30.959	1.00	19.94
BBBBBATOM	3220	O	PHE	B	82	-2.777	-66.444	-31.970	1.00	19.64
BBBBBATOM	3221	N	ASN	B	83	-2.832	-66.923	-29.764	1.00	19.29
BBBBBATOM	3222	CA	ASN	B	83	-4.150	-66.332	-29.577	1.00	20.90
BBBBBATOM	3223	CB	ASN	B	83	-4.693	-66.641	-28.178	1.00	20.55
BBBBBATOM	3224	CG	ASN	B	83	-6.158	-66.244	-28.028	1.00	22.79
BBBBBATOM	3225	OD1	ASN	B	83	-6.505	-65.374	-27.229	1.00	25.14
BBBBBATOM	3226	ND2	ASN	B	83	-7.018	-66.877	-28.807	1.00	20.47
BBBBBATOM	3227	C	ASN	B	83	-4.178	-64.821	-29.812	1.00	20.83
BBBBBATOM	3228	O	ASN	B	83	-5.086	-64.316	-30.472	1.00	21.92
BBBBBATOM	3229	N	ALA	B	84	-3.203	-64.092	-29.275	1.00	19.74
BBBBBATOM	3230	CA	ALA	B	84	-3.177	-62.647	-29.484	1.00	19.30
BBBBBATOM	3231	CB	ALA	B	84	-2.060	-62.008	-28.662	1.00	18.59
BBBBBATOM	3232	C	ALA	B	84	-2.967	-62.380	-30.981	1.00	19.94
BBBBBATOM	3233	O	ALA	B	84	-3.561	-61.459	-31.552	1.00	19.69
BBBBBATOM	3234	N	TRP	B	85	-2.118	-63.197	-31.603	1.00	19.77
BBBBBATOM	3235	CA	TRP	B	85	-1.820	-63.111	-33.032	1.00	20.56
BBBBBATOM	3236	CB	TRP	B	85	-0.754	-64.148	-33.396	1.00	21.46
BBBBBATOM	3237	CG	TRP	B	85	-0.365	-64.167	-34.856	1.00	23.00
BBBBBATOM	3238	CD2	TRP	B	85	-0.588	-65.232	-35.785	1.00	23.69
BBBBBATOM	3239	CE2	TRP	B	85	-0.024	-64.835	-37.022	1.00	24.14
BBBBBATOM	3240	CE3	TRP	B	85	-1.206	-66.486	-35.693	1.00	24.79
BBBBBATOM	3241	CD1	TRP	B	85	0.301	-63.189	-35.548	1.00	23.17
BBBBBATOM	3242	NE1	TRP	B	85	0.509	-63.585	-36.848	1.00	24.28
BBBBBATOM	3243	CZ2	TRP	B	85	-0.060	-65.650	-38.160	1.00	24.90
BBBBBATOM	3244	CZ3	TRP	B	85	-1.243	-67.299	-36.827	1.00	25.45
BBBBBATOM	3245	CH2	TRP	B	85	-0.671	-66.875	-38.045	1.00	25.15
BBBBBATOM	3246	C	TRP	B	85	-3.090	-63.354	-33.865	1.00	21.76
BBBBBATOM	3247	O	TRP	B	85	-3.339	-62.658	-34.859	1.00	20.40
BBBBBATOM	3248	N	ARG	B	86	-3.885	-64.346	-33.467	1.00	22.03
BBBBBATOM	3249	CA	ARG	B	86	-5.140	-64.660	-34.166	1.00	23.28
BBBBBATOM	3250	CB	ARG	B	86	-5.754	-65.965	-33.623	1.00	24.72
BBBBBATOM	3251	CG	ARG	B	86	-4.999	-67.236	-34.021	1.00	27.21
BBBBBATOM	3252	CD	ARG	B	86	-5.368	-67.725	-35.418	1.00	29.60
BBBBBATOM	3253	NE	ARG	B	86	-6.626	-68.477	-35.422	1.00	31.45
BBBBBATOM	3254	CZ	ARG	B	86	-7.185	-69.004	-36.508	1.00	31.37
BBBBBATOM	3255	NH1	ARG	B	86	-6.607	-68.862	-37.696	1.00	32.19
BBBBBATOM	3256	NH2	ARG	B	86	-8.314	-69.694	-36.405	1.00	31.39
BBBBBATOM	3257	C	ARG	B	86	-6.151	-63.517	-34.007	1.00	22.98
BBBBBATOM	3258	O	ARG	B	86	-6.890	-63.195	-34.942	1.00	21.37
BBBBBATOM	3259	N	GLN	B	87	-6.190	-62.916	-32.821	1.00	22.90
BBBBBATOM	3260	CA	GLN	B	87	-7.101	-61.802	-32.567	1.00	24.07

BBBBATOM	3261	CB	GLN	B	87	-7.046	-61.382	-31.097	1.00	24.33
BBBBATOM	3262	CG	GLN	B	87	-7.873	-62.280	-30.187	1.00	27.24
BBBBATOM	3263	CD	GLN	B	87	-7.720	-61.943	-28.723	1.00	28.81
BBBBATOM	3264	OE1	GLN	B	87	-8.567	-62.296	-27.908	1.00	33.25
BBBBATOM	3265	NE2	GLN	B	87	-6.632	-61.275	-28.375	1.00	29.95
BBBBATOM	3266	C	GLN	B	87	-6.738	-60.618	-33.457	1.00	23.85
BBBBATOM	3267	O	GLN	B	87	-7.613	-60.012	-34.077	1.00	24.02
BBBBATOM	3268	N	ALA	B	88	-5.449	-60.293	-33.521	1.00	23.39
BBBBATOM	3269	CA	ALA	B	88	-4.996	-59.183	-34.355	1.00	23.78
BBBBATOM	3270	CB	ALA	B	88	-3.508	-58.909	-34.116	1.00	23.33
BBBBATOM	3271	C	ALA	B	88	-5.257	-59.485	-35.831	1.00	24.73
BBBBATOM	3272	O	ALA	B	88	-5.655	-58.595	-36.592	1.00	24.72
BBBBATOM	3273	N	ARG	B	89	-5.038	-60.735	-36.244	1.00	24.26
BBBBATOM	3274	CA	ARG	B	89	-5.285	-61.111	-37.636	1.00	24.94
BBBBATOM	3275	CB	ARG	B	89	-4.904	-62.575	-37.893	1.00	25.14
BBBBATOM	3276	CG	ARG	B	89	-3.461	-62.774	-38.353	1.00	24.54
BBBBATOM	3277	CD	ARG	B	89	-3.142	-64.253	-38.510	1.00	25.50
BBBBATOM	3278	NE	ARG	B	89	-3.809	-64.901	-39.641	1.00	24.93
BBBBATOM	3279	CZ	ARG	B	89	-3.329	-64.930	-40.882	1.00	25.90
BBBBATOM	3280	NH1	ARG	B	89	-2.178	-64.336	-41.170	1.00	25.98
BBBBATOM	3281	NH2	ARG	B	89	-3.979	-65.596	-41.831	1.00	26.36
BBBBATOM	3282	C	ARG	B	89	-6.752	-60.909	-38.013	1.00	25.29
BBBBATOM	3283	O	ARG	B	89	-7.056	-60.420	-39.104	1.00	24.27
BBBBATOM	3284	N	ALA	B	90	-7.658	-61.296	-37.118	1.00	24.61
BBBBATOM	3285	CA	ALA	B	90	-9.088	-61.151	-37.383	1.00	26.16
BBBBATOM	3286	CB	ALA	B	90	-9.907	-61.775	-36.254	1.00	25.77
BBBBATOM	3287	C	ALA	B	90	-9.440	-59.673	-37.538	1.00	26.83
BBBBATOM	3288	O	ALA	B	90	-10.213	-59.301	-38.421	1.00	27.71
BBBBATOM	3289	N	ILE	B	91	-8.862	-58.837	-36.685	1.00	26.92
BBBBATOM	3290	CA	ILE	B	91	-9.108	-57.400	-36.733	1.00	26.97
BBBBATOM	3291	CB	ILE	B	91	-8.408	-56.682	-35.565	1.00	27.03
BBBBATOM	3292	CG2	ILE	B	91	-8.327	-55.175	-35.837	1.00	25.82
BBBBATOM	3293	CG1	ILE	B	91	-9.161	-56.962	-34.260	1.00	24.58
BBBBATOM	3294	CD1	ILE	B	91	-8.435	-56.490	-33.021	1.00	24.65
BBBBATOM	3295	C	ILE	B	91	-8.618	-56.787	-38.040	1.00	28.07
BBBBATOM	3296	O	ILE	B	91	-9.289	-55.934	-38.629	1.00	28.41
BBBBATOM	3297	N	MET	B	92	-7.451	-57.227	-38.496	1.00	27.92
BBBBATOM	3298	CA	MET	B	92	-6.872	-56.693	-39.717	1.00	29.03
BBBBATOM	3299	CB	MET	B	92	-5.366	-56.912	-39.712	1.00	27.34
BBBBATOM	3300	CG	MET	B	92	-4.686	-56.235	-38.536	1.00	26.09
BBBBATOM	3301	SD	MET	B	92	-2.919	-56.413	-38.602	1.00	25.72
BBBBATOM	3302	CE	MET	B	92	-2.413	-55.394	-37.218	1.00	24.09
BBBBATOM	3303	C	MET	B	92	-7.488	-57.257	-40.988	1.00	30.07
BBBBATOM	3304	O	MET	B	92	-7.417	-56.628	-42.046	1.00	30.66
BBBBATOM	3305	N	LYS	B	93	-8.082	-58.441	-40.894	1.00	30.96
BBBBATOM	3306	CA	LYS	B	93	-8.735	-59.038	-42.050	1.00	33.20
BBBBATOM	3307	CB	LYS	B	93	-8.969	-60.537	-41.826	1.00	34.31
BBBBATOM	3308	CG	LYS	B	93	-7.689	-61.369	-41.860	1.00	36.71
BBBBATOM	3309	CD	LYS	B	93	-7.956	-62.847	-41.576	1.00	38.43
BBBBATOM	3310	CE	LYS	B	93	-8.781	-63.491	-42.683	1.00	38.82
BBBBATOM	3311	NZ	LYS	B	93	-9.197	-64.881	-42.344	1.00	40.70
BBBBATOM	3312	C	LYS	B	93	-10.067	-58.314	-42.252	1.00	33.65
BBBBATOM	3313	O	LYS	B	93	-10.524	-58.143	-43.382	1.00	34.76
BBBBATOM	3314	N	ALA	B	94	-10.672	-57.877	-41.147	1.00	33.00
BBBBATOM	3315	CA	ALA	B	94	-11.943	-57.157	-41.183	1.00	33.62
BBBBATOM	3316	CB	ALA	B	94	-12.641	-57.260	-39.833	1.00	33.62
BBBBATOM	3317	C	ALA	B	94	-11.752	-55.684	-41.559	1.00	33.95
BBBBATOM	3318	O	ALA	B	94	-12.484	-55.153	-42.397	1.00	33.20
BBBBATOM	3319	N	TYR	B	95	-10.772	-55.028	-40.943	1.00	33.15
BBBBATOM	3320	CA	TYR	B	95	-10.504	-53.620	-41.224	1.00	33.83
BBBBATOM	3321	CB	TYR	B	95	-9.722	-52.992	-40.060	1.00	33.92
BBBBATOM	3322	CG	TYR	B	95	-9.383	-51.525	-40.249	1.00	34.38
BBBBATOM	3323	CD1	TYR	B	95	-10.381	-50.585	-40.499	1.00	36.04
BBBBATOM	3324	CE1	TYR	B	95	-10.071	-49.240	-40.702	1.00	36.49
BBBBATOM	3325	CD2	TYR	B	95	-8.063	-51.082	-40.202	1.00	34.89
BBBBATOM	3326	CE2	TYR	B	95	-7.741	-49.741	-40.401	1.00	35.72

BBBBATOM	3327	CZ	TYR	B	95	-8.750	-48.826	-40.655	1.00	36.79
BBBBATOM	3328	OH	TYR	B	95	-8.436	-47.502	-40.874	1.00	37.60
BBBBATOM	3329	C	TYR	B	95	-9.743	-53.418	-42.538	1.00	34.06
BBBBATOM	3330	O	TYR	B	95	-9.919	-52.404	-43.214	1.00	33.85
BBBBATOM	3331	N	LYS	B	96	-8.902	-54.386	-42.896	1.00	33.76
BBBBATOM	3332	CA	LYS	B	96	-8.104	-54.327	-44.122	1.00	33.85
BBBBATOM	3333	CB	LYS	B	96	-9.004	-54.476	-45.353	1.00	35.14
BBBBATOM	3334	CG	LYS	B	96	-9.707	-55.812	-45.463	1.00	37.16
BBBBATOM	3335	CD	LYS	B	96	-10.649	-55.843	-46.661	1.00	38.58
BBBBATOM	3336	CE	LYS	B	96	-11.388	-57.170	-46.752	1.00	40.07
BBBBATOM	3337	NZ	LYS	B	96	-12.319	-57.218	-47.925	1.00	41.29
BBBBATOM	3338	C	LYS	B	96	-7.278	-53.049	-44.262	1.00	33.75
BBBBATOM	3339	O	LYS	B	96	-7.489	-52.258	-45.189	1.00	34.55
BBBBATOM	3340	N	PRO	B	97	-6.326	-52.825	-43.345	1.00	32.59
BBBBATOM	3341	CD	PRO	B	97	-6.004	-53.620	-42.143	1.00	32.37
BBBBATOM	3342	CA	PRO	B	97	-5.490	-51.623	-43.419	1.00	31.82
BBBBATOM	3343	CB	PRO	B	97	-4.850	-51.568	-42.038	1.00	31.66
BBBBATOM	3344	CG	PRO	B	97	-4.686	-53.025	-41.704	1.00	31.53
BBBBATOM	3345	C	PRO	B	97	-4.458	-51.769	-44.530	1.00	31.60
BBBBATOM	3346	O	PRO	B	97	-4.052	-52.881	-44.860	1.00	32.52
BBBBATOM	3347	N	ASP	B	98	-4.037	-50.651	-45.112	1.00	31.25
BBBBATOM	3348	CA	ASP	B	98	-3.049	-50.685	-46.188	1.00	29.78
BBBBATOM	3349	CB	ASP	B	98	-3.234	-49.488	-47.117	1.00	32.00
BBBBATOM	3350	CG	ASP	B	98	-4.562	-49.519	-47.837	1.00	34.21
BBBBATOM	3351	OD1	ASP	B	98	-5.281	-48.498	-47.795	1.00	35.37
BBBBATOM	3352	OD2	ASP	B	98	-4.888	-50.566	-48.443	1.00	35.10
BBBBATOM	3353	C	ASP	B	98	-1.654	-50.660	-45.603	1.00	28.70
BBBBATOM	3354	O	ASP	B	98	-0.672	-50.973	-46.274	1.00	26.48
BBBBATOM	3355	N	VAL	B	99	-1.573	-50.278	-44.337	1.00	26.88
BBBBATOM	3356	CA	VAL	B	99	-0.296	-50.214	-43.660	1.00	26.75
BBBBATOM	3357	CB	VAL	B	99	0.500	-48.973	-44.132	1.00	27.35
BBBBATOM	3358	CG1	VAL	B	99	-0.305	-47.718	-43.867	1.00	29.45
BBBBATOM	3359	CG2	VAL	B	99	1.841	-48.908	-43.443	1.00	27.48
BBBBATOM	3360	C	VAL	B	99	-0.552	-50.134	-42.162	1.00	25.92
BBBBATOM	3361	O	VAL	B	99	-1.585	-49.627	-41.723	1.00	25.04
BBBBATOM	3362	N	VAL	B	100	0.374	-50.664	-41.377	1.00	24.63
BBBBATOM	3363	CA	VAL	B	100	0.227	-50.613	-39.936	1.00	23.59
BBBBATOM	3364	CB	VAL	B	100	0.120	-52.026	-39.327	1.00	24.97
BBBBATOM	3365	CG1	VAL	B	100	0.139	-51.941	-37.811	1.00	24.71
BBBBATOM	3366	CG2	VAL	B	100	-1.172	-52.683	-39.782	1.00	22.62
BBBBATOM	3367	C	VAL	B	100	1.428	-49.881	-39.382	1.00	22.74
BBBBATOM	3368	O	VAL	B	100	2.551	-50.093	-39.830	1.00	24.62
BBBBATOM	3369	N	LEU	B	101	1.178	-49.001	-38.419	1.00	21.89
BBBBATOM	3370	CA	LEU	B	101	2.214	-48.199	-37.797	1.00	21.59
BBBBATOM	3371	CB	LEU	B	101	1.823	-46.716	-37.853	1.00	22.86
BBBBATOM	3372	CG	LEU	B	101	2.850	-45.580	-37.892	1.00	24.72
BBBBATOM	3373	CD1	LEU	B	101	2.237	-44.385	-37.174	1.00	25.30
BBBBATOM	3374	CD2	LEU	B	101	4.168	-45.954	-37.273	1.00	24.45
BBBBATOM	3375	C	LEU	B	101	2.349	-48.604	-36.336	1.00	20.83
BBBBATOM	3376	O	LEU	B	101	1.370	-48.581	-35.595	1.00	21.35
BBBBATOM	3377	N	GLY	B	102	3.556	-48.986	-35.936	1.00	20.96
BBBBATOM	3378	CA	GLY	B	102	3.796	-49.357	-34.549	1.00	19.23
BBBBATOM	3379	C	GLY	B	102	4.655	-48.282	-33.918	1.00	18.45
BBBBATOM	3380	O	GLY	B	102	5.765	-48.016	-34.381	1.00	18.70
BBBBATOM	3381	N	MET	B	103	4.155	-47.660	-32.857	1.00	18.01
BBBBATOM	3382	CA	MET	B	103	4.892	-46.597	-32.191	1.00	18.93
BBBBATOM	3383	CB	MET	B	103	3.928	-45.477	-31.781	1.00	20.02
BBBBATOM	3384	CG	MET	B	103	3.121	-44.888	-32.944	1.00	21.61
BBBBATOM	3385	SD	MET	B	103	4.212	-44.135	-34.157	1.00	23.45
BBBBATOM	3386	CE	MET	B	103	4.718	-42.680	-33.271	1.00	21.40
BBBBATOM	3387	C	MET	B	103	5.612	-47.128	-30.957	1.00	18.98
BBBBATOM	3388	O	MET	B	103	6.134	-46.357	-30.158	1.00	17.96
BBBBATOM	3389	N	GLY	B	104	5.640	-48.450	-30.827	1.00	21.56
BBBBATOM	3390	CA	GLY	B	104	6.275	-49.080	-29.686	1.00	21.89
BBBBATOM	3391	C	GLY	B	104	5.192	-49.614	-28.764	1.00	23.28
BBBBATOM	3392	O	GLY	B	104	4.009	-49.353	-28.980	1.00	22.50

BBBBATOM	3393	N	GLY	B	105	5.583	-50.364	-27.741	1.00	23.01
BBBBATOM	3394	CA	GLY	B	105	4.593	-50.905	-26.827	1.00	23.54
BBBBATOM	3395	C	GLY	B	105	4.358	-52.380	-27.078	1.00	23.17
BBBBATOM	3396	O	GLY	B	105	4.449	-52.844	-28.214	1.00	22.69
BBBBATOM	3397	N	TYR	B	106	4.018	-53.118	-26.026	1.00	22.87
BBBBATOM	3398	CA	TYR	B	106	3.818	-54.554	-26.159	1.00	22.37
BBBBATOM	3399	CB	TYR	B	106	3.632	-55.181	-24.774	1.00	25.08
BBBBATOM	3400	CG	TYR	B	106	4.864	-55.008	-23.929	1.00	28.19
BBBBATOM	3401	CD1	TYR	B	106	4.869	-54.153	-22.830	1.00	31.96
BBBBATOM	3402	CE1	TYR	B	106	6.043	-53.915	-22.108	1.00	33.13
BBBBATOM	3403	CD2	TYR	B	106	6.058	-55.631	-24.282	1.00	31.27
BBBBATOM	3404	CE2	TYR	B	106	7.234	-55.400	-23.569	1.00	32.27
BBBBATOM	3405	CZ	TYR	B	106	7.219	-54.541	-22.487	1.00	33.19
BBBBATOM	3406	OH	TYR	B	106	8.388	-54.291	-21.802	1.00	35.95
BBBBATOM	3407	C	TYR	B	106	2.719	-55.018	-27.100	1.00	20.52
BBBBATOM	3408	O	TYR	B	106	2.867	-56.052	-27.746	1.00	20.50
BBBBATOM	3409	N	VAL	B	107	1.628	-54.270	-27.205	1.00	19.06
BBBBATOM	3410	CA	VAL	B	107	0.557	-54.694	-28.099	1.00	18.06
BBBBATOM	3411	CB	VAL	B	107	-0.690	-53.774	-27.978	1.00	20.95
BBBBATOM	3412	CG1	VAL	B	107	-0.407	-52.407	-28.589	1.00	21.39
BBBBATOM	3413	CG2	VAL	B	107	-1.879	-54.433	-28.658	1.00	21.30
BBBBATOM	3414	C	VAL	B	107	1.015	-54.743	-29.559	1.00	17.45
BBBBATOM	3415	O	VAL	B	107	0.502	-55.536	-30.346	1.00	16.99
BBBBATOM	3416	N	SER	B	108	1.991	-53.916	-29.918	1.00	17.96
BBBBATOM	3417	CA	SER	B	108	2.488	-53.892	-31.290	1.00	19.67
BBBBATOM	3418	CB	SER	B	108	3.424	-52.691	-31.508	1.00	19.56
BBBBATOM	3419	OG	SER	B	108	4.666	-52.824	-30.837	1.00	19.63
BBBBATOM	3420	C	SER	B	108	3.197	-55.187	-31.694	1.00	20.38
BBBBATOM	3421	O	SER	B	108	3.385	-55.449	-32.884	1.00	21.25
BBBBATOM	3422	N	GLY	B	109	3.595	-55.995	-30.710	1.00	19.59
BBBBATOM	3423	CA	GLY	B	109	4.251	-57.256	-31.023	1.00	20.03
BBBBATOM	3424	C	GLY	B	109	3.311	-58.170	-31.792	1.00	19.61
BBBBATOM	3425	O	GLY	B	109	3.579	-58.517	-32.940	1.00	19.24
BBBBATOM	3426	N	PRO	B	110	2.206	-58.606	-31.173	1.00	19.20
BBBBATOM	3427	CD	PRO	B	110	1.914	-58.528	-29.729	1.00	19.94
BBBBATOM	3428	CA	PRO	B	110	1.251	-59.478	-31.855	1.00	18.99
BBBBATOM	3429	CB	PRO	B	110	0.198	-59.737	-30.778	1.00	20.41
BBBBATOM	3430	CG	PRO	B	110	0.998	-59.720	-29.515	1.00	19.81
BBBBATOM	3431	C	PRO	B	110	0.651	-58.761	-33.075	1.00	19.22
BBBBATOM	3432	O	PRO	B	110	0.406	-59.371	-34.116	1.00	17.13
BBBBATOM	3433	N	GLY	B	111	0.407	-57.462	-32.927	1.00	19.03
BBBBATOM	3434	CA	GLY	B	111	-0.160	-56.702	-34.025	1.00	19.60
BBBBATOM	3435	C	GLY	B	111	0.764	-56.714	-35.226	1.00	19.59
BBBBATOM	3436	O	GLY	B	111	0.330	-56.979	-36.339	1.00	21.10
BBBBATOM	3437	N	GLY	B	112	2.043	-56.429	-34.995	1.00	19.78
BBBBATOM	3438	CA	GLY	B	112	3.014	-56.417	-36.074	1.00	19.97
BBBBATOM	3439	C	GLY	B	112	3.147	-57.783	-36.724	1.00	20.43
BBBBATOM	3440	O	GLY	B	112	3.233	-57.896	-37.949	1.00	19.94
BBBBATOM	3441	N	LEU	B	113	3.167	-58.828	-35.903	1.00	19.26
BBBBATOM	3442	CA	LEU	B	113	3.265	-60.184	-36.429	1.00	19.49
BBBBATOM	3443	CB	LEU	B	113	3.405	-61.198	-35.289	1.00	18.38
BBBBATOM	3444	CG	LEU	B	113	4.777	-61.270	-34.605	1.00	20.59
BBBBATOM	3445	CD1	LEU	B	113	4.656	-62.059	-33.311	1.00	20.01
BBBBATOM	3446	CD2	LEU	B	113	5.794	-61.914	-35.538	1.00	20.23
BBBBATOM	3447	C	LEU	B	113	2.040	-60.521	-37.274	1.00	18.73
BBBBATOM	3448	O	LEU	B	113	2.143	-61.252	-38.255	1.00	18.44
BBBBATOM	3449	N	ALA	B	114	0.875	-60.010	-36.892	1.00	18.96
BBBBATOM	3450	CA	ALA	B	114	-0.334	-60.292	-37.661	1.00	18.70
BBBBATOM	3451	CB	ALA	B	114	-1.562	-59.855	-36.889	1.00	16.45
BBBBATOM	3452	C	ALA	B	114	-0.288	-59.578	-39.019	1.00	19.30
BBBBATOM	3453	O	ALA	B	114	-0.602	-60.167	-40.052	1.00	20.62
BBBBATOM	3454	N	ALA	B	115	0.082	-58.303	-39.000	1.00	20.57
BBBBATOM	3455	CA	ALA	B	115	0.167	-57.516	-40.229	1.00	21.84
BBBBATOM	3456	CB	ALA	B	115	0.636	-56.108	-39.911	1.00	19.85
BBBBATOM	3457	C	ALA	B	115	1.140	-58.192	-41.189	1.00	21.58
BBBBATOM	3458	O	ALA	B	115	0.815	-58.464	-42.345	1.00	22.14

BBBBATOM	3459	N	TRP	B	116	2.334	-58.476	-40.688	1.00	22.12
BBBBATOM	3460	CA	TRP	B	116	3.365	-59.126	-41.478	1.00	23.22
BBBBATOM	3461	CB	TRP	B	116	4.584	-59.367	-40.579	1.00	26.08
BBBBATOM	3462	CG	TRP	B	116	5.699	-60.136	-41.204	1.00	27.40
BBBBATOM	3463	CD2	TRP	B	116	6.168	-61.418	-40.793	1.00	28.77
BBBBATOM	3464	CE2	TRP	B	116	7.234	-61.771	-41.655	1.00	30.37
BBBBATOM	3465	CE3	TRP	B	116	5.794	-62.308	-39.778	1.00	30.49
BBBBATOM	3466	CD1	TRP	B	116	6.473	-59.761	-42.271	1.00	28.30
BBBBATOM	3467	NE1	TRP	B	116	7.401	-60.742	-42.547	1.00	29.04
BBBBATOM	3468	CZ2	TRP	B	116	7.929	-62.981	-41.529	1.00	31.08
BBBBATOM	3469	CZ3	TRP	B	116	6.485	-63.510	-39.653	1.00	31.85
BBBBATOM	3470	CH2	TRP	B	116	7.541	-63.834	-40.527	1.00	32.27
BBBBATOM	3471	C	TRP	B	116	2.871	-60.434	-42.123	1.00	23.55
BBBBATOM	3472	O	TRP	B	116	3.048	-60.643	-43.329	1.00	22.19
BBBBATOM	3473	N	SER	B	117	2.231	-61.304	-41.338	1.00	21.35
BBBBATOM	3474	CA	SER	B	117	1.735	-62.573	-41.873	1.00	22.61
BBBBATOM	3475	CB	SER	B	117	1.167	-63.462	-40.756	1.00	20.72
BBBBATOM	3476	OG	SER	B	117	0.010	-62.889	-40.169	1.00	22.72
BBBBATOM	3477	C	SER	B	117	0.665	-62.383	-42.940	1.00	23.56
BBBBATOM	3478	O	SER	B	117	0.463	-63.262	-43.780	1.00	23.11
BBBBATOM	3479	N	LEU	B	118	-0.020	-61.242	-42.905	1.00	24.40
BBBBATOM	3480	CA	LEU	B	118	-1.069	-60.957	-43.882	1.00	25.70
BBBBATOM	3481	CB	LEU	B	118	-2.195	-60.155	-43.227	1.00	25.80
BBBBATOM	3482	CG	LEU	B	118	-3.012	-60.889	-42.159	1.00	26.56
BBBBATOM	3483	CD1	LEU	B	118	-3.905	-59.895	-41.433	1.00	26.62
BBBBATOM	3484	CD2	LEU	B	118	-3.841	-62.000	-42.801	1.00	26.51
BBBBATOM	3485	C	LEU	B	118	-0.539	-60.193	-45.094	1.00	26.87
BBBBATOM	3486	O	LEU	B	118	-1.292	-59.878	-46.021	1.00	26.69
BBBBATOM	3487	N	GLY	B	119	0.755	-59.898	-45.085	1.00	26.39
BBBBATOM	3488	CA	GLY	B	119	1.354	-59.174	-46.192	1.00	27.80
BBBBATOM	3489	C	GLY	B	119	1.142	-57.671	-46.120	1.00	27.64
BBBBATOM	3490	O	GLY	B	119	1.293	-56.972	-47.122	1.00	28.49
BBBBATOM	3491	N	ILE	B	120	0.786	-57.173	-44.940	1.00	25.88
BBBBATOM	3492	CA	ILE	B	120	0.568	-55.744	-44.731	1.00	24.85
BBBBATOM	3493	CB	ILE	B	120	-0.507	-55.497	-43.652	1.00	24.64
BBBBATOM	3494	CG2	ILE	B	120	-0.648	-54.000	-43.397	1.00	24.49
BBBBATOM	3495	CG1	ILE	B	120	-1.839	-56.112	-44.093	1.00	24.61
BBBBATOM	3496	CD1	ILE	B	120	-2.891	-56.170	-42.991	1.00	23.34
BBBBATOM	3497	C	ILE	B	120	1.879	-55.121	-44.272	1.00	24.55
BBBBATOM	3498	O	ILE	B	120	2.465	-55.551	-43.275	1.00	23.69
BBBBATOM	3499	N	PRO	B	121	2.365	-54.098	-44.995	1.00	23.85
BBBBATOM	3500	CD	PRO	B	121	1.780	-53.400	-46.154	1.00	23.64
BBBBATOM	3501	CA	PRO	B	121	3.625	-53.477	-44.591	1.00	22.63
BBBBATOM	3502	CB	PRO	B	121	3.872	-52.440	-45.691	1.00	23.83
BBBBATOM	3503	CG	PRO	B	121	2.485	-52.053	-46.102	1.00	23.96
BBBBATOM	3504	C	PRO	B	121	3.583	-52.869	-43.196	1.00	22.21
BBBBATOM	3505	O	PRO	B	121	2.617	-52.208	-42.810	1.00	22.46
BBBBATOM	3506	N	VAL	B	122	4.641	-53.114	-42.437	1.00	21.69
BBBBATOM	3507	CA	VAL	B	122	4.743	-52.594	-41.083	1.00	22.03
BBBBATOM	3508	CB	VAL	B	122	5.184	-53.694	-40.095	1.00	21.80
BBBBATOM	3509	CG1	VAL	B	122	5.426	-53.085	-38.724	1.00	21.97
BBBBATOM	3510	CG2	VAL	B	122	4.133	-54.789	-40.035	1.00	22.19
BBBBATOM	3511	C	VAL	B	122	5.754	-51.465	-41.021	1.00	21.29
BBBBATOM	3512	O	VAL	B	122	6.892	-51.605	-41.479	1.00	22.83
BBBBATOM	3513	N	VAL	B	123	5.330	-50.338	-40.464	1.00	20.94
BBBBATOM	3514	CA	VAL	B	123	6.200	-49.184	-40.310	1.00	20.82
BBBBATOM	3515	CB	VAL	B	123	5.580	-47.902	-40.932	1.00	22.16
BBBBATOM	3516	CG1	VAL	B	123	6.516	-46.722	-40.709	1.00	20.83
BBBBATOM	3517	CG2	VAL	B	123	5.322	-48.111	-42.420	1.00	22.66
BBBBATOM	3518	C	VAL	B	123	6.338	-48.953	-38.812	1.00	21.09
BBBBATOM	3519	O	VAL	B	123	5.341	-48.986	-38.093	1.00	21.48
BBBBATOM	3520	N	LEU	B	124	7.557	-48.720	-38.340	1.00	20.53
BBBBATOM	3521	CA	LEU	B	124	7.749	-48.485	-36.915	1.00	22.10
BBBBATOM	3522	CB	LEU	B	124	8.578	-49.606	-36.286	1.00	22.00
BBBBATOM	3523	CG	LEU	B	124	8.160	-51.051	-36.551	1.00	22.45
BBBBATOM	3524	CD1	LEU	B	124	9.196	-51.974	-35.905	1.00	23.90

BBBBATOM	3525	CD2	LEU	B	124	6.765	-51.313	-36.003	1.00	22.34
BBBBATOM	3526	C	LEU	B	124	8.452	-47.172	-36.633	1.00	22.36
BBBBATOM	3527	O	LEU	B	124	9.218	-46.660	-37.461	1.00	20.75
BBBBATOM	3528	N	HIS	B	125	8.182	-46.638	-35.447	1.00	21.40
BBBBATOM	3529	CA	HIS	B	125	8.814	-45.413	-34.981	1.00	21.42
BBBBATOM	3530	CB	HIS	B	125	7.858	-44.218	-35.067	1.00	21.57
BBBBATOM	3531	CG	HIS	B	125	8.432	-42.948	-34.511	1.00	23.73
BBBBATOM	3532	CD2	HIS	B	125	8.300	-42.368	-33.295	1.00	22.15
BBBBATOM	3533	ND1	HIS	B	125	9.274	-42.127	-35.236	1.00	26.23
BBBBATOM	3534	CE1	HIS	B	125	9.631	-41.095	-34.490	1.00	24.20
BBBBATOM	3535	NE2	HIS	B	125	9.054	-41.218	-33.307	1.00	26.07
BBBBATOM	3536	C	HIS	B	125	9.196	-45.642	-33.519	1.00	21.70
BBBBATOM	3537	O	HIS	B	125	8.378	-46.117	-32.725	1.00	19.81
BBBBATOM	3538	N	GLU	B	126	10.444	-45.332	-33.186	1.00	21.20
BBBBATOM	3539	CA	GLU	B	126	10.947	-45.452	-31.817	1.00	22.15
BBBBATOM	3540	CB	GLU	B	126	12.252	-46.246	-31.790	1.00	21.99
BBBBATOM	3541	CG	GLU	B	126	12.958	-46.206	-30.439	1.00	22.04
BBBBATOM	3542	CD	GLU	B	126	12.119	-46.824	-29.338	1.00	21.43
BBBBATOM	3543	OE1	GLU	B	126	11.767	-48.014	-29.471	1.00	21.92
BBBBATOM	3544	OE2	GLU	B	126	11.807	-46.124	-28.349	1.00	21.08
BBBBATOM	3545	C	GLU	B	126	11.205	-44.027	-31.326	1.00	21.93
BBBBATOM	3546	O	GLU	B	126	12.016	-43.300	-31.908	1.00	21.33
BBBBATOM	3547	N	GLN	B	127	10.520	-43.624	-30.259	1.00	22.62
BBBBATOM	3548	CA	GLN	B	127	10.682	-42.270	-29.735	1.00	22.81
BBBBATOM	3549	CB	GLN	B	127	9.414	-41.814	-28.989	1.00	23.56
BBBBATOM	3550	CG	GLN	B	127	8.147	-41.783	-29.830	1.00	24.46
BBBBATOM	3551	CD	GLN	B	127	7.312	-43.041	-29.687	1.00	25.85
BBBBATOM	3552	OE1	GLN	B	127	6.842	-43.366	-28.591	1.00	23.78
BBBBATOM	3553	NE2	GLN	B	127	7.119	-43.758	-30.797	1.00	24.91
BBBBATOM	3554	C	GLN	B	127	11.874	-42.087	-28.809	1.00	22.39
BBBBATOM	3555	O	GLN	B	127	12.399	-40.976	-28.682	1.00	22.43
BBBBATOM	3556	N	ASN	B	128	12.314	-43.173	-28.177	1.00	22.35
BBBBATOM	3557	CA	ASN	B	128	13.406	-43.097	-27.216	1.00	22.96
BBBBATOM	3558	CB	ASN	B	128	13.136	-44.080	-26.064	1.00	22.85
BBBBATOM	3559	CG	ASN	B	128	11.742	-43.919	-25.474	1.00	23.25
BBBBATOM	3560	OD1	ASN	B	128	10.804	-44.632	-25.848	1.00	26.04
BBBBATOM	3561	ND2	ASN	B	128	11.597	-42.975	-24.556	1.00	22.68
BBBBATOM	3562	C	ASN	B	128	14.824	-43.314	-27.742	1.00	23.87
BBBBATOM	3563	O	ASN	B	128	15.026	-43.856	-28.830	1.00	24.05
BBBBATOM	3564	N	GLY	B	129	15.798	-42.885	-26.940	1.00	24.35
BBBBATOM	3565	CA	GLY	B	129	17.203	-43.019	-27.294	1.00	25.36
BBBBATOM	3566	C	GLY	B	129	17.642	-44.468	-27.280	1.00	25.97
BBBBATOM	3567	O	GLY	B	129	18.643	-44.836	-27.891	1.00	25.48
BBBBATOM	3568	N	ILE	B	130	16.886	-45.290	-26.565	1.00	26.18
BBBBATOM	3569	CA	ILE	B	130	17.160	-46.716	-26.488	1.00	28.00
BBBBATOM	3570	CB	ILE	B	130	17.480	-47.145	-25.033	1.00	28.45
BBBBATOM	3571	CG2	ILE	B	130	16.323	-46.785	-24.102	1.00	28.52
BBBBATOM	3572	CG1	ILE	B	130	17.776	-48.642	-24.986	1.00	29.33
BBBBATOM	3573	CD1	ILE	B	130	18.097	-49.149	-23.593	1.00	31.39
BBBBATOM	3574	C	ILE	B	130	15.909	-47.435	-26.999	1.00	27.44
BBBBATOM	3575	O	ILE	B	130	14.793	-47.103	-26.610	1.00	28.58
BBBBATOM	3576	N	ALA	B	131	16.097	-48.405	-27.887	1.00	26.98
BBBBATOM	3577	CA	ALA	B	131	14.978	-49.139	-28.461	1.00	25.88
BBBBATOM	3578	CB	ALA	B	131	15.485	-50.102	-29.525	1.00	25.02
BBBBATOM	3579	C	ALA	B	131	14.171	-49.901	-27.413	1.00	25.20
BBBBATOM	3580	O	ALA	B	131	14.732	-50.544	-26.533	1.00	25.01
BBBBATOM	3581	N	GLY	B	132	12.851	-49.814	-27.506	1.00	24.52
BBBBATOM	3582	CA	GLY	B	132	12.007	-50.532	-26.568	1.00	24.05
BBBBATOM	3583	C	GLY	B	132	12.150	-52.019	-26.831	1.00	23.35
BBBBATOM	3584	O	GLY	B	132	12.582	-52.419	-27.904	1.00	22.89
BBBBATOM	3585	N	LEU	B	133	11.788	-52.846	-25.860	1.00	23.38
BBBBATOM	3586	CA	LEU	B	133	11.903	-54.293	-26.020	1.00	24.54
BBBBATOM	3587	CB	LEU	B	133	11.328	-54.996	-24.786	1.00	25.48
BBBBATOM	3588	CG	LEU	B	133	11.388	-56.527	-24.780	1.00	27.50
BBBBATOM	3589	CD1	LEU	B	133	12.840	-56.984	-24.866	1.00	28.69
BBBBATOM	3590	CD2	LEU	B	133	10.735	-57.059	-23.509	1.00	28.04

BBBBATOM	3591	C	LEU B 133	11.209	-54.833	-27.276	1.00	22.84
BBBBATOM	3592	O	LEU B 133	11.784	-55.619	-28.027	1.00	21.86
BBBBATOM	3593	N	THR B 134	9.975	-54.401	-27.499	1.00	21.72
BBBBATOM	3594	CA	THR B 134	9.202	-54.860	-28.639	1.00	21.22
BBBBATOM	3595	CB	THR B 134	7.716	-54.509	-28.449	1.00	20.99
BBBBATOM	3596	OG1	THR B 134	7.257	-55.075	-27.210	1.00	20.94
BBBBATOM	3597	CG2	THR B 134	6.872	-55.073	-29.600	1.00	20.64
BBBBATOM	3598	C	THR B 134	9.693	-54.326	-29.986	1.00	20.62
BBBBATOM	3599	O	THR B 134	9.843	-55.091	-30.932	1.00	20.33
BBBBATOM	3600	N	ASN B 135	9.932	-53.021	-30.075	1.00	21.24
BBBBATOM	3601	CA	ASN B 135	10.407	-52.419	-31.324	1.00	20.50
BBBBATOM	3602	CB	ASN B 135	10.637	-50.911	-31.142	1.00	19.58
BBBBATOM	3603	CG	ASN B 135	9.457	-50.058	-31.597	1.00	19.93
BBBBATOM	3604	OD1	ASN B 135	9.454	-48.837	-31.390	1.00	21.78
BBBBATOM	3605	ND2	ASN B 135	8.467	-50.677	-32.219	1.00	17.21
BBBBATOM	3606	C	ASN B 135	11.724	-53.064	-31.767	1.00	20.78
BBBBATOM	3607	O	ASN B 135	11.945	-53.290	-32.953	1.00	20.41
BBBBATOM	3608	N	LYS B 136	12.595	-53.366	-30.809	1.00	21.46
BBBBATOM	3609	CA	LYS B 136	13.886	-53.949	-31.144	1.00	22.79
BBBBATOM	3610	CB	LYS B 136	14.713	-54.196	-29.879	1.00	24.70
BBBBATOM	3611	CG	LYS B 136	16.183	-54.424	-30.178	1.00	27.75
BBBBATOM	3612	CD	LYS B 136	16.998	-54.494	-28.902	1.00	30.17
BBBBATOM	3613	CE	LYS B 136	18.479	-54.671	-29.203	1.00	32.33
BBBBATOM	3614	NZ	LYS B 136	19.278	-54.641	-27.944	1.00	33.37
BBBBATOM	3615	C	LYS B 136	13.793	-55.229	-31.966	1.00	23.46
BBBBATOM	3616	O	LYS B 136	14.561	-55.407	-32.912	1.00	23.71
BBBBATOM	3617	N	TRP B 137	12.868	-56.127	-31.633	1.00	21.78
BBBBATOM	3618	CA	TRP B 137	12.753	-57.345	-32.424	1.00	22.06
BBBBATOM	3619	CB	TRP B 137	12.361	-58.552	-31.553	1.00	21.20
BBBBATOM	3620	CG	TRP B 137	10.990	-58.525	-30.922	1.00	20.23
BBBBATOM	3621	CD2	TRP B 137	9.748	-58.877	-31.544	1.00	18.68
BBBBATOM	3622	CE2	TRP B 137	8.743	-58.780	-30.555	1.00	18.97
BBBBATOM	3623	CE3	TRP B 137	9.383	-59.270	-32.840	1.00	19.75
BBBBATOM	3624	CD1	TRP B 137	10.696	-58.231	-29.618	1.00	19.62
BBBBATOM	3625	NE1	TRP B 137	9.349	-58.385	-29.390	1.00	19.31
BBBBATOM	3626	CZ2	TRP B 137	7.401	-59.058	-30.821	1.00	18.18
BBBBATOM	3627	CZ3	TRP B 137	8.046	-59.549	-33.107	1.00	18.87
BBBBATOM	3628	CH2	TRP B 137	7.072	-59.440	-32.099	1.00	18.94
BBBBATOM	3629	C	TRP B 137	11.768	-57.202	-33.574	1.00	21.75
BBBBATOM	3630	O	TRP B 137	11.936	-57.822	-34.623	1.00	21.76
BBBBATOM	3631	N	LEU B 138	10.741	-56.381	-33.386	1.00	21.61
BBBBATOM	3632	CA	LEU B 138	9.744	-56.188	-34.431	1.00	23.15
BBBBATOM	3633	CB	LEU B 138	8.618	-55.305	-33.886	1.00	23.87
BBBBATOM	3634	CG	LEU B 138	7.312	-55.155	-34.664	1.00	26.48
BBBBATOM	3635	CD1	LEU B 138	6.672	-56.508	-34.915	1.00	25.34
BBBBATOM	3636	CD2	LEU B 138	6.383	-54.267	-33.851	1.00	25.90
BBBBATOM	3637	C	LEU B 138	10.384	-55.558	-35.676	1.00	23.07
BBBBATOM	3638	O	LEU B 138	9.958	-55.801	-36.809	1.00	22.68
BBBBATOM	3639	N	ALA B 139	11.423	-54.763	-35.453	1.00	23.34
BBBBATOM	3640	CA	ALA B 139	12.128	-54.092	-36.542	1.00	25.29
BBBBATOM	3641	CB	ALA B 139	13.298	-53.287	-35.984	1.00	24.97
BBBBATOM	3642	C	ALA B 139	12.624	-55.064	-37.610	1.00	26.83
BBBBATOM	3643	O	ALA B 139	12.829	-54.672	-38.754	1.00	27.29
BBBBATOM	3644	N	LYS B 140	12.801	-56.332	-37.241	1.00	27.38
BBBBATOM	3645	CA	LYS B 140	13.279	-57.337	-38.182	1.00	28.05
BBBBATOM	3646	CB	LYS B 140	13.893	-58.501	-37.401	1.00	29.91
BBBBATOM	3647	CG	LYS B 140	15.134	-58.057	-36.635	1.00	31.62
BBBBATOM	3648	CD	LYS B 140	15.719	-59.149	-35.757	1.00	33.53
BBBBATOM	3649	CE	LYS B 140	16.974	-58.634	-35.055	1.00	34.46
BBBBATOM	3650	NZ	LYS B 140	17.692	-59.713	-34.320	1.00	36.17
BBBBATOM	3651	C	LYS B 140	12.254	-57.833	-39.212	1.00	27.83
BBBBATOM	3652	O	LYS B 140	12.602	-58.562	-40.142	1.00	27.80
BBBBATOM	3653	N	ILE B 141	10.992	-57.445	-39.052	1.00	26.40
BBBBATOM	3654	CA	ILE B 141	9.963	-57.818	-40.016	1.00	26.09
BBBBATOM	3655	CB	ILE B 141	8.854	-58.721	-39.405	1.00	26.39
BBBBATOM	3656	CG2	ILE B 141	9.401	-60.118	-39.145	1.00	28.33

BBBBATOM	3657	CG1	ILE	B	141	8.298	-58.092	-38.127	1.00	26.45
BBBBATOM	3658	CD1	ILE	B	141	7.136	-58.845	-37.549	1.00	26.95
BBBBATOM	3659	C	ILE	B	141	9.316	-56.542	-40.530	1.00	25.81
BBBBATOM	3660	O	ILE	B	141	8.353	-56.586	-41.305	1.00	26.10
BBBBATOM	3661	N	ALA	B	142	9.856	-55.405	-40.097	1.00	23.78
BBBBATOM	3662	CA	ALA	B	142	9.331	-54.107	-40.498	1.00	25.03
BBBBATOM	3663	CB	ALA	B	142	9.717	-53.046	-39.466	1.00	24.89
BBBBATOM	3664	C	ALA	B	142	9.816	-53.680	-41.880	1.00	25.08
BBBBATOM	3665	O	ALA	B	142	10.973	-53.894	-42.237	1.00	24.93
BBBBATOM	3666	N	THR	B	143	8.920	-53.075	-42.651	1.00	25.03
BBBBATOM	3667	CA	THR	B	143	9.262	-52.595	-43.984	1.00	26.10
BBBBATOM	3668	CB	THR	B	143	7.987	-52.318	-44.816	1.00	25.75
BBBBATOM	3669	OG1	THR	B	143	7.249	-53.534	-44.970	1.00	25.54
BBBBATOM	3670	CG2	THR	B	143	8.345	-51.782	-46.207	1.00	26.92
BBBBATOM	3671	C	THR	B	143	10.079	-51.310	-43.863	1.00	26.63
BBBBATOM	3672	O	THR	B	143	10.996	-51.061	-44.656	1.00	27.13
BBBBATOM	3673	N	LYS	B	144	9.753	-50.506	-42.853	1.00	24.95
BBBBATOM	3674	CA	LYS	B	144	10.436	-49.238	-42.618	1.00	24.73
BBBBATOM	3675	CB	LYS	B	144	9.688	-48.103	-43.329	1.00	26.20
BBBBATOM	3676	CG	LYS	B	144	10.202	-46.710	-43.013	1.00	27.44
BBBBATOM	3677	CD	LYS	B	144	11.602	-46.480	-43.558	1.00	29.01
BBBBATOM	3678	CE	LYS	B	144	12.055	-45.051	-43.293	1.00	29.74
BBBBATOM	3679	NZ	LYS	B	144	13.406	-44.774	-43.854	1.00	31.29
BBBBATOM	3680	C	LYS	B	144	10.506	-48.943	-41.125	1.00	24.61
BBBBATOM	3681	O	LYS	B	144	9.493	-49.008	-40.423	1.00	23.36
BBBBATOM	3682	N	VAL	B	145	11.707	-48.623	-40.656	1.00	23.68
BBBBATOM	3683	CA	VAL	B	145	11.947	-48.311	-39.252	1.00	23.62
BBBBATOM	3684	CB	VAL	B	145	12.981	-49.279	-38.617	1.00	23.66
BBBBATOM	3685	CG1	VAL	B	145	13.083	-49.014	-37.114	1.00	24.44
BBBBATOM	3686	CG2	VAL	B	145	12.589	-50.724	-38.878	1.00	23.51
BBBBATOM	3687	C	VAL	B	145	12.510	-46.900	-39.125	1.00	24.09
BBBBATOM	3688	O	VAL	B	145	13.473	-46.545	-39.808	1.00	23.68
BBBBATOM	3689	N	MET	B	146	11.902	-46.103	-38.251	1.00	23.84
BBBBATOM	3690	CA	MET	B	146	12.338	-44.736	-37.993	1.00	23.15
BBBBATOM	3691	CB	MET	B	146	11.274	-43.729	-38.446	1.00	24.72
BBBBATOM	3692	CG	MET	B	146	11.130	-43.577	-39.970	1.00	21.76
BBBBATOM	3693	SD	MET	B	146	9.649	-42.636	-40.468	1.00	25.05
BBBBATOM	3694	CE	MET	B	146	8.376	-43.846	-40.325	1.00	21.96
BBBBATOM	3695	C	MET	B	146	12.567	-44.593	-36.488	1.00	24.69
BBBBATOM	3696	O	MET	B	146	11.963	-45.311	-35.689	1.00	22.43
BBBBATOM	3697	N	GLN	B	147	13.456	-43.678	-36.112	1.00	23.37
BBBBATOM	3698	CA	GLN	B	147	13.762	-43.418	-34.712	1.00	25.05
BBBBATOM	3699	CB	GLN	B	147	15.067	-44.114	-34.301	1.00	24.99
BBBBATOM	3700	CG	GLN	B	147	16.259	-43.750	-35.169	1.00	26.10
BBBBATOM	3701	CD	GLN	B	147	17.527	-44.508	-34.803	1.00	26.65
BBBBATOM	3702	OE1	GLN	B	147	18.425	-44.671	-35.637	1.00	28.62
BBBBATOM	3703	NE2	GLN	B	147	17.615	-44.966	-33.558	1.00	26.05
BBBBATOM	3704	C	GLN	B	147	13.880	-41.911	-34.515	1.00	26.28
BBBBATOM	3705	O	GLN	B	147	14.292	-41.177	-35.430	1.00	25.02
BBBBATOM	3706	N	ALA	B	148	13.518	-41.452	-33.323	1.00	26.58
BBBBATOM	3707	CA	ALA	B	148	13.559	-40.032	-33.009	1.00	26.88
BBBBATOM	3708	CB	ALA	B	148	12.853	-39.776	-31.685	1.00	26.71
BBBBATOM	3709	C	ALA	B	148	14.983	-39.502	-32.954	1.00	27.88
BBBBATOM	3710	O	ALA	B	148	15.293	-38.463	-33.545	1.00	27.38
BBBBATOM	3711	N	PHE	B	149	15.847	-40.219	-32.242	1.00	27.92
BBBBATOM	3712	CA	PHE	B	149	17.239	-39.820	-32.098	1.00	29.39
BBBBATOM	3713	CB	PHE	B	149	17.596	-39.631	-30.617	1.00	28.95
BBBBATOM	3714	CG	PHE	B	149	16.549	-38.910	-29.821	1.00	28.91
BBBBATOM	3715	CD1	PHE	B	149	15.745	-39.603	-28.929	1.00	27.96
BBBBATOM	3716	CD2	PHE	B	149	16.372	-37.537	-29.957	1.00	29.03
BBBBATOM	3717	CE1	PHE	B	149	14.779	-38.945	-28.178	1.00	28.64
BBBBATOM	3718	CE2	PHE	B	149	15.406	-36.966	-29.211	1.00	30.10
BBBBATOM	3719	CZ	PHE	B	149	14.608	-37.575	-28.317	1.00	29.02
BBBBATOM	3720	C	PHE	B	149	18.153	-40.893	-32.673	1.00	30.03
BBBBATOM	3721	O	PHE	B	149	17.750	-42.036	-32.849	1.00	30.05
BBBBATOM	3722	N	PRO	B	150	19.401	-40.530	-32.991	1.00	31.73

BBBBATOM	3723	CD	PRO	B	150	20.018	-39.192	-33.018	1.00	32.39
BBBBATOM	3724	CA	PRO	B	150	20.310	-41.541	-33.535	1.00	31.87
BBBBATOM	3725	CB	PRO	B	150	21.418	-40.698	-34.154	1.00	33.07
BBBBATOM	3726	CG	PRO	B	150	21.480	-39.517	-33.238	1.00	33.70
BBBBATOM	3727	C	PRO	B	150	20.809	-42.411	-32.376	1.00	31.93
BBBBATOM	3728	O	PRO	B	150	20.873	-41.945	-31.239	1.00	31.39
BBBBATOM	3729	N	GLY	B	151	21.130	-43.671	-32.651	1.00	31.67
BBBBATOM	3730	CA	GLY	B	151	21.629	-44.537	-31.595	1.00	32.62
BBBBATOM	3731	C	GLY	B	151	20.717	-45.655	-31.112	1.00	32.88
BBBBATOM	3732	O	GLY	B	151	21.206	-46.690	-30.657	1.00	32.98
BBBBATOM	3733	N	ALA	B	152	19.403	-45.458	-31.196	1.00	32.24
BBBBATOM	3734	CA	ALA	B	152	18.447	-46.476	-30.753	1.00	32.71
BBBBATOM	3735	CB	ALA	B	152	17.020	-45.924	-30.817	1.00	31.78
BBBBATOM	3736	C	ALA	B	152	18.582	-47.708	-31.643	1.00	33.00
BBBBATOM	3737	O	ALA	B	152	18.528	-48.842	-31.169	1.00	32.08
BBBBATOM	3738	N	PHE	B	153	18.732	-47.462	-32.941	1.00	33.66
BBBBATOM	3739	CA	PHE	B	153	18.925	-48.506	-33.937	1.00	34.83
BBBBATOM	3740	CB	PHE	B	153	17.734	-48.611	-34.893	1.00	33.64
BBBBATOM	3741	CG	PHE	B	153	16.518	-49.244	-34.289	1.00	32.97
BBBBATOM	3742	CD1	PHE	B	153	15.468	-48.461	-33.823	1.00	31.93
BBBBATOM	3743	CD2	PHE	B	153	16.421	-50.628	-34.184	1.00	32.46
BBBBATOM	3744	CE1	PHE	B	153	14.339	-49.049	-33.265	1.00	32.18
BBBBATOM	3745	CE2	PHE	B	153	15.294	-51.224	-33.626	1.00	31.75
BBBBATOM	3746	CZ	PHE	B	153	14.254	-50.435	-33.166	1.00	31.22
BBBBATOM	3747	C	PHE	B	153	20.155	-48.075	-34.723	1.00	36.90
BBBBATOM	3748	O	PHE	B	153	20.407	-46.878	-34.879	1.00	37.54
BBBBATOM	3749	N	PRO	B	154	20.944	-49.040	-35.220	1.00	38.15
BBBBATOM	3750	CD	PRO	B	154	20.845	-50.482	-34.932	1.00	38.37
BBBBATOM	3751	CA	PRO	B	154	22.158	-48.751	-35.993	1.00	38.97
BBBBATOM	3752	CB	PRO	B	154	22.706	-50.143	-36.302	1.00	39.31
BBBBATOM	3753	CG	PRO	B	154	22.274	-50.941	-35.108	1.00	39.50
BBBBATOM	3754	C	PRO	B	154	21.964	-47.921	-37.266	1.00	39.90
BBBBATOM	3755	O	PRO	B	154	22.697	-46.958	-37.496	1.00	39.89
BBBBATOM	3756	N	ASN	B	155	20.979	-48.280	-38.088	1.00	40.46
BBBBATOM	3757	CA	ASN	B	155	20.765	-47.568	-39.346	1.00	41.08
BBBBATOM	3758	CB	ASN	B	155	21.135	-48.488	-40.510	1.00	43.63
BBBBATOM	3759	CG	ASN	B	155	22.618	-48.753	-40.585	1.00	45.00
BBBBATOM	3760	OD1	ASN	B	155	23.401	-47.861	-40.922	1.00	46.41
BBBBATOM	3761	ND2	ASN	B	155	23.019	-49.978	-40.259	1.00	45.20
BBBBATOM	3762	C	ASN	B	155	19.393	-46.966	-39.627	1.00	40.73
BBBBATOM	3763	O	ASN	B	155	19.145	-46.501	-40.742	1.00	41.01
BBBBATOM	3764	N	ALA	B	156	18.507	-46.956	-38.638	1.00	38.93
BBBBATOM	3765	CA	ALA	B	156	17.170	-46.407	-38.843	1.00	37.55
BBBBATOM	3766	CB	ALA	B	156	16.304	-46.689	-37.618	1.00	37.34
BBBBATOM	3767	C	ALA	B	156	17.209	-44.909	-39.123	1.00	36.36
BBBBATOM	3768	O	ALA	B	156	17.934	-44.171	-38.459	1.00	36.95
BBBBATOM	3769	N	GLU	B	157	16.428	-44.464	-40.107	1.00	35.76
BBBBATOM	3770	CA	GLU	B	157	16.367	-43.044	-40.460	1.00	34.40
BBBBATOM	3771	CB	GLU	B	157	15.375	-42.815	-41.613	1.00	34.84
BBBBATOM	3772	CG	GLU	B	157	15.246	-41.349	-42.055	1.00	34.91
BBBBATOM	3773	CD	GLU	B	157	14.171	-41.123	-43.117	1.00	36.66
BBBBATOM	3774	OE1	GLU	B	157	13.952	-39.951	-43.509	1.00	37.67
BBBBATOM	3775	OE2	GLU	B	157	13.543	-42.107	-43.563	1.00	35.62
BBBBATOM	3776	C	GLU	B	157	15.922	-42.249	-39.231	1.00	33.89
BBBBATOM	3777	O	GLU	B	157	14.941	-42.605	-38.574	1.00	33.04
BBBBATOM	3778	N	VAL	B	158	16.655	-41.185	-38.915	1.00	32.73
BBBBATOM	3779	CA	VAL	B	158	16.337	-40.344	-37.764	1.00	31.16
BBBBATOM	3780	CB	VAL	B	158	17.606	-39.680	-37.202	1.00	31.85
BBBBATOM	3781	CG1	VAL	B	158	17.238	-38.729	-36.073	1.00	31.22
BBBBATOM	3782	CG2	VAL	B	158	18.574	-40.752	-36.708	1.00	31.41
BBBBATOM	3783	C	VAL	B	158	15.352	-39.260	-38.178	1.00	30.27
BBBBATOM	3784	O	VAL	B	158	15.649	-38.445	-39.053	1.00	30.18
BBBBATOM	3785	N	VAL	B	159	14.186	-39.241	-37.544	1.00	28.57
BBBBATOM	3786	CA	VAL	B	159	13.155	-38.265	-37.889	1.00	28.10
BBBBATOM	3787	CB	VAL	B	159	11.942	-38.963	-38.535	1.00	27.81
BBBBATOM	3788	CG1	VAL	B	159	12.365	-39.667	-39.819	1.00	28.61

BBBBATOM	3789	CG2	VAL	B	159	11.336	-39.962	-37.548	1.00	27.61
BBBBATOM	3790	C	VAL	B	159	12.636	-37.430	-36.725	1.00	27.64
BBBBATOM	3791	O	VAL	B	159	11.757	-36.591	-36.918	1.00	27.97
BBBBATOM	3792	N	GLY	B	160	13.168	-37.662	-35.527	1.00	27.60
BBBBATOM	3793	CA	GLY	B	160	12.724	-36.921	-34.355	1.00	26.93
BBBBATOM	3794	C	GLY	B	160	11.331	-37.312	-33.883	1.00	26.66
BBBBATOM	3795	O	GLY	B	160	10.757	-38.275	-34.384	1.00	26.71
BBBBATOM	3796	N	ASN	B	161	10.797	-36.569	-32.914	1.00	25.68
BBBBATOM	3797	CA	ASN	B	161	9.456	-36.807	-32.375	1.00	25.27
BBBBATOM	3798	CB	ASN	B	161	9.481	-36.963	-30.849	1.00	23.89
BBBBATOM	3799	CG	ASN	B	161	10.042	-38.285	-30.401	1.00	22.91
BBBBATOM	3800	OD1	ASN	B	161	9.600	-39.335	-30.850	1.00	22.70
BBBBATOM	3801	ND2	ASN	B	161	11.017	-38.243	-29.496	1.00	22.71
BBBBATOM	3802	C	ASN	B	161	8.556	-35.618	-32.670	1.00	25.39
BBBBATOM	3803	O	ASN	B	161	9.028	-34.499	-32.821	1.00	25.45
BBBBATOM	3804	N	PRO	B	162	7.241	-35.849	-32.741	1.00	26.08
BBBBATOM	3805	CD	PRO	B	162	6.533	-37.140	-32.710	1.00	25.20
BBBBATOM	3806	CA	PRO	B	162	6.315	-34.747	-33.004	1.00	26.14
BBBBATOM	3807	CB	PRO	B	162	4.952	-35.431	-32.976	1.00	25.76
BBBBATOM	3808	CG	PRO	B	162	5.255	-36.821	-33.430	1.00	26.48
BBBBATOM	3809	C	PRO	B	162	6.455	-33.728	-31.866	1.00	27.00
BBBBATOM	3810	O	PRO	B	162	6.652	-34.102	-30.703	1.00	25.08
BBBBATOM	3811	N	VAL	B	163	6.355	-32.446	-32.203	1.00	27.54
BBBBATOM	3812	CA	VAL	B	163	6.456	-31.379	-31.216	1.00	27.75
BBBBATOM	3813	CB	VAL	B	163	7.748	-30.561	-31.421	1.00	28.81
BBBBATOM	3814	CG1	VAL	B	163	7.839	-29.451	-30.381	1.00	28.20
BBBBATOM	3815	CG2	VAL	B	163	8.958	-31.471	-31.335	1.00	27.87
BBBBATOM	3816	C	VAL	B	163	5.261	-30.440	-31.365	1.00	29.43
BBBBATOM	3817	O	VAL	B	163	4.777	-30.227	-32.476	1.00	28.49
BBBBATOM	3818	N	ARG	B	164	4.790	-29.891	-30.246	1.00	29.93
BBBBATOM	3819	CA	ARG	B	164	3.667	-28.953	-30.246	1.00	32.36
BBBBATOM	3820	CB	ARG	B	164	3.430	-28.411	-28.833	1.00	34.56
BBBBATOM	3821	CG	ARG	B	164	2.967	-29.439	-27.832	1.00	38.34
BBBBATOM	3822	CD	ARG	B	164	3.067	-28.889	-26.417	1.00	41.59
BBBBATOM	3823	NE	ARG	B	164	2.481	-27.555	-26.299	1.00	44.08
BBBBATOM	3824	CZ	ARG	B	164	2.307	-26.919	-25.144	1.00	45.79
BBBBATOM	3825	NH1	ARG	B	164	2.673	-27.499	-24.008	1.00	46.89
BBBBATOM	3826	NH2	ARG	B	164	1.769	-25.705	-25.123	1.00	47.50
BBBBATOM	3827	C	ARG	B	164	3.939	-27.775	-31.187	1.00	31.56
BBBBATOM	3828	O	ARG	B	164	5.031	-27.212	-31.191	1.00	30.03
BBBBATOM	3829	N	THR	B	165	2.928	-27.401	-31.965	1.00	32.06
BBBBATOM	3830	CA	THR	B	165	3.038	-26.307	-32.924	1.00	31.74
BBBBATOM	3831	CB	THR	B	165	1.701	-26.104	-33.678	1.00	32.51
BBBBATOM	3832	OG1	THR	B	165	1.198	-27.375	-34.094	1.00	32.54
BBBBATOM	3833	CG2	THR	B	165	1.907	-25.239	-34.916	1.00	32.14
BBBBATOM	3834	C	THR	B	165	3.445	-24.976	-32.295	1.00	31.49
BBBBATOM	3835	O	THR	B	165	4.236	-24.238	-32.872	1.00	31.48
BBBBATOM	3836	N	ASP	B	166	2.907	-24.664	-31.120	1.00	30.86
BBBBATOM	3837	CA	ASP	B	166	3.252	-23.404	-30.466	1.00	30.64
BBBBATOM	3838	CB	ASP	B	166	2.358	-23.163	-29.242	1.00	33.08
BBBBATOM	3839	CG	ASP	B	166	2.185	-24.400	-28.384	1.00	35.24
BBBBATOM	3840	OD1	ASP	B	166	1.315	-24.373	-27.485	1.00	38.19
BBBBATOM	3841	OD2	ASP	B	166	2.908	-25.393	-28.603	1.00	37.17
BBBBATOM	3842	C	ASP	B	166	4.729	-23.338	-30.084	1.00	28.64
BBBBATOM	3843	O	ASP	B	166	5.321	-22.259	-30.076	1.00	27.92
BBBBATOM	3844	N	VAL	B	167	5.328	-24.485	-29.773	1.00	27.08
BBBBATOM	3845	CA	VAL	B	167	6.746	-24.503	-29.440	1.00	25.91
BBBBATOM	3846	CB	VAL	B	167	7.171	-25.824	-28.757	1.00	25.96
BBBBATOM	3847	CG1	VAL	B	167	8.687	-25.844	-28.586	1.00	24.67
BBBBATOM	3848	CG2	VAL	B	167	6.482	-25.964	-27.396	1.00	26.22
BBBBATOM	3849	C	VAL	B	167	7.548	-24.361	-30.736	1.00	25.54
BBBBATOM	3850	O	VAL	B	167	8.548	-23.642	-30.787	1.00	25.58
BBBBATOM	3851	N	LEU	B	168	7.108	-25.059	-31.778	1.00	26.75
BBBBATOM	3852	CA	LEU	B	168	7.780	-25.002	-33.075	1.00	28.46
BBBBATOM	3853	CB	LEU	B	168	7.085	-25.930	-34.080	1.00	28.40
BBBBATOM	3854	CG	LEU	B	168	7.205	-27.440	-33.890	1.00	28.67

BBBBBATOM	3855	CD1	LEU	B	168	6.254	-28.161	-34.854	1.00	30.19
BBBBBATOM	3856	CD2	LEU	B	168	8.647	-27.868	-34.129	1.00	28.82
BBBBBATOM	3857	C	LEU	B	168	7.766	-23.584	-33.632	1.00	29.14
BBBBBATOM	3858	O	LEU	B	168	8.667	-23.186	-34.369	1.00	29.57
BBBBBATOM	3859	N	ALA	B	169	6.741	-22.823	-33.267	1.00	30.35
BBBBBATOM	3860	CA	ALA	B	169	6.580	-21.455	-33.756	1.00	31.43
BBBBBATOM	3861	CB	ALA	B	169	5.118	-21.030	-33.624	1.00	33.26
BBBBBATOM	3862	C	ALA	B	169	7.472	-20.427	-33.078	1.00	32.03
BBBBBATOM	3863	O	ALA	B	169	7.562	-19.284	-33.536	1.00	31.95
BBBBBATOM	3864	N	LEU	B	170	8.131	-20.824	-31.993	1.00	30.53
BBBBBATOM	3865	CA	LEU	B	170	9.002	-19.905	-31.268	1.00	29.60
BBBBBATOM	3866	CB	LEU	B	170	9.601	-20.595	-30.041	1.00	28.66
BBBBBATOM	3867	CG	LEU	B	170	8.623	-20.954	-28.923	1.00	28.67
BBBBBATOM	3868	CD1	LEU	B	170	9.322	-21.845	-27.907	1.00	27.66
BBBBBATOM	3869	CD2	LEU	B	170	8.096	-19.675	-28.277	1.00	27.21
BBBBBATOM	3870	C	LEU	B	170	10.138	-19.363	-32.127	1.00	29.76
BBBBBATOM	3871	O	LEU	B	170	10.670	-20.064	-32.983	1.00	29.07
BBBBBATOM	3872	N	PRO	B	171	10.525	-18.099	-31.897	1.00	29.71
BBBBBATOM	3873	CD	PRO	B	171	9.874	-17.138	-30.989	1.00	30.67
BBBBBATOM	3874	CA	PRO	B	171	11.611	-17.457	-32.642	1.00	30.11
BBBBBATOM	3875	CB	PRO	B	171	11.665	-16.054	-32.033	1.00	29.54
BBBBBATOM	3876	CG	PRO	B	171	10.261	-15.810	-31.605	1.00	30.96
BBBBBATOM	3877	C	PRO	B	171	12.900	-18.226	-32.374	1.00	30.39
BBBBBATOM	3878	O	PRO	B	171	12.999	-18.933	-31.363	1.00	30.16
BBBBBATOM	3879	N	LEU	B	172	13.883	-18.097	-33.263	1.00	28.62
BBBBBATOM	3880	CA	LEU	B	172	15.157	-18.780	-33.062	1.00	28.33
BBBBBATOM	3881	CB	LEU	B	172	16.106	-18.557	-34.247	1.00	29.88
BBBBBATOM	3882	CG	LEU	B	172	15.800	-19.149	-35.628	1.00	32.18
BBBBBATOM	3883	CD1	LEU	B	172	15.593	-20.656	-35.510	1.00	32.75
BBBBBATOM	3884	CD2	LEU	B	172	14.573	-18.476	-36.222	1.00	33.92
BBBBBATOM	3885	C	LEU	B	172	15.805	-18.206	-31.805	1.00	26.61
BBBBBATOM	3886	O	LEU	B	172	15.478	-17.093	-31.388	1.00	26.45
BBBBBATOM	3887	N	PRO	B	173	16.735	-18.959	-31.190	1.00	25.73
BBBBBATOM	3888	CD	PRO	B	173	17.093	-20.345	-31.550	1.00	24.63
BBBBBATOM	3889	CA	PRO	B	173	17.450	-18.550	-29.977	1.00	25.25
BBBBBATOM	3890	CB	PRO	B	173	18.512	-19.635	-29.827	1.00	25.04
BBBBBATOM	3891	CG	PRO	B	173	17.818	-20.831	-30.309	1.00	24.90
BBBBBATOM	3892	C	PRO	B	173	18.066	-17.145	-29.999	1.00	24.24
BBBBBATOM	3893	O	PRO	B	173	17.791	-16.337	-29.116	1.00	22.89
BBBBBATOM	3894	N	GLN	B	174	18.899	-16.850	-30.995	1.00	24.48
BBBBBATOM	3895	CA	GLN	B	174	19.526	-15.527	-31.049	1.00	25.46
BBBBBATOM	3896	CB	GLN	B	174	20.384	-15.382	-32.313	1.00	26.10
BBBBBATOM	3897	CG	GLN	B	174	21.173	-14.070	-32.382	1.00	26.21
BBBBBATOM	3898	CD	GLN	B	174	20.325	-12.883	-32.812	1.00	26.24
BBBBBATOM	3899	OE1	GLN	B	174	20.634	-11.732	-32.491	1.00	26.98
BBBBBATOM	3900	NE2	GLN	B	174	19.258	-13.154	-33.550	1.00	25.58
BBBBBATOM	3901	C	GLN	B	174	18.485	-14.408	-30.981	1.00	25.33
BBBBBATOM	3902	O	GLN	B	174	18.646	-13.432	-30.249	1.00	24.63
BBBBBATOM	3903	N	GLN	B	175	17.402	-14.555	-31.726	1.00	26.49
BBBBBATOM	3904	CA	GLN	B	175	16.365	-13.525	-31.718	1.00	28.47
BBBBBATOM	3905	CB	GLN	B	175	15.333	-13.819	-32.809	1.00	29.48
BBBBBATOM	3906	CG	GLN	B	175	14.206	-12.805	-32.888	1.00	33.70
BBBBBATOM	3907	CD	GLN	B	175	13.324	-13.006	-34.109	1.00	35.20
BBBBBATOM	3908	OE1	GLN	B	175	12.247	-12.422	-34.215	1.00	38.98
BBBBBATOM	3909	NE2	GLN	B	175	13.785	-13.828	-35.042	1.00	37.92
BBBBBATOM	3910	C	GLN	B	175	15.678	-13.430	-30.355	1.00	27.54
BBBBBATOM	3911	O	GLN	B	175	15.521	-12.346	-29.796	1.00	26.49
BBBBBATOM	3912	N	ARG	B	176	15.288	-14.578	-29.818	1.00	28.19
BBBBBATOM	3913	CA	ARG	B	176	14.611	-14.635	-28.525	1.00	29.01
BBBBBATOM	3914	CB	ARG	B	176	14.183	-16.088	-28.260	1.00	32.12
BBBBBATOM	3915	CG	ARG	B	176	13.783	-16.410	-26.825	1.00	34.95
BBBBBATOM	3916	CD	ARG	B	176	12.879	-17.638	-26.779	1.00	36.93
BBBBBATOM	3917	NE	ARG	B	176	13.401	-18.749	-27.566	1.00	37.99
BBBBBATOM	3918	CZ	ARG	B	176	14.458	-19.480	-27.231	1.00	40.44
BBBBBATOM	3919	NH1	ARG	B	176	15.121	-19.233	-26.107	1.00	41.22
BBBBBATOM	3920	NH2	ARG	B	176	14.866	-20.451	-28.040	1.00	42.79

BBBBATOM	3921	C	ARG	B	176	15.449	-14.094	-27.357	1.00	28.58
BBBBATOM	3922	O	ARG	B	176	14.933	-13.414	-26.467	1.00	26.70
BBBBATOM	3923	N	LEU	B	177	16.744	-14.382	-27.384	1.00	28.60
BBBBATOM	3924	CA	LEU	B	177	17.673	-13.970	-26.331	1.00	29.90
BBBBATOM	3925	CB	LEU	B	177	18.729	-15.071	-26.140	1.00	30.05
BBBBATOM	3926	CG	LEU	B	177	18.323	-16.402	-25.484	1.00	31.35
BBBBATOM	3927	CD1	LEU	B	177	16.893	-16.755	-25.807	1.00	31.63
BBBBATOM	3928	CD2	LEU	B	177	19.266	-17.504	-25.948	1.00	30.16
BBBBATOM	3929	C	LEU	B	177	18.384	-12.637	-26.594	1.00	30.48
BBBBATOM	3930	O	LEU	B	177	19.148	-12.161	-25.752	1.00	30.67
BBBBATOM	3931	N	ALA	B	178	18.128	-12.036	-27.752	1.00	31.18
BBBBATOM	3932	CA	ALA	B	178	18.766	-10.776	-28.131	1.00	30.78
BBBBATOM	3933	CB	ALA	B	178	18.238	-10.319	-29.496	1.00	32.30
BBBBATOM	3934	C	ALA	B	178	18.639	-9.636	-27.123	1.00	31.11
BBBBATOM	3935	O	ALA	B	178	17.537	-9.253	-26.726	1.00	30.59
BBBBATOM	3936	N	GLY	B	179	19.792	-9.105	-26.718	1.00	30.45
BBBBATOM	3937	CA	GLY	B	179	19.846	-7.993	-25.784	1.00	30.10
BBBBATOM	3938	C	GLY	B	179	19.392	-8.298	-24.374	1.00	29.54
BBBBATOM	3939	O	GLY	B	179	19.288	-7.405	-23.537	1.00	28.79
BBBBATOM	3940	N	ARG	B	180	19.129	-9.568	-24.101	1.00	29.31
BBBBATOM	3941	CA	ARG	B	180	18.676	-9.965	-22.787	1.00	28.97
BBBBATOM	3942	CB	ARG	B	180	18.120	-11.391	-22.868	1.00	28.73
BBBBATOM	3943	CG	ARG	B	180	17.281	-11.815	-21.693	1.00	25.80
BBBBATOM	3944	CD	ARG	B	180	16.813	-13.245	-21.869	1.00	24.21
BBBBATOM	3945	NE	ARG	B	180	15.595	-13.363	-22.665	1.00	23.27
BBBBATOM	3946	CZ	ARG	B	180	14.898	-14.489	-22.776	1.00	24.65
BBBBATOM	3947	NH1	ARG	B	180	15.316	-15.579	-22.146	1.00	21.06
BBBBATOM	3948	NH2	ARG	B	180	13.777	-14.529	-23.491	1.00	23.07
BBBBATOM	3949	C	ARG	B	180	19.818	-9.874	-21.769	1.00	30.52
BBBBATOM	3950	O	ARG	B	180	20.916	-10.398	-21.980	1.00	30.32
BBBBATOM	3951	N	GLU	B	181	19.562	-9.171	-20.677	1.00	30.40
BBBBATOM	3952	CA	GLU	B	181	20.545	-9.027	-19.621	1.00	31.79
BBBBATOM	3953	CB	GLU	B	181	21.157	-7.617	-19.650	1.00	34.59
BBBBATOM	3954	CG	GLU	B	181	22.130	-7.422	-20.826	1.00	38.85
BBBBATOM	3955	CD	GLU	B	181	22.659	-6.001	-20.957	1.00	41.19
BBBBATOM	3956	OE1	GLU	B	181	23.274	-5.495	-19.996	1.00	43.24
BBBBATOM	3957	OE2	GLU	B	181	22.467	-5.392	-22.032	1.00	43.11
BBBBATOM	3958	C	GLU	B	181	19.815	-9.307	-18.313	1.00	31.51
BBBBATOM	3959	O	GLU	B	181	18.605	-9.543	-18.313	1.00	33.44
BBBBATOM	3960	N	GLY	B	182	20.535	-9.314	-17.203	1.00	29.65
BBBBATOM	3961	CA	GLY	B	182	19.871	-9.586	-15.943	1.00	27.75
BBBBATOM	3962	C	GLY	B	182	19.989	-11.051	-15.565	1.00	25.32
BBBBATOM	3963	O	GLY	B	182	20.573	-11.830	-16.311	1.00	22.00
BBBBATOM	3964	N	PRO	B	183	19.414	-11.455	-14.423	1.00	23.79
BBBBATOM	3965	CD	PRO	B	183	18.562	-10.609	-13.572	1.00	24.07
BBBBATOM	3966	CA	PRO	B	183	19.450	-12.832	-13.913	1.00	22.93
BBBBATOM	3967	CB	PRO	B	183	18.480	-12.796	-12.727	1.00	23.23
BBBBATOM	3968	CG	PRO	B	183	18.549	-11.381	-12.271	1.00	24.61
BBBBATOM	3969	C	PRO	B	183	19.063	-13.912	-14.905	1.00	21.77
BBBBATOM	3970	O	PRO	B	183	18.117	-13.758	-15.683	1.00	21.04
BBBBATOM	3971	N	VAL	B	184	19.805	-15.011	-14.867	1.00	19.40
BBBBATOM	3972	CA	VAL	B	184	19.524	-16.146	-15.729	1.00	18.01
BBBBATOM	3973	CB	VAL	B	184	20.597	-17.248	-15.549	1.00	17.45
BBBBATOM	3974	CG1	VAL	B	184	20.171	-18.534	-16.249	1.00	15.59
BBBBATOM	3975	CG2	VAL	B	184	21.931	-16.753	-16.121	1.00	18.46
BBBBATOM	3976	C	VAL	B	184	18.155	-16.650	-15.283	1.00	18.17
BBBBATOM	3977	O	VAL	B	184	17.931	-16.882	-14.092	1.00	16.37
BBBBATOM	3978	N	ARG	B	185	17.244	-16.771	-16.245	1.00	17.91
BBBBATOM	3979	CA	ARG	B	185	15.873	-17.216	-16.011	1.00	17.62
BBBBATOM	3980	CB	ARG	B	185	14.966	-16.622	-17.092	1.00	17.65
BBBBATOM	3981	CG	ARG	B	185	15.036	-15.110	-17.160	1.00	18.62
BBBBATOM	3982	CD	ARG	B	185	14.344	-14.624	-18.420	1.00	20.39
BBBBATOM	3983	NE	ARG	B	185	14.307	-13.173	-18.516	1.00	19.72
BBBBATOM	3984	CZ	ARG	B	185	13.647	-12.520	-19.466	1.00	20.23
BBBBATOM	3985	NH1	ARG	B	185	12.977	-13.197	-20.391	1.00	19.85
BBBBATOM	3986	NH2	ARG	B	185	13.650	-11.197	-19.487	1.00	23.44

BBBBATOM	3987	C	ARG	B	185	15.804	-18.740	-16.037	1.00	16.88
BBBBATOM	3988	O	ARG	B	185	15.971	-19.367	-17.087	1.00	15.75
BBBBATOM	3989	N	VAL	B	186	15.566	-19.326	-14.870	1.00	15.97
BBBBATOM	3990	CA	VAL	B	186	15.508	-20.771	-14.741	1.00	16.47
BBBBATOM	3991	CB	VAL	B	186	16.259	-21.245	-13.476	1.00	15.51
BBBBATOM	3992	CG1	VAL	B	186	16.316	-22.770	-13.448	1.00	17.66
BBBBATOM	3993	CG2	VAL	B	186	17.652	-20.626	-13.430	1.00	16.97
BBBBATOM	3994	C	VAL	B	186	14.076	-21.282	-14.644	1.00	16.41
BBBBATOM	3995	O	VAL	B	186	13.343	-20.920	-13.732	1.00	18.33
BBBBATOM	3996	N	LEU	B	187	13.695	-22.128	-15.588	1.00	15.92
BBBBATOM	3997	CA	LEU	B	187	12.361	-22.710	-15.604	1.00	16.75
BBBBATOM	3998	CB	LEU	B	187	11.813	-22.701	-17.035	1.00	16.85
BBBBATOM	3999	CG	LEU	B	187	10.445	-23.340	-17.276	1.00	18.63
BBBBATOM	4000	CD1	LEU	B	187	9.368	-22.478	-16.625	1.00	19.42
BBBBATOM	4001	CD2	LEU	B	187	10.198	-23.449	-18.783	1.00	19.11
BBBBATOM	4002	C	LEU	B	187	12.450	-24.146	-15.085	1.00	16.85
BBBBATOM	4003	O	LEU	B	187	13.115	-24.982	-15.688	1.00	17.18
BBBBATOM	4004	N	VAL	B	188	11.788	-24.426	-13.964	1.00	18.20
BBBBATOM	4005	CA	VAL	B	188	11.774	-25.775	-13.381	1.00	18.41
BBBBATOM	4006	CB	VAL	B	188	11.902	-25.714	-11.842	1.00	18.98
BBBBATOM	4007	CG1	VAL	B	188	12.088	-27.126	-11.270	1.00	18.50
BBBBATOM	4008	CG2	VAL	B	188	13.061	-24.818	-11.449	1.00	18.83
BBBBATOM	4009	G	VAL	B	188	10.434	-26.440	-13.739	1.00	19.88
BBBBATOM	4010	O	VAL	B	188	9.371	-25.967	-13.336	1.00	20.39
BBBBATOM	4011	N	VAL	B	189	10.493	-27.532	-14.496	1.00	21.55
BBBBATOM	4012	CA	VAL	B	189	9.298	-28.234	-14.948	1.00	22.11
BBBBATOM	4013	CB	VAL	B	189	9.299	-28.342	-16.488	1.00	22.50
BBBBATOM	4014	CG1	VAL	B	189	8.009	-29.013	-16.981	1.00	22.70
BBBBATOM	4015	CG2	VAL	B	189	9.470	-26.943	-17.101	1.00	21.26
BBBBATOM	4016	C	VAL	B	189	9.191	-29.639	-14.351	1.00	23.90
BBBBATOM	4017	O	VAL	B	189	10.067	-30.478	-14.559	1.00	23.61
BBBBATOM	4018	N	GLY	B	190	8.111	-29.887	-13.615	1.00	25.60
BBBBATOM	4019	CA	GLY	B	190	7.914	-31.188	-12.994	1.00	27.28
BBBBATOM	4020	C	GLY	B	190	6.808	-32.026	-13.604	1.00	29.67
BBBBATOM	4021	O	GLY	B	190	6.668	-33.208	-13.283	1.00	29.86
BBBBATOM	4022	N	GLY	B	191	6.025	-31.430	-14.497	1.00	30.56
BBBBATOM	4023	CA	GLY	B	191	4.935	-32.163	-15.115	1.00	31.94
BBBBATOM	4024	C	GLY	B	191	3.676	-32.104	-14.269	1.00	33.11
BBBBATOM	4025	O	GLY	B	191	3.691	-31.556	-13.165	1.00	32.14
BBBBATOM	4026	N	SER	B	192	2.587	-32.673	-14.779	1.00	34.23
BBBBATOM	4027	CA	SER	B	192	1.313	-32.665	-14.064	1.00	35.91
BBBBATOM	4028	CB	SER	B	192	0.283	-33.532	-14.801	1.00	36.87
BBBBATOM	4029	OG	SER	B	192	0.702	-34.887	-14.877	1.00	39.58
BBBBATOM	4030	C	SER	B	192	1.419	-33.128	-12.609	1.00	36.41
BBBBATOM	4031	O	SER	B	192	0.862	-32.499	-11.714	1.00	35.78
BBBBATOM	4032	N	GLN	B	193	2.134	-34.225	-12.380	1.00	37.60
BBBBATOM	4033	CA	GLN	B	193	2.292	-34.763	-11.033	1.00	38.53
BBBBATOM	4034	CB	GLN	B	193	2.584	-36.263	-11.096	1.00	41.10
BBBBATOM	4035	CG	GLN	B	193	1.501	-37.082	-11.779	1.00	45.38
BBBBATOM	4036	CD	GLN	B	193	0.152	-36.948	-11.099	1.00	47.81
BBBBATOM	4037	OE1	GLN	B	193	-0.484	-35.892	-11.149	1.00	49.50
BBBBATOM	4038	NE2	GLN	B	193	-0.290	-38.023	-10.452	1.00	49.36
BBBBATOM	4039	C	GLN	B	193	3.405	-34.072	-10.260	1.00	37.76
BBBBATOM	4040	O	GLN	B	193	3.458	-34.146	-9.030	1.00	37.02
BBBBATOM	4041	N	GLY	B	194	4.291	-33.398	-10.986	1.00	36.47
BBBBATOM	4042	CA	GLY	B	194	5.398	-32.711	-10.350	1.00	35.02
BBBBATOM	4043	C	GLY	B	194	6.584	-33.630	-10.146	1.00	34.51
BBBBATOM	4044	O	GLY	B	194	6.442	-34.851	-10.191	1.00	34.26
BBBBATOM	4045	N	ALA	B	195	7.761	-33.045	-9.938	1.00	33.54
BBBBATOM	4046	CA	ALA	B	195	8.977	-33.819	-9.709	1.00	33.12
BBBBATOM	4047	CB	ALA	B	195	10.073	-33.387	-10.679	1.00	33.17
BBBBATOM	4048	C	ALA	B	195	9.423	-33.590	-8.267	1.00	32.87
BBBBATOM	4049	O	ALA	B	195	9.955	-32.533	-7.923	1.00	31.47
BBBBATOM	4050	N	ARG	B	196	9.195	-34.592	-7.426	1.00	32.81
BBBBATOM	4051	CA	ARG	B	196	9.538	-34.512	-6.010	1.00	32.63
BBBBATOM	4052	CB	ARG	B	196	9.373	-35.891	-5.361	1.00	35.51

BBBBATOM	4053	CG	ARG	B	196	10.382	-36.954	-5.830	1.00	39.68
BBBBATOM	4054	CD	ARG	B	196	10.317	-37.224	-7.329	1.00	41.52
BBBBATOM	4055	NE	ARG	B	196	9.007	-37.722	-7.738	1.00	43.02
BBBBATOM	4056	CZ	ARG	B	196	8.661	-37.955	-8.997	1.00	42.91
BBBBATOM	4057	NH1	ARG	B	196	9.527	-37.735	-9.975	1.00	44.39
BBBBATOM	4058	NH2	ARG	B	196	7.449	-38.408	-9.279	1.00	45.18
BBBBATOM	4059	C	ARG	B	196	10.940	-33.977	-5.729	1.00	30.96
BBBBATOM	4060	O	ARG	B	196	11.108	-33.035	-4.957	1.00	29.99
BBBBATOM	4061	N	ILE	B	197	11.942	-34.573	-6.367	1.00	29.47
BBBBATOM	4062	CA	ILE	B	197	13.329	-34.168	-6.164	1.00	28.10
BBBBATOM	4063	CB	ILE	B	197	14.284	-35.109	-6.946	1.00	28.46
BBBBATOM	4064	CG2	ILE	B	197	13.984	-35.041	-8.430	1.00	27.99
BBBBATOM	4065	CG1	ILE	B	197	15.742	-34.749	-6.657	1.00	28.64
BBBBATOM	4066	CD1	ILE	B	197	16.212	-35.158	-5.281	1.00	30.51
BBBBATOM	4067	C	ILE	B	197	13.579	-32.703	-6.554	1.00	27.65
BBBBATOM	4068	O	ILE	B	197	14.378	-32.013	-5.921	1.00	27.21
BBBBATOM	4069	N	LEU	B	198	12.897	-32.223	-7.590	1.00	27.07
BBBBATOM	4070	CA	LEU	B	198	13.069	-30.833	-8.003	1.00	26.58
BBBBATOM	4071	CB	LEU	B	198	12.504	-30.616	-9.412	1.00	25.88
BBBBATOM	4072	CG	LEU	B	198	13.196	-31.408	-10.524	1.00	25.40
BBBBATOM	4073	CD1	LEU	B	198	12.625	-31.007	-11.874	1.00	26.54
BBBBATOM	4074	CD2	LEU	B	198	14.692	-31.146	-10.493	1.00	25.94
BBBBATOM	4075	C	LEU	B	198	12.388	-29.893	-7.006	1.00	26.41
BBBBATOM	4076	O	LEU	B	198	12.930	-28.835	-6.667	1.00	26.35
BBBBATOM	4077	N	ASN	B	199	11.205	-30.274	-6.532	1.00	26.01
BBBBATOM	4078	CA	ASN	B	199	10.497	-29.447	-5.563	1.00	27.07
BBBBATOM	4079	CB	ASN	B	199	9.123	-30.035	-5.238	1.00	26.63
BBBBATOM	4080	CG	ASN	B	199	8.212	-30.050	-6.434	1.00	27.62
BBBBATOM	4081	OD1	ASN	B	199	8.519	-29.434	-7.460	1.00	26.33
BBBBATOM	4082	ND2	ASN	B	199	7.080	-30.749	-6.320	1.00	24.20
BBBBATOM	4083	C	ASN	B	199	11.308	-29.319	-4.282	1.00	27.65
BBBBATOM	4084	O	ASN	B	199	11.207	-28.321	-3.581	1.00	28.19
BBBBATOM	4085	N	GLN	B	200	12.124	-30.328	-3.994	1.00	28.38
BBBBATOM	4086	CA	GLN	B	200	12.955	-30.326	-2.794	1.00	30.10
BBBBATOM	4087	CB	GLN	B	200	13.158	-31.764	-2.301	1.00	31.91
BBBBATOM	4088	CG	GLN	B	200	11.883	-32.453	-1.827	1.00	35.02
BBBBATOM	4089	CD	GLN	B	200	12.056	-33.956	-1.632	1.00	37.49
BBBBATOM	4090	OE1	GLN	B	200	11.204	-34.619	-1.032	1.00	38.76
BBBBATOM	4091	NE2	GLN	B	200	13.155	-34.502	-2.151	1.00	37.28
BBBBATOM	4092	C	GLN	B	200	14.319	-29.675	-3.011	1.00	30.18
BBBBATOM	4093	O	GLN	B	200	14.834	-28.975	-2.135	1.00	31.13
BBBBATOM	4094	N	THR	B	201	14.897	-29.884	-4.187	1.00	28.94
BBBBATOM	4095	CA	THR	B	201	16.215	-29.345	-4.474	1.00	27.34
BBBBATOM	4096	CB	THR	B	201	16.915	-30.181	-5.567	1.00	28.81
BBBBATOM	4097	OG1	THR	B	201	16.988	-31.553	-5.149	1.00	28.92
BBBBATOM	4098	CG2	THR	B	201	18.331	-29.654	-5.817	1.00	28.29
BBBBATOM	4099	C	THR	B	201	16.313	-27.871	-4.869	1.00	25.78
BBBBATOM	4100	O	THR	B	201	17.137	-27.138	-4.331	1.00	24.91
BBBBATOM	4101	N	MET	B	202	15.479	-27.430	-5.800	1.00	24.08
BBBBATOM	4102	CA	MET	B	202	15.567	-26.048	-6.268	1.00	23.68
BBBBATOM	4103	CB	MET	B	202	14.558	-25.827	-7.397	1.00	22.29
BBBBATOM	4104	CG	MET	B	202	14.856	-26.685	-8.633	1.00	22.80
BBBBATOM	4105	SD	MET	B	202	16.590	-26.614	-9.190	1.00	25.93
BBBBATOM	4106	CE	MET	B	202	16.814	-24.877	-9.345	1.00	22.63
BBBBATOM	4107	C	MET	B	202	15.489	-24.926	-5.229	1.00	23.47
BBBBATOM	4108	O	MET	B	202	16.189	-23.929	-5.354	1.00	24.40
BBBBATOM	4109	N	PRO	B	203	14.636	-25.059	-4.192	1.00	24.12
BBBBATOM	4110	CD	PRO	B	203	13.518	-25.991	-3.970	1.00	22.27
BBBBATOM	4111	CA	PRO	B	203	14.608	-23.963	-3.220	1.00	23.84
BBBBATOM	4112	CB	PRO	B	203	13.553	-24.424	-2.217	1.00	24.46
BBBBATOM	4113	CG	PRO	B	203	12.593	-25.178	-3.084	1.00	24.04
BBBBATOM	4114	C	PRO	B	203	15.987	-23.731	-2.573	1.00	24.07
BBBBATOM	4115	O	PRO	B	203	16.395	-22.593	-2.343	1.00	23.18
BBBBATOM	4116	N	GLN	B	204	16.706	-24.814	-2.290	1.00	25.26
BBBBATOM	4117	CA	GLN	B	204	18.033	-24.708	-1.684	1.00	26.34
BBBBATOM	4118	CB	GLN	B	204	18.474	-26.078	-1.157	1.00	28.67

BBBBATOM	4119	CG	GLN	B	204	17.555	-26.626	-0.065	1.00	33.65
BBBBATOM	4120	CD	GLN	B	204	17.885	-28.059	0.328	1.00	37.09
BBBBATOM	4121	OE1	GLN	B	204	18.991	-28.354	0.792	1.00	39.30
BBBBATOM	4122	NE2	GLN	B	204	16.924	-28.960	0.140	1.00	38.32
BBBBATOM	4123	C	GLN	B	204	19.030	-24.177	-2.717	1.00	25.36
BBBBATOM	4124	O	GLN	B	204	19.985	-23.466	-2.385	1.00	24.98
BBBBATOM	4125	N	VAL	B	205	18.806	-24.522	-3.978	1.00	24.46
BBBBATOM	4126	CA	VAL	B	205	19.672	-24.033	-5.043	1.00	24.44
BBBBATOM	4127	CB	VAL	B	205	19.288	-24.634	-6.409	1.00	24.84
BBBBATOM	4128	CG1	VAL	B	205	20.039	-23.906	-7.534	1.00	23.72
BBBBATOM	4129	CG2	VAL	B	205	19.614	-26.110	-6.428	1.00	22.91
BBBBATOM	4130	C	VAL	B	205	19.511	-22.515	-5.110	1.00	23.79
BBBBATOM	4131	O	VAL	B	205	20.487	-21.789	-5.270	1.00	25.25
BBBBATOM	4132	N	ALA	B	206	18.273	-22.044	-4.972	1.00	24.12
BBBBATOM	4133	CA	ALA	B	206	17.980	-20.610	-5.013	1.00	22.84
BBBBATOM	4134	CB	ALA	B	206	16.466	-20.377	-4.908	1.00	21.55
BBBBATOM	4135	C	ALA	B	206	18.700	-19.862	-3.890	1.00	24.09
BBBBATOM	4136	O	ALA	B	206	19.174	-18.740	-4.081	1.00	24.90
BBBBATOM	4137	N	ALA	B	207	18.768	-20.477	-2.713	1.00	25.15
BBBBATOM	4138	CA	ALA	B	207	19.442	-19.857	-1.576	1.00	26.65
BBBBATOM	4139	CB	ALA	B	207	19.260	-20.710	-0.324	1.00	27.83
BBBBATOM	4140	C	ALA	B	207	20.924	-19.686	-1.879	1.00	26.96
BBBBATOM	4141	O	ALA	B	207	21.537	-18.693	-1.493	1.00	27.82
BBBBATOM	4142	N	LYS	B	208	21.498	-20.651	-2.586	1.00	27.19
BBBBATOM	4143	CA	LYS	B	208	22.915	-20.595	-2.919	1.00	28.31
BBBBATOM	4144	CB	LYS	B	208	23.432	-21.989	-3.300	1.00	29.85
BBBBATOM	4145	CG	LYS	B	208	23.030	-23.088	-2.329	1.00	32.97
BBBBATOM	4146	CD	LYS	B	208	23.264	-22.667	-0.886	1.00	35.74
BBBBATOM	4147	CE	LYS	B	208	22.689	-23.689	0.084	1.00	37.28
BBBBATOM	4148	NZ	LYS	B	208	21.227	-23.899	-0.135	1.00	35.29
BBBBATOM	4149	C	LYS	B	208	23.237	-19.624	-4.050	1.00	27.83
BBBBATOM	4150	O	LYS	B	208	24.286	-18.978	-4.033	1.00	27.46
BBBBATOM	4151	N	LEU	B	209	22.341	-19.517	-5.028	1.00	26.04
BBBBATOM	4152	CA	LEU	B	209	22.577	-18.640	-6.171	1.00	25.68
BBBBATOM	4153	CB	LEU	B	209	21.975	-19.268	-7.435	1.00	25.08
BBBBATOM	4154	CG	LEU	B	209	22.534	-20.638	-7.844	1.00	25.01
BBBBATOM	4155	CD1	LEU	B	209	21.797	-21.151	-9.074	1.00	25.67
BBBBATOM	4156	CD2	LEU	B	209	24.029	-20.528	-8.119	1.00	25.13
BBBBATOM	4157	C	LEU	B	209	22.075	-17.200	-6.007	1.00	25.59
BBBBATOM	4158	O	LEU	B	209	22.496	-16.313	-6.742	1.00	25.26
BBBBATOM	4159	N	GLY	B	210	21.185	-16.970	-5.045	1.00	26.27
BBBBATOM	4160	CA	GLY	B	210	20.675	-15.628	-4.804	1.00	26.56
BBBBATOM	4161	C	GLY	B	210	20.238	-14.836	-6.030	1.00	27.75
BBBBATOM	4162	O	GLY	B	210	19.518	-15.349	-6.889	1.00	27.68
BBBBATOM	4163	N	ASP	B	211	20.696	-13.585	-6.105	1.00	27.93
BBBBATOM	4164	CA	ASP	B	211	20.370	-12.647	-7.190	1.00	28.28
BBBBATOM	4165	CB	ASP	B	211	21.011	-11.283	-6.906	1.00	29.89
BBBBATOM	4166	CG	ASP	B	211	20.351	-10.545	-5.768	1.00	31.43
BBBBATOM	4167	OD1	ASP	B	211	20.864	-9.469	-5.398	1.00	32.43
BBBBATOM	4168	OD2	ASP	B	211	19.323	-11.025	-5.249	1.00	33.41
BBBBATOM	4169	C	ASP	B	211	20.768	-13.035	-8.615	1.00	27.77
BBBBATOM	4170	O	ASP	B	211	20.320	-12.397	-9.578	1.00	26.32
BBBBATOM	4171	N	SER	B	212	21.616	-14.048	-8.753	1.00	25.75
BBBBATOM	4172	CA	SER	B	212	22.098	-14.474	-10.067	1.00	25.73
BBBBATOM	4173	CB	SER	B	212	23.331	-15.376	-9.904	1.00	26.63
BBBBATOM	4174	OG	SER	B	212	22.971	-16.596	-9.282	1.00	26.71
BBBBATOM	4175	C	SER	B	212	21.062	-15.185	-10.943	1.00	23.61
BBBBATOM	4176	O	SER	B	212	21.262	-15.334	-12.147	1.00	22.28
BBBBATOM	4177	N	VAL	B	213	19.969	-15.644	-10.344	1.00	23.16
BBBBATOM	4178	CA	VAL	B	213	18.925	-16.308	-11.116	1.00	20.76
BBBBATOM	4179	CB	VAL	B	213	18.952	-17.867	-10.989	1.00	21.69
BBBBATOM	4180	CG1	VAL	B	213	20.318	-18.423	-11.375	1.00	19.84
BBBBATOM	4181	CG2	VAL	B	213	18.564	-18.288	-9.576	1.00	20.36
BBBBATOM	4182	C	VAL	B	213	17.535	-15.871	-10.677	1.00	21.41
BBBBATOM	4183	O	VAL	B	213	17.328	-15.396	-9.554	1.00	20.58
BBBBATOM	4184	N	THR	B	214	16.593	-16.021	-11.595	1.00	19.82

BBBBATOM	4185	CA	THR	B	214	15.204	-15.726	-11.337	1.00	19.60
BBBBATOM	4186	CB	THR	B	214	14.718	-14.478	-12.126	1.00	21.35
BBBBATOM	4187	OG1	THR	B	214	13.323	-14.273	-11.870	1.00	21.93
BBBBATOM	4188	CG2	THR	B	214	14.983	-14.633	-13.622	1.00	19.52
BBBBATOM	4189	C	THR	B	214	14.543	-17.021	-11.791	1.00	20.24
BBBBATOM	4190	O	THR	B	214	14.803	-17.533	-12.893	1.00	18.70
BBBBATOM	4191	N	ILE	B	215	13.706	-17.569	-10.921	1.00	19.21
BBBBATOM	4192	CA	ILE	B	215	13.076	-18.850	-11.169	1.00	18.75
BBBBATOM	4193	CB	ILE	B	215	13.417	-19.828	-10.008	1.00	18.82
BBBBATOM	4194	CG2	ILE	B	215	12.690	-21.157	-10.194	1.00	19.53
BBBBATOM	4195	CG1	ILE	B	215	14.934	-20.030	-9.931	1.00	19.76
BBBBATOM	4196	CD1	ILE	B	215	15.421	-20.656	-8.600	1.00	19.40
BBBBATOM	4197	C	ILE	B	215	11.568	-18.837	-11.315	1.00	19.26
BBBBATOM	4198	O	ILE	B	215	10.874	-18.025	-10.699	1.00	18.28
BBBBATOM	4199	N	TRP	B	216	11.089	-19.737	-12.167	1.00	18.93
BBBBATOM	4200	CA	TRP	B	216	9.661	-19.973	-12.378	1.00	19.34
BBBBATOM	4201	CB	TRP	B	216	9.222	-19.631	-13.797	1.00	18.97
BBBBATOM	4202	CG	TRP	B	216	7.757	-19.897	-14.065	1.00	20.09
BBBBATOM	4203	CD2	TRP	B	216	7.015	-19.467	-15.211	1.00	19.61
BBBBATOM	4204	CE2	TRP	B	216	5.705	-19.988	-15.085	1.00	19.98
BBBBATOM	4205	CE3	TRP	B	216	7.329	-18.690	-16.333	1.00	19.39
BBBBATOM	4206	CD1	TRP	B	216	6.888	-20.639	-13.303	1.00	19.30
BBBBATOM	4207	NE1	TRP	B	216	5.653	-20.700	-13.914	1.00	20.95
BBBBATOM	4208	CZ2	TRP	B	216	4.713	-19.759	-16.043	1.00	22.06
BBBBATOM	4209	CZ3	TRP	B	216	6.336	-18.459	-17.288	1.00	20.42
BBBBATOM	4210	CH2	TRP	B	216	5.047	-18.993	-17.134	1.00	21.16
BBBBATOM	4211	C	TRP	B	216	9.629	-21.479	-12.176	1.00	19.95
BBBBATOM	4212	O	TRP	B	216	10.114	-22.241	-13.010	1.00	19.91
BBBBATOM	4213	N	HIS	B	217	9.067	-21.897	-11.050	1.00	21.62
BBBBATOM	4214	CA	HIS	B	217	9.015	-23.303	-10.680	1.00	21.06
BBBBATOM	4215	CB	HIS	B	217	9.553	-23.419	-9.242	1.00	20.56
BBBBATOM	4216	CG	HIS	B	217	9.717	-24.824	-8.747	1.00	21.95
BBBBATOM	4217	CD2	HIS	B	217	8.915	-25.910	-8.846	1.00	22.12
BBBBATOM	4218	ND1	HIS	B	217	10.807	-25.219	-8.002	1.00	23.39
BBBBATOM	4219	CE1	HIS	B	217	10.670	-26.490	-7.663	1.00	21.82
BBBBATOM	4220	NE2	HIS	B	217	9.530	-26.933	-8.162	1.00	22.14
BBBBATOM	4221	C	HIS	B	217	7.596	-23.870	-10.795	1.00	21.27
BBBBATOM	4222	O	HIS	B	217	6.655	-23.334	-10.214	1.00	21.69
BBBBATOM	4223	N	GLN	B	218	7.448	-24.940	-11.567	1.00	20.83
BBBBATOM	4224	CA	GLN	B	218	6.149	-25.594	-11.735	1.00	24.30
BBBBATOM	4225	CB	GLN	B	218	5.915	-25.935	-13.206	1.00	23.84
BBBBATOM	4226	CG	GLN	B	218	4.561	-26.558	-13.495	1.00	25.91
BBBBATOM	4227	CD	GLN	B	218	4.637	-28.060	-13.673	1.00	26.52
BBBBATOM	4228	OE1	GLN	B	218	3.757	-28.793	-13.214	1.00	28.05
BBBBATOM	4229	NE2	GLN	B	218	5.680	-28.529	-14.360	1.00	25.20
BBBBATOM	4230	C	GLN	B	218	6.173	-26.854	-10.854	1.00	24.64
BBBBATOM	4231	O	GLN	B	218	6.780	-27.866	-11.199	1.00	25.73
BBBBATOM	4232	N	SER	B	219	5.502	-26.756	-9.709	1.00	26.38
BBBBATOM	4233	CA	SER	B	219	5.463	-27.800	-8.684	1.00	26.73
BBBBATOM	4234	CB	SER	B	219	4.947	-27.188	-7.380	1.00	28.26
BBBBATOM	4235	OG	SER	B	219	3.563	-26.881	-7.488	1.00	26.22
BBBBATOM	4236	C	SER	B	219	4.689	-29.096	-8.914	1.00	27.58
BBBBATOM	4237	O	SER	B	219	5.014	-30.122	-8.320	1.00	26.39
BBBBATOM	4238	N	GLY	B	220	3.662	-29.054	-9.750	1.00	28.58
BBBBATOM	4239	CA	GLY	B	220	2.855	-30.242	-9.961	1.00	30.53
BBBBATOM	4240	C	GLY	B	220	1.596	-30.110	-9.111	1.00	31.96
BBBBATOM	4241	O	GLY	B	220	1.523	-29.248	-8.233	1.00	30.92
BBBBATOM	4242	N	LYS	B	221	0.608	-30.965	-9.358	1.00	33.93
BBBBATOM	4243	CA	LYS	B	221	-0.657	-30.914	-8.628	1.00	35.12
BBBBATOM	4244	CB	LYS	B	221	-1.573	-32.049	-9.094	1.00	37.88
BBBBATOM	4245	CG	LYS	B	221	-2.942	-32.055	-8.427	1.00	40.51
BBBBATOM	4246	CD	LYS	B	221	-3.792	-33.215	-8.934	1.00	42.62
BBBBATOM	4247	CE	LYS	B	221	-5.162	-33.249	-8.260	1.00	43.67
BBBBATOM	4248	NZ	LYS	B	221	-6.002	-34.383	-8.763	1.00	45.38
BBBBATOM	4249	C	LYS	B	221	-0.545	-30.950	-7.103	1.00	35.13
BBBBATOM	4250	O	LYS	B	221	0.110	-31.823	-6.531	1.00	34.60

BBBBATOM	4251	N	GLY	B	222	-1.187	-29.979	-6.461	1.00	34.79
BBBBATOM	4252	CA	GLY	B	222	-1.195	-29.899	-5.011	1.00	35.34
BBBBATOM	4253	C	GLY	B	222	0.111	-29.594	-4.299	1.00	35.61
BBBBATOM	4254	O	GLY	B	222	0.163	-29.678	-3.071	1.00	35.51
BBBBATOM	4255	N	SER	B	223	1.158	-29.234	-5.038	1.00	34.65
BBBBATOM	4256	CA	SER	B	223	2.451	-28.934	-4.418	1.00	33.98
BBBBATOM	4257	CB	SER	B	223	3.552	-29.781	-5.062	1.00	35.02
BBBBATOM	4258	OG	SER	B	223	3.303	-31.168	-4.897	1.00	36.07
BBBBATOM	4259	C	SER	B	223	2.839	-27.454	-4.504	1.00	33.55
BBBBATOM	4260	O	SER	B	223	3.930	-27.063	-4.086	1.00	31.72
BBBBATOM	4261	N	GLN	B	224	1.941	-26.639	-5.044	1.00	33.22
BBBBATOM	4262	CA	GLN	B	224	2.187	-25.208	-5.186	1.00	33.71
BBBBATOM	4263	CB	GLN	B	224	0.954	-24.539	-5.799	1.00	35.45
BBBBATOM	4264	CG	GLN	B	224	1.160	-23.120	-6.337	1.00	37.82
BBBBATOM	4265	CD	GLN	B	224	1.344	-22.076	-5.249	1.00	40.08
BBBBATOM	4266	OE1	GLN	B	224	0.669	-22.111	-4.217	1.00	40.97
BBBBATOM	4267	NE2	GLN	B	224	2.244	-21.124	-5.486	1.00	40.08
BBBBATOM	4268	C	GLN	B	224	2.510	-24.560	-3.840	1.00	33.86
BBBBATOM	4269	O	GLN	B	224	3.512	-23.856	-3.697	1.00	33.38
BBBBATOM	4270	N	GLN	B	225	1.659	-24.814	-2.850	1.00	33.06
BBBBATOM	4271	CA	GLN	B	225	1.823	-24.239	-1.519	1.00	32.32
BBBBATOM	4272	CB	GLN	B	225	0.624	-24.619	-0.640	1.00	35.12
BBBBATOM	4273	CG	GLN	B	225	-0.743	-24.143	-1.151	1.00	36.85
BBBBATOM	4274	CD	GLN	B	225	-1.144	-24.751	-2.495	1.00	39.09
BBBBATOM	4275	OE1	GLN	B	225	-0.914	-25.937	-2.759	1.00	39.42
BBBBATOM	4276	NE2	GLN	B	225	-1.768	-23.937	-3.345	1.00	40.13
BBBBATOM	4277	C	GLN	B	225	3.117	-24.606	-0.788	1.00	30.73
BBBBATOM	4278	O	GLN	B	225	3.766	-23.742	-0.202	1.00	30.36
BBBBATOM	4279	N	SER	B	226	3.494	-25.878	-0.817	1.00	29.26
BBBBATOM	4280	CA	SER	B	226	4.701	-26.309	-0.122	1.00	28.30
BBBBATOM	4281	CB	SER	B	226	4.727	-27.834	0.003	1.00	29.10
BBBBATOM	4282	OG	SER	B	226	4.563	-28.461	-1.254	1.00	32.61
BBBBATOM	4283	C	SER	B	226	5.991	-25.809	-0.771	1.00	26.41
BBBBATOM	4284	O	SER	B	226	6.950	-25.486	-0.073	1.00	25.24
BBBBATOM	4285	N	VAL	B	227	6.019	-25.738	-2.099	1.00	25.21
BBBBATOM	4286	CA	VAL	B	227	7.214	-25.247	-2.791	1.00	24.28
BBBBATOM	4287	CB	VAL	B	227	7.150	-25.527	-4.317	1.00	23.32
BBBBATOM	4288	CG1	VAL	B	227	8.368	-24.914	-5.028	1.00	20.67
BBBBATOM	4289	CG2	VAL	B	227	7.117	-27.024	-4.563	1.00	22.45
BBBBATOM	4290	C	VAL	B	227	7.335	-23.743	-2.545	1.00	24.34
BBBBATOM	4291	O	VAL	B	227	8.421	-23.240	-2.281	1.00	25.50
BBBBATOM	4292	N	GLU	B	228	6.209	-23.035	-2.623	1.00	26.12
BBBBATOM	4293	CA	GLU	B	228	6.178	-21.592	-2.387	1.00	27.23
BBBBATOM	4294	CB	GLU	B	228	4.735	-21.075	-2.476	1.00	28.60
BBBBATOM	4295	CG	GLU	B	228	4.558	-19.586	-2.184	1.00	30.24
BBBBATOM	4296	CD	GLU	B	228	4.938	-18.688	-3.356	1.00	31.99
BBBBATOM	4297	OE1	GLU	B	228	5.012	-17.452	-3.159	1.00	31.68
BBBBATOM	4298	OE2	GLU	B	228	5.154	-19.212	-4.471	1.00	32.04
BBBBATOM	4299	C	GLU	B	228	6.746	-21.327	-0.994	1.00	27.95
BBBBATOM	4300	O	GLU	B	228	7.511	-20.383	-0.787	1.00	27.32
BBBBATOM	4301	N	GLN	B	229	6.374	-22.178	-0.041	1.00	28.66
BBBBATOM	4302	CA	GLN	B	229	6.853	-22.046	1.329	1.00	28.38
BBBBATOM	4303	CB	GLN	B	229	6.082	-22.990	2.261	1.00	31.03
BBBBATOM	4304	CG	GLN	B	229	6.570	-22.946	3.700	1.00	35.48
BBBBATOM	4305	CD	GLN	B	229	5.780	-23.860	4.615	1.00	38.01
BBBBATOM	4306	OE1	GLN	B	229	4.548	-23.810	4.645	1.00	39.26
BBBBATOM	4307	NE2	GLN	B	229	6.484	-24.697	5.370	1.00	38.61
BBBBATOM	4308	C	GLN	B	229	8.338	-22.362	1.407	1.00	27.09
BBBBATOM	4309	O	GLN	B	229	9.084	-21.697	2.124	1.00	28.29
BBBBATOM	4310	N	ALA	B	230	8.771	-23.385	0.677	1.00	26.97
BBBBATOM	4311	CA	ALA	B	230	10.185	-23.754	0.682	1.00	26.18
BBBBATOM	4312	CB	ALA	B	230	10.412	-24.984	-0.184	1.00	25.07
BBBBATOM	4313	C	ALA	B	230	11.054	-22.588	0.192	1.00	26.36
BBBBATOM	4314	O	ALA	B	230	12.119	-22.317	0.755	1.00	25.04
BBBBATOM	4315	N	TYR	B	231	10.605	-21.895	-0.854	1.00	25.85
BBBBATOM	4316	CA	TYR	B	231	11.371	-20.766	-1.366	1.00	25.47

BBBBATOM	4317	CB	TYR	B	231	10.762	-20.248	-2.678	1.00	24.72
BBBBATOM	4318	CG	TYR	B	231	11.236	-21.014	-3.905	1.00	23.66
BBBBATOM	4319	CD1	TYR	B	231	12.546	-20.869	-4.381	1.00	23.97
BBBBATOM	4320	CE1	TYR	B	231	13.006	-21.599	-5.488	1.00	21.40
BBBBATOM	4321	CD2	TYR	B	231	10.393	-21.905	-4.567	1.00	22.63
BBBBATOM	4322	CE2	TYR	B	231	10.841	-22.641	-5.681	1.00	22.71
BBBBATOM	4323	CZ	TYR	B	231	12.151	-22.480	-6.128	1.00	21.91
BBBBATOM	4324	OH	TYR	B	231	12.600	-23.214	-7.199	1.00	21.69
BBBBATOM	4325	C	TYR	B	231	11.450	-19.639	-0.336	1.00	26.53
BBBBATOM	4326	O	TYR	B	231	12.498	-19.011	-0.175	1.00	26.32
BBBBATOM	4327	N	ALA	B	232	10.345	-19.380	0.361	1.00	26.28
BBBBATOM	4328	CA	ALA	B	232	10.342	-18.322	1.368	1.00	27.51
BBBBATOM	4329	CB	ALA	B	232	8.930	-18.109	1.910	1.00	28.09
BBBBATOM	4330	C	ALA	B	232	11.303	-18.695	2.499	1.00	28.03
BBBBATOM	4331	O	ALA	B	232	12.069	-17.858	2.983	1.00	27.93
BBBBATOM	4332	N	GLU	B	233	11.263	-19.958	2.911	1.00	29.43
BBBBATOM	4333	CA	GLU	B	233	12.145	-20.441	3.966	1.00	30.87
BBBBATOM	4334	CB	GLU	B	233	11.772	-21.877	4.344	1.00	33.60
BBBBATOM	4335	CG	GLU	B	233	10.491	-21.973	5.170	1.00	37.67
BBBBATOM	4336	CD	GLU	B	233	10.077	-23.404	5.461	1.00	40.35
BBBBATOM	4337	OE1	GLU	B	233	10.964	-24.283	5.525	1.00	42.97
BBBBATOM	4338	OE2	GLU	B	233	8.864	-23.649	5.641	1.00	41.95
BBBBATOM	4339	C	GLU	B	233	13.606	-20.369	3.530	1.00	30.58
BBBBATOM	4340	O	GLU	B	233	14.499	-20.202	4.359	1.00	30.82
BBBBATOM	4341	N	ALA	B	234	13.850	-20.485	2.227	1.00	29.17
BBBBATOM	4342	CA	ALA	B	234	15.215	-20.417	1.714	1.00	28.48
BBBBATOM	4343	CB	ALA	B	234	15.310	-21.110	0.354	1.00	27.71
BBBBATOM	4344	C	ALA	B	234	15.649	-18.961	1.588	1.00	27.73
BBBBATOM	4345	O	ALA	B	234	16.787	-18.677	1.213	1.00	27.34
BBBBATOM	4346	N	GLY	B	235	14.731	-18.045	1.890	1.00	26.74
BBBBATOM	4347	CA	GLY	B	235	15.033	-16.627	1.815	1.00	26.23
BBBBATOM	4348	C	GLY	B	235	14.946	-16.009	0.426	1.00	26.13
BBBBATOM	4349	O	GLY	B	235	15.483	-14.924	0.198	1.00	25.67
BBBBATOM	4350	N	GLN	B	236	14.284	-16.696	-0.502	1.00	25.36
BBBBATOM	4351	CA	GLN	B	236	14.121	-16.198	-1.870	1.00	25.53
BBBBATOM	4352	CB	GLN	B	236	14.940	-17.043	-2.852	1.00	25.84
BBBBATOM	4353	CG	GLN	B	236	16.436	-17.074	-2.603	1.00	27.18
BBBBATOM	4354	CD	GLN	B	236	17.080	-15.705	-2.661	1.00	28.96
BBBBATOM	4355	OE1	GLN	B	236	16.686	-14.850	-3.456	1.00	30.03
BBBBATOM	4356	NE2	GLN	B	236	18.092	-15.495	-1.829	1.00	29.39
BBBBATOM	4357	C	GLN	B	236	12.641	-16.298	-2.232	1.00	24.12
BBBBATOM	4358	O	GLN	B	236	12.262	-17.002	-3.167	1.00	23.31
BBBBATOM	4359	N	PRO	B	237	11.783	-15.578	-1.497	1.00	24.40
BBBBATOM	4360	CD	PRO	B	237	12.143	-14.580	-0.473	1.00	24.52
BBBBATOM	4361	CA	PRO	B	237	10.336	-15.587	-1.720	1.00	24.65
BBBBATOM	4362	CB	PRO	B	237	9.808	-14.798	-0.527	1.00	25.37
BBBBATOM	4363	CG	PRO	B	237	10.862	-13.773	-0.340	1.00	25.24
BBBBATOM	4364	C	PRO	B	237	9.837	-15.012	-3.043	1.00	25.33
BBBBATOM	4365	O	PRO	B	237	8.720	-15.313	-3.465	1.00	24.93
BBBBATOM	4366	N	GLN	B	238	10.663	-14.197	-3.690	1.00	24.47
BBBBATOM	4367	CA	GLN	B	238	10.277	-13.558	-4.945	1.00	24.29
BBBBATOM	4368	CB	GLN	B	238	11.281	-12.455	-5.306	1.00	23.76
BBBBATOM	4369	CG	GLN	B	238	12.622	-12.945	-5.852	1.00	25.22
BBBBATOM	4370	CD	GLN	B	238	13.535	-13.523	-4.783	1.00	26.90
BBBBATOM	4371	OE1	GLN	B	238	13.188	-13.550	-3.600	1.00	28.05
BBBBATOM	4372	NE2	GLN	B	238	14.712	-13.983	-5.195	1.00	25.61
BBBBATOM	4373	C	GLN	B	238	10.108	-14.489	-6.143	1.00	23.41
BBBBATOM	4374	O	GLN	B	238	9.485	-14.112	-7.139	1.00	20.49
BBBBATOM	4375	N	HIS	B	239	10.655	-15.700	-6.069	1.00	22.66
BBBBATOM	4376	CA	HIS	B	239	10.526	-16.608	-7.201	1.00	22.08
BBBBATOM	4377	CB	HIS	B	239	11.432	-17.829	-7.008	1.00	22.41
BBBBATOM	4378	CG	HIS	B	239	12.891	-17.488	-6.998	1.00	20.93
BBBBATOM	4379	CD2	HIS	B	239	13.869	-17.774	-6.104	1.00	20.09
BBBBATOM	4380	ND1	HIS	B	239	13.488	-16.743	-7.992	1.00	20.30
BBBBATOM	4381	CE1	HIS	B	239	14.769	-16.582	-7.711	1.00	22.38
BBBBATOM	4382	NE2	HIS	B	239	15.025	-17.197	-6.569	1.00	19.62

BBBBATOM	4383	C	HIS	B	239
BBBBATOM	4384	O	HIS	B	239
BBBBATOM	4385	N	LYS	B	240
BBBBATOM	4386	CA	LYS	B	240
BBBBATOM	4387	CB	LYS	B	240
BBBBATOM	4388	CG	LYS	B	240
BBBBATOM	4389	CD	LYS	B	240
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BBBBATOM	4391	NZ	LYS	B	240
BBBBATOM	4392	C	LYS	B	240
BBBBATOM	4393	O	LYS	B	240
BBBBATOM	4394	N	VAL	B	241
BBBBATOM	4395	CA	VAL	B	241
BBBBATOM	4396	CB	VAL	B	241
BBBBATOM	4397	CG1	VAL	B	241
BBBBATOM	4398	CG2	VAL	B	241
BBBBATOM	4399	C	VAL	B	241
BBBBATOM	4400	O	VAL	B	241
BBBBATOM	4401	N	THR	B	242
BBBBATOM	4402	CA	THR	B	242
BBBBATOM	4403	CB	THR	B	242
BBBBATOM	4404	OG1	THR	B	242
BBBBATOM	4405	OG2	THR	B	242
BBBBATOM	4406	C	THR	B	242
BBBBATOM	4407	O	THR	B	242
BBBBATOM	4408	N	GLU	B	243
BBBBATOM	4409	CA	GLU	B	243
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BBBBATOM	4414	OE2	GLU	B	243
BBBBATOM	4415	C	GLU	B	243
BBBBATOM	4416	O	GLU	B	243
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BBBBATOM	4418	CA	PHE	B	244
BBBBATOM	4419	CB	PHE	B	244
BBBBATOM	4420	CG	PHE	B	244
BBBBATOM	4421	CD1	PHE	B	244
BBBBATOM	4422	CD2	PHE	B	244
BBBBATOM	4423	CE1	PHE	B	244
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BBBBATOM	4429	CA	ILE	B	245
BBBBATOM	4430	CB	ILE	B	245
BBBBATOM	4431	CG2	ILE	B	245
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BBBBATOM	4434	C	ILE	B	245
BBBBATOM	4435	O	ILE	B	245
BBBBATOM	4436	N	ASP	B	246
BBBBATOM	4437	CA	ASP	B	246
BBBBATOM	4438	CB	ASP	B	246
BBBBATOM	4439	CG	ASP	B	246
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BBBBATOM	4442	C	ASP	B	246
BBBBATOM	4443	O	ASP	B	246
BBBBATOM	4444	N	ASP	B	247
BBBBATOM	4445	CA	ASP	B	247
BBBBATOM	4446	CB	ASP	B	247
BBBBATOM	4447	CG	ASP	B	247
BBBBATOM	4448	OD1	ASP	B	247

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8.727	-17.209	-8.703	1.00	21.76
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7.112	-17.102	-10.534	1.00	23.38
5.718	-17.385	-11.079	1.00	24.06
5.701	-17.155	-12.585	1.00	23.93
4.315	-17.309	-13.193	1.00	23.72
3.478	-16.129	-12.884	1.00	21.82
7.149	-19.091	-9.046	1.00	23.38
7.922	-19.871	-9.607	1.00	23.06
6.075	-19.497	-8.378	1.00	23.98
5.740	-20.911	-8.277	1.00	23.78
5.858	-21.428	-6.833	1.00	24.03
5.548	-22.923	-6.803	1.00	24.14
7.242	-21.144	-6.281	1.00	23.49
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3.380	-20.528	-8.184	1.00	24.63
4.103	-22.000	-9.710	1.00	24.22
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3.503	-24.577	-10.303	1.00	26.75
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1.256	-26.289	-11.202	1.00	26.61
1.841	-27.370	-11.304	1.00	26.48
0.807	-25.602	-12.248	1.00	26.54
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-2.318	-27.172	-12.716	1.00	31.10
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-2.678	-21.511	-19.962	1.00	45.41
-0.088	-24.020	-20.780	1.00	35.70
-0.155	-24.768	-21.758	1.00	38.58
0.582	-22.876	-20.794	1.00	33.18
1.245	-22.392	-21.999	1.00	30.74
0.936	-20.904	-22.182	1.00	29.62
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2.161	-21.036	-24.225	1.00	27.57

BBBBBATOM	4449	OD2	ASP	B	247	0.854	-19.296	-23.935	1.00	29.19
BBBBBATOM	4450	C	ASP	B	247	2.754	-22.607	-21.892	1.00	28.87
BBBBBATOM	4451	O	ASP	B	247	3.494	-21.695	-21.525	1.00	27.28
BBBBBATOM	4452	N	MET	B	248	3.204	-23.818	-22.205	1.00	27.72
BBBBBATOM	4453	CA	MET	B	248	4.625	-24.136	-22.138	1.00	28.41
BBBBBATOM	4454	CB	MET	B	248	4.856	-25.623	-22.405	1.00	29.48
BBBBBATOM	4455	CG	MET	B	248	4.952	-26.469	-21.150	1.00	34.21
BBBBBATOM	4456	SD	MET	B	248	6.277	-25.936	-20.049	1.00	38.21
BBBBBATOM	4457	CE	MET	B	248	5.611	-26.499	-18.479	1.00	37.90
BBBBBATOM	4458	C	MET	B	248	5.429	-23.313	-23.132	1.00	27.22
BBBBBATOM	4459	O	MET	B	248	6.578	-22.965	-22.873	1.00	27.06
BBBBBATOM	4460	N	ALA	B	249	4.827	-23.009	-24.279	1.00	26.23
BBBBBATOM	4461	CA	ALA	B	249	5.512	-22.216	-25.290	1.00	24.67
BBBBBATOM	4462	CB	ALA	B	249	4.625	-22.069	-26.537	1.00	25.39
BBBBBATOM	4463	C	ALA	B	249	5.870	-20.843	-24.721	1.00	24.03
BBBBBATOM	4464	O	ALA	B	249	6.971	-20.338	-24.932	1.00	23.78
BBBBBATOM	4465	N	ALA	B	250	4.942	-20.241	-23.983	1.00	23.39
BBBBBATOM	4466	CA	ALA	B	250	5.188	-18.933	-23.390	1.00	21.78
BBBBBATOM	4467	CB	ALA	B	250	3.898	-18.376	-22.797	1.00	23.21
BBBBBATOM	4468	C	ALA	B	250	6.277	-19.011	-22.313	1.00	21.84
BBBBBATOM	4469	O	ALA	B	250	7.091	-18.092	-22.176	1.00	20.78
BBBBBATOM	4470	N	ALA	B	251	6.291	-20.099	-21.548	1.00	20.34
BBBBBATOM	4471	CA	ALA	B	251	7.301	-20.259	-20.501	1.00	20.85
BBBBBATOM	4472	CB	ALA	B	251	6.920	-21.405	-19.568	1.00	19.79
BBBBBATOM	4473	C	ALA	B	251	8.685	-20.512	-21.123	1.00	20.95
BBBBBATOM	4474	O	ALA	B	251	9.689	-19.980	-20.648	1.00	21.14
BBBBBATOM	4475	N	TYR	B	252	8.723	-21.314	-22.184	1.00	21.27
BBBBBATOM	4476	CA	TYR	B	252	9.972	-21.616	-22.886	1.00	22.78
BBBBBATOM	4477	CB	TYR	B	252	9.726	-22.661	-23.980	1.00	21.62
BBBBBATOM	4478	CG	TYR	B	252	9.662	-24.100	-23.505	1.00	23.34
BBBBBATOM	4479	CD1	TYR	B	252	9.003	-25.065	-24.261	1.00	22.88
BBBBBATOM	4480	CE1	TYR	B	252	8.961	-26.392	-23.861	1.00	24.81
BBBBBATOM	4481	CD2	TYR	B	252	10.288	-24.505	-22.319	1.00	22.30
BBBBBATOM	4482	CE2	TYR	B	252	10.253	-25.838	-21.912	1.00	23.56
BBBBBATOM	4483	CZ	TYR	B	252	9.590	-26.772	-22.687	1.00	24.26
BBBBBATOM	4484	OH	TYR	B	252	9.554	-28.088	-22.305	1.00	25.57
BBBBBATOM	4485	C	TYR	B	252	10.566	-20.354	-23.516	1.00	23.57
BBBBBATOM	4486	O	TYR	B	252	11.784	-20.180	-23.550	1.00	23.91
BBBBBATOM	4487	N	ALA	B	253	9.699	-19.473	-24.007	1.00	23.22
BBBBBATOM	4488	CA	ALA	B	253	10.131	-18.224	-24.636	1.00	23.54
BBBBBATOM	4489	CB	ALA	B	253	8.931	-17.512	-25.275	1.00	24.59
BBBBBATOM	4490	C	ALA	B	253	10.783	-17.305	-23.617	1.00	23.30
BBBBBATOM	4491	O	ALA	B	253	11.699	-16.546	-23.945	1.00	23.04
BBBBBATOM	4492	N	TRP	B	254	10.299	-17.369	-22.379	1.00	20.49
BBBBBATOM	4493	CA	TRP	B	254	10.829	-16.534	-21.303	1.00	19.76
BBBBBATOM	4494	CB	TRP	B	254	9.808	-16.467	-20.151	1.00	19.57
BBBBBATOM	4495	CG	TRP	B	254	10.381	-15.981	-18.841	1.00	19.57
BBBBBATOM	4496	CD2	TRP	B	254	10.870	-16.796	-17.762	1.00	19.25
BBBBBATOM	4497	CE2	TRP	B	254	11.369	-15.922	-16.771	1.00	18.94
BBBBBATOM	4498	CE3	TRP	B	254	10.939	-18.178	-17.543	1.00	19.18
BBBBBATOM	4499	CD1	TRP	B	254	10.591	-14.691	-18.470	1.00	19.03
BBBBBATOM	4500	NE1	TRP	B	254	11.185	-14.643	-17.226	1.00	20.30
BBBBBATOM	4501	CZ2	TRP	B	254	11.931	-16.382	-15.572	1.00	20.01
BBBBBATOM	4502	CZ3	TRP	B	254	11.504	-18.642	-16.346	1.00	20.05
BBBBBATOM	4503	CH2	TRP	B	254	11.991	-17.743	-15.380	1.00	18.31
BBBBBATOM	4504	C	TRP	B	254	12.156	-17.059	-20.755	1.00	19.33
BBBBBATOM	4505	O	TRP	B	254	13.084	-16.293	-20.496	1.00	19.25
BBBBBATOM	4506	N	ALA	B	255	12.234	-18.373	-20.597	1.00	18.90
BBBBBATOM	4507	CA	ALA	B	255	13.399	-19.025	-20.003	1.00	19.51
BBBBBATOM	4508	CB	ALA	B	255	13.082	-20.507	-19.788	1.00	18.83
BBBBBATOM	4509	C	ALA	B	255	14.737	-18.901	-20.713	1.00	18.88
BBBBBATOM	4510	O	ALA	B	255	14.803	-18.688	-21.918	1.00	19.40
BBBBBATOM	4511	N	ASP	B	256	15.803	-19.036	-19.927	1.00	19.01
BBBBBATOM	4512	CA	ASP	B	256	17.176	-19.026	-20.434	1.00	17.58
BBBBBATOM	4513	CB	ASP	B	256	18.078	-18.185	-19.534	1.00	18.47
BBBBBATOM	4514	CG	ASP	B	256	17.954	-16.699	-19.795	1.00	18.05

BBBBBATOM	4515	OD1	ASP	B	256
BBBBBATOM	4516	OD2	ASP	B	256
BBBBBATOM	4517	C	ASP	B	256
BBBBBATOM	4518	O	ASP	B	256
BBBBBATOM	4519	N	VAL	B	257
BBBBBATOM	4520	CA	VAL	B	257
BBBBBATOM	4521	CB	VAL	B	257
BBBBBATOM	4522	CG1	VAL	B	257
BBBBBATOM	4523	CG2	VAL	B	257
BBBBBATOM	4524	C	VAL	B	257
BBBBBATOM	4525	O	VAL	B	257
BBBBBATOM	4526	N	VAL	B	258
BBBBBATOM	4527	CA	VAL	B	258
BBBBBATOM	4528	CB	VAL	B	258
BBBBBATOM	4529	CG1	VAL	B	258
BBBBBATOM	4530	CG2	VAL	B	258
BBBBBATOM	4531	C	VAL	B	258
BBBBBATOM	4532	O	VAL	B	258
BBBBBATOM	4533	N	VAL	B	259
BBBBBATOM	4534	CA	VAL	B	259
BBBBBATOM	4535	CB	VAL	B	259
BBBBBATOM	4536	CG1	VAL	B	259
BBBBBATOM	4537	CG2	VAL	B	259
BBBBBATOM	4538	C	VAL	B	259
BBBBBATOM	4539	O	VAL	B	259
BBBBBATOM	4540	N	CYS	B	260
BBBBBATOM	4541	CA	CYS	B	260
BBBBBATOM	4542	CB	CYS	B	260
BBBBBATOM	4543	SG	CYS	B	260
BBBBBATOM	4544	C	CYS	B	260
BBBBBATOM	4545	O	CYS	B	260
BBBBBATOM	4546	N	ARG	B	261
BBBBBATOM	4547	CA	ARG	B	261
BBBBBATOM	4548	CB	ARG	B	261
BBBBBATOM	4549	CG	ARG	B	261
BBBBBATOM	4550	CD	ARG	B	261
BBBBBATOM	4551	NE	ARG	B	261
BBBBBATOM	4552	CZ	ARG	B	261
BBBBBATOM	4553	NH1	ARG	B	261
BBBBBATOM	4554	NH2	ARG	B	261
BBBBBATOM	4555	C	ARG	B	261
BBBBBATOM	4556	O	ARG	B	261
BBBBBATOM	4557	N	SER	B	262
BBBBBATOM	4558	CA	SER	B	262
BBBBBATOM	4559	CB	SER	B	262
BBBBBATOM	4560	OG	SER	B	262
BBBBBATOM	4561	C	SER	B	262
BBBBBATOM	4562	O	SER	B	262
BBBBBATOM	4563	N	GLY	B	263
BBBBBATOM	4564	CA	GLY	B	263
BBBBBATOM	4565	C	GLY	B	263
BBBBBATOM	4566	O	GLY	B	263
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BBBBBATOM	4568	CA	ALA	B	264
BBBBBATOM	4569	CB	ALA	B	264
BBBBBATOM	4570	C	ALA	B	264
BBBBBATOM	4571	O	ALA	B	264
BBBBBATOM	4572	N	LEU	B	265
BBBBBATOM	4573	CA	LEU	B	265
BBBBBATOM	4574	CB	LEU	B	265
BBBBBATOM	4575	CG	LEU	B	265
BBBBBATOM	4576	CD1	LEU	B	265
BBBBBATOM	4577	CD2	LEU	B	265
BBBBBATOM	4578	C	LEU	B	265
BBBBBATOM	4579	O	LEU	B	265
BBBBBATOM	4580	N	THR	B	266

17.845	-15.944	-18.806	1.00	16.89
17.983	-16.287	-20.982	1.00	19.53
17.657	-20.481	-20.379	1.00	18.01
18.459	-20.929	-21.198	1.00	16.11
17.147	-21.216	-19.396	1.00	17.49
17.535	-22.603	-19.194	1.00	18.53
18.831	-22.681	-18.332	1.00	17.72
18.586	-22.069	-16.966	1.00	19.19
19.286	-24.129	-18.200	1.00	20.40
16.400	-23.363	-18.501	1.00	18.31
15.659	-22.795	-17.703	1.00	19.74
16.263	-24.643	-18.818	1.00	18.74
15.208	-25.456	-18.234	1.00	19.32
14.328	-26.100	-19.337	1.00	19.89
13.101	-26.754	-18.714	1.00	19.81
13.907	-25.041	-20.364	1.00	21.59
15.799	-26.585	-17.389	1.00	19.70
16.808	-27.175	-17.758	1.00	18.96
15.167	-26.861	-16.253	1.00	20.24
15.581	-27.957	-15.374	1.00	19.85
15.850	-27.483	-13.936	1.00	20.08
16.222	-28.689	-13.059	1.00	20.22
16.966	-26.453	-13.930	1.00	17.86
14.382	-28.890	-15.371	1.00	20.02
13.301	-28.500	-14.942	1.00	21.88
14.562	-30.111	-15.867	1.00	21.70
13.454	-31.055	-15.946	1.00	22.00
12.494	-30.618	-17.057	1.00	22.77
13.297	-30.506	-18.711	1.00	22.15
13.903	-32.478	-16.242	1.00	21.86
15.087	-32.730	-16.496	1.00	21.34
12.937	-33.397	-16.212	1.00	22.34
13.170	-34.800	-16.515	1.00	23.75
11.964	-35.663	-16.104	1.00	27.16
11.376	-35.337	-14.738	1.00	31.82
11.490	-36.473	-13.732	1.00	36.33
12.865	-36.721	-13.323	1.00	38.48
13.218	-37.176	-12.125	1.00	37.25
12.295	-37.433	-11.204	1.00	38.46
14.499	-37.370	-11.848	1.00	36.79
13.351	-34.871	-18.032	1.00	23.98
13.117	-33.883	-18.746	1.00	22.44
13.740	-36.038	-18.527	1.00	22.00
13.975	-36.189	-19.948	1.00	23.18
15.481	-36.377	-20.203	1.00	24.45
16.043	-37.326	-19.311	1.00	25.79
13.173	-37.263	-20.676	1.00	22.90
13.738	-38.179	-21.274	1.00	23.25
11.850	-37.151	-20.619	1.00	22.74
11.026	-38.079	-21.361	1.00	22.85
11.392	-37.793	-22.813	1.00	24.06
11.908	-36.705	-23.121	1.00	22.75
11.130	-38.739	-23.708	1.00	23.37
11.482	-38.564	-25.115	1.00	24.25
11.133	-39.829	-25.894	1.00	24.58
10.843	-37.343	-25.783	1.00	24.29
11.523	-36.572	-26.470	1.00	24.33
9.541	-37.167	-25.596	1.00	24.44
8.846	-36.037	-26.205	1.00	24.66
7.332	-36.183	-26.011	1.00	25.33
6.760	-37.544	-26.426	1.00	27.97
5.242	-37.541	-26.258	1.00	28.21
7.146	-37.856	-27.878	1.00	27.40
9.331	-34.717	-25.613	1.00	24.47
9.374	-33.693	-26.301	1.00	23.85
9.702	-34.747	-24.338	1.00	22.12

BBBBATOM	4581	CA	THR	B	266	10.194	-33.557	-23.657	1.00	22.34
BBBBATOM	4582	CB	THR	B	266	10.348	-33.803	-22.140	1.00	22.35
BBBBATOM	4583	OG1	THR	B	266	9.061	-34.087	-21.583	1.00	24.46
BBBBATOM	4584	CG2	THR	B	266	10.945	-32.573	-21.444	1.00	24.00
BBBBATOM	4585	C	THR	B	266	11.535	-33.117	-24.226	1.00	21.15
BBBBATOM	4586	O	THR	B	266	11.761	-31.926	-24.442	1.00	20.35
BBBBATOM	4587	N	VAL	B	267	12.427	-34.075	-24.461	1.00	20.46
BBBBATOM	4588	CA	VAL	B	267	13.730	-33.762	-25.023	1.00	21.11
BBBBATOM	4589	CB	VAL	B	267	14.614	-35.039	-25.114	1.00	21.54
BBBBATOM	4590	CG1	VAL	B	267	15.903	-34.740	-25.865	1.00	20.72
BBBBATOM	4591	CG2	VAL	B	267	14.938	-35.541	-23.708	1.00	20.45
BBBBATOM	4592	C	VAL	B	267	13.548	-33.138	-26.416	1.00	21.34
BBBBATOM	4593	O	VAL	B	267	14.188	-32.135	-26.747	1.00	19.99
BBBBATOM	4594	N	SER	B	268	12.663	-33.717	-27.222	1.00	21.61
BBBBATOM	4595	CA	SER	B	268	12.411	-33.191	-28.567	1.00	21.96
BBBBATOM	4596	CB	SER	B	268	11.474	-34.121	-29.344	1.00	21.57
BBBBATOM	4597	OG	SER	B	268	12.141	-35.316	-29.721	1.00	24.06
BBBBATOM	4598	C	SER	B	268	11.817	-31.790	-28.519	1.00	21.81
BBBBATOM	4599	O	SER	B	268	12.158	-30.933	-29.336	1.00	22.60
BBBBATOM	4600	N	GLU	B	269	10.928	-31.563	-27.557	1.00	21.64
BBBBATOM	4601	CA	GLU	B	269	10.282	-30.272	-27.378	1.00	21.95
BBBBATOM	4602	CB	GLU	B	269	9.213	-30.399	-26.292	1.00	24.72
BBBBATOM	4603	CG	GLU	B	269	8.480	-29.128	-25.940	1.00	27.67
BBBBATOM	4604	CD	GLU	B	269	7.385	-29.380	-24.908	1.00	30.05
BBBBATOM	4605	OE1	GLU	B	269	6.325	-29.915	-25.287	1.00	31.50
BBBBATOM	4606	OE2	GLU	B	269	7.591	-29.057	-23.719	1.00	29.84
BBBBATOM	4607	C	GLU	B	269	11.321	-29.214	-26.999	1.00	21.68
BBBBATOM	4608	O	GLU	B	269	11.301	-28.095	-27.518	1.00	18.12
BBBBATOM	4609	N	ILE	B	270	12.224	-29.581	-26.092	1.00	19.43
BBBBATOM	4610	CA	ILE	B	270	13.295	-28.698	-25.638	1.00	20.62
BBBBATOM	4611	CB	ILE	B	270	14.157	-29.391	-24.533	1.00	20.30
BBBBATOM	4612	CG2	ILE	B	270	15.415	-28.595	-24.266	1.00	19.17
BBBBATOM	4613	CG1	ILE	B	270	13.337	-29.574	-23.254	1.00	21.32
BBBBATOM	4614	CD1	ILE	B	270	12.926	-28.291	-22.583	1.00	23.40
BBBBATOM	4615	C	ILE	B	270	14.214	-28.314	-26.806	1.00	20.58
BBBBATOM	4616	O	ILE	B	270	14.595	-27.151	-26.954	1.00	20.50
BBBBATOM	4617	N	ALA	B	271	14.574	-29.298	-27.624	1.00	21.29
BBBBATOM	4618	CA	ALA	B	271	15.440	-29.058	-28.776	1.00	22.45
BBBBATOM	4619	CB	ALA	B	271	15.741	-30.376	-29.485	1.00	23.36
BBBBATOM	4620	C	ALA	B	271	14.766	-28.084	-29.745	1.00	23.03
BBBBATOM	4621	O	ALA	B	271	15.400	-27.156	-30.259	1.00	23.57
BBBBATOM	4622	N	ALA	B	272	13.479	-28.301	-29.988	1.00	21.81
BBBBATOM	4623	CA	ALA	B	272	12.719	-27.451	-30.898	1.00	22.17
BBBBATOM	4624	CB	ALA	B	272	11.335	-28.053	-31.131	1.00	22.15
BBBBATOM	4625	C	ALA	B	272	12.590	-26.030	-30.355	1.00	22.78
BBBBATOM	4626	O	ALA	B	272	12.585	-25.058	-31.122	1.00	21.77
BBBBATOM	4627	N	ALA	B	273	12.474	-25.907	-29.034	1.00	21.06
BBBBATOM	4628	CA	ALA	B	273	12.361	-24.596	-28.407	1.00	21.97
BBBBATOM	4629	CB	ALA	B	273	11.919	-24.737	-26.949	1.00	20.63
BBBBATOM	4630	C	ALA	B	273	13.699	-23.867	-28.468	1.00	21.83
BBBBATOM	4631	O	ALA	B	273	13.754	-22.642	-28.344	1.00	22.67
BBBBATOM	4632	N	GLY	B	274	14.773	-24.621	-28.656	1.00	20.90
BBBBATOM	4633	CA	GLY	B	274	16.093	-24.023	-28.709	1.00	21.07
BBBBATOM	4634	C	GLY	B	274	16.498	-23.549	-27.327	1.00	21.48
BBBBATOM	4635	O	GLY	B	274	16.961	-22.421	-27.154	1.00	20.01
BBBBATOM	4636	N	LEU	B	275	16.331	-24.420	-26.333	1.00	19.66
BBBBATOM	4637	CA	LEU	B	275	16.666	-24.057	-24.966	1.00	19.78
BBBBATOM	4638	CB	LEU	B	275	15.402	-24.068	-24.102	1.00	21.30
BBBBATOM	4639	CG	LEU	B	275	14.451	-22.870	-24.202	1.00	24.60
BBBBATOM	4640	CD1	LEU	B	275	13.220	-23.136	-23.349	1.00	26.44
BBBBATOM	4641	CD2	LEU	B	275	15.159	-21.609	-23.725	1.00	24.02
BBBBATOM	4642	C	LEU	B	275	17.698	-24.970	-24.318	1.00	18.79
BBBBATOM	4643	O	LEU	B	275	17.679	-26.180	-24.524	1.00	19.36
BBBBATOM	4644	N	PRO	B	276	18.634	-24.389	-23.554	1.00	17.27
BBBBATOM	4645	CD	PRO	B	276	18.925	-22.955	-23.416	1.00	16.95
BBBBATOM	4646	CA	PRO	B	276	19.651	-25.199	-22.875	1.00	16.62

BBBBBATOM	4647	CB	PRO B 276	20.619	-24.162	-22.317	1.00	17.27
BBBBBATOM	4648	CG	PRO B 276	20.408	-22.957	-23.195	1.00	18.59
BBBBBATOM	4649	C	PRO B 276	18.900	-25.900	-21.746	1.00	17.23
BBBBBATOM	4650	O	PRO B 276	17.944	-25.340	-21.189	1.00	15.14
BBBBBATOM	4651	N	ALA B 277	19.316	-27.110	-21.396	1.00	17.01
BBBBBATOM	4652	CA	ALA B 277	18.638	-27.807	-20.321	1.00	15.80
BBBBBATOM	4653	CB	ALA B 277	17.641	-28.805	-20.895	1.00	17.01
BBBBBATOM	4654	C	ALA B 277	19.591	-28.526	-19.382	1.00	17.37
BBBBBATOM	4655	O	ALA B 277	20.710	-28.891	-19.755	1.00	17.09
BBBBBATOM	4656	N	LEU B 278	19.147	-28.673	-18.138	1.00	17.14
BBBBBATOM	4657	CA	LEU B 278	19.896	-29.429	-17.145	1.00	18.48
BBBBBATOM	4658	CB	LEU B 278	20.140	-28.619	-15.869	1.00	19.19
BBBBBATOM	4659	CG	LEU B 278	21.084	-29.308	-14.868	1.00	20.85
BBBBBATOM	4660	CD1	LEU B 278	21.283	-28.411	-13.668	1.00	21.11
BBBBBATOM	4661	CD2	LEU B 278	20.497	-30.647	-14.433	1.00	19.16
BBBBBATOM	4662	C	LEU B 278	18.884	-30.535	-16.898	1.00	19.62
BBBBBATOM	4663	O	LEU B 278	17.870	-30.330	-16.218	1.00	20.77
BBBBBATOM	4664	N	PHE B 279	19.149	-31.691	-17.495	1.00	19.50
BBBBBATOM	4665	CA	PHE B 279	18.266	-32.838	-17.392	1.00	21.59
BBBBBATOM	4666	CB	PHE B 279	18.385	-33.700	-18.651	1.00	21.07
BBBBBATOM	4667	CG	PHE B 279	17.740	-33.099	-19.876	1.00	19.35
BBBBBATOM	4668	CD1	PHE B 279	18.481	-32.898	-21.035	1.00	19.42
BBBBBATOM	4669	CD2	PHE B 279	16.379	-32.794	-19.888	1.00	18.16
BBBBBATOM	4670	CE1	PHE B 279	17.874	-32.405	-22.203	1.00	19.06
BBBBBATOM	4671	CE2	PHE B 279	15.759	-32.298	-21.052	1.00	17.65
BBBBBATOM	4672	CZ	PHE B 279	16.515	-32.108	-22.208	1.00	15.61
BBBBBATOM	4673	C	PHE B 279	18.525	-33.709	-16.167	1.00	22.86
BBBBBATOM	4674	O	PHE B 279	19.671	-34.065	-15.871	1.00	23.32
BBBBBATOM	4675	N	VAL B 280	17.445	-34.037	-15.461	1.00	23.88
BBBBBATOM	4676	CA	VAL B 280	17.502	-34.902	-14.281	1.00	25.67
BBBBBATOM	4677	CB	VAL B 280	16.883	-34.223	-13.048	1.00	26.89
BBBBBATOM	4678	CG1	VAL B 280	16.954	-35.159	-11.847	1.00	28.12
BBBBBATOM	4679	CG2	VAL B 280	17.631	-32.929	-12.742	1.00	27.70
BBBBBATOM	4680	C	VAL B 280	16.690	-36.136	-14.658	1.00	25.65
BBBBBATOM	4681	O	VAL B 280	15.509	-36.239	-14.346	1.00	24.57
BBBBBATOM	4682	N	PRO B 281	17.324	-37.080	-15.370	1.00	27.08
BBBBBATOM	4683	CD	PRO B 281	18.750	-37.057	-15.726	1.00	27.31
BBBBBATOM	4684	CA	PRO B 281	16.698	-38.320	-15.824	1.00	29.05
BBBBBATOM	4685	CB	PRO B 281	17.851	-39.071	-16.492	1.00	29.44
BBBBBATOM	4686	CG	PRO B 281	18.791	-37.992	-16.895	1.00	29.67
BBBBBATOM	4687	C	PRO B 281	16.092	-39.121	-14.684	1.00	31.51
BBBBBATOM	4688	O	PRO B 281	16.675	-39.223	-13.603	1.00	32.26
BBBBBATOM	4689	N	PHE B 282	14.908	-39.668	-14.923	1.00	33.83
BBBBBATOM	4690	CA	PHE B 282	14.246	-40.496	-13.926	1.00	37.13
BBBBBATOM	4691	CB	PHE B 282	12.818	-40.808	-14.372	1.00	38.38
BBBBBATOM	4692	CG	PHE B 282	12.032	-41.606	-13.377	1.00	40.57
BBBBBATOM	4693	CD1	PHE B 282	11.720	-41.074	-12.130	1.00	41.80
BBBBBATOM	4694	CD2	PHE B 282	11.590	-42.886	-13.689	1.00	41.65
BBBBBATOM	4695	CE1	PHE B 282	10.975	-41.806	-11.209	1.00	42.03
BBBBBATOM	4696	CE2	PHE B 282	10.843	-43.628	-12.773	1.00	42.49
BBBBBATOM	4697	CZ	PHE B 282	10.536	-43.085	-11.532	1.00	41.74
BBBBBATOM	4698	C	PHE B 282	15.078	-41.776	-13.880	1.00	38.09
BBBBBATOM	4699	O	PHE B 282	15.357	-42.373	-14.921	1.00	38.33
BBBBBATOM	4700	N	GLN B 283	15.492	-42.197	-12.690	1.00	39.70
BBBBBATOM	4701	CA	GLN B 283	16.319	-43.395	-12.591	1.00	41.11
BBBBBATOM	4702	CB	GLN B 283	17.010	-43.477	-11.223	1.00	41.41
BBBBBATOM	4703	CG	GLN B 283	17.953	-44.676	-11.096	1.00	42.60
BBBBBATOM	4704	CD	GLN B 283	19.143	-44.605	-12.051	1.00	42.87
BBBBBATOM	4705	OE1	GLN B 283	20.199	-44.068	-11.712	1.00	43.66
BBBBBATOM	4706	NE2	GLN B 283	18.969	-45.135	-13.254	1.00	42.46
BBBBBATOM	4707	C	GLN B 283	15.543	-44.679	-12.846	1.00	41.60
BBBBBATOM	4708	O	GLN B 283	14.382	-44.809	-12.462	1.00	40.91
BBBBBATOM	4709	N	HIS B 284	16.211	-45.618	-13.511	1.00	42.92
BBBBBATOM	4710	CA	HIS B 284	15.641	-46.917	-13.843	1.00	43.69
BBBBBATOM	4711	CB	HIS B 284	14.508	-46.760	-14.858	1.00	43.91
BBBBBATOM	4712	CG	HIS B 284	13.795	-48.039	-15.165	1.00	44.71

BBBBATOM	4713	CD2	HIS	B	284	12.574	-48.489	-14.793	1.00	44.80
BBBBATOM	4714	ND1	HIS	B	284	14.360	-49.044	-15.923	1.00	44.69
BBBBATOM	4715	CE1	HIS	B	284	13.516	-50.058	-16.002	1.00	45.06
BBBBATOM	4716	NE2	HIS	B	284	12.425	-49.747	-15.325	1.00	44.90
BBBBATOM	4717	C	HIS	B	284	16.749	-47.788	-14.424	1.00	44.09
BBBBATOM	4718	O	HIS	B	284	17.602	-47.302	-15.164	1.00	43.02
BBBBATOM	4719	N	LYS	B	285	16.740	-49.074	-14.085	1.00	44.90
BBBBATOM	4720	CA	LYS	B	285	17.767	-49.993	-14.571	1.00	45.34
BBBBATOM	4721	CB	LYS	B	285	17.386	-51.436	-14.222	1.00	46.84
BBBBATOM	4722	CG	LYS	B	285	18.541	-52.425	-14.327	1.00	49.53
BBBBATOM	4723	CD	LYS	B	285	18.140	-53.802	-13.807	1.00	51.08
BBBBATOM	4724	CE	LYS	B	285	19.325	-54.759	-13.780	1.00	51.58
BBBBATOM	4725	NZ	LYS	B	285	18.931	-56.115	-13.292	1.00	52.11
BBBBATOM	4726	C	LYS	B	285	17.969	-49.853	-16.079	1.00	45.02
BBBBATOM	4727	O	LYS	B	285	19.067	-50.070	-16.595	1.00	45.49
BBBBATOM	4728	N	ASP	B	286	16.903	-49.478	-16.777	1.00	44.33
BBBBATOM	4729	CA	ASP	B	286	16.949	-49.299	-18.222	1.00	43.26
BBBBATOM	4730	CB	ASP	B	286	15.532	-49.379	-18.794	1.00	45.91
BBBBATOM	4731	CG	ASP	B	286	15.511	-49.354	-20.304	1.00	48.32
BBBBATOM	4732	OD1	ASP	B	286	15.971	-50.338	-20.925	1.00	49.52
BBBBATOM	4733	OD2	ASP	B	286	15.037	-48.346	-20.872	1.00	51.04
BBBBATOM	4734	C	ASP	B	286	17.573	-47.947	-18.582	1.00	40.92
BBBBATOM	4735	O	ASP	B	286	18.179	-47.796	-19.643	1.00	40.31
BBBBATOM	4736	N	ARG	B	287	17.415	-46.972	-17.689	1.00	38.60
BBBBATOM	4737	CA	ARG	B	287	17.951	-45.623	-17.883	1.00	36.28
BBBBATOM	4738	CB	ARG	B	287	19.477	-45.650	-17.910	1.00	37.28
BBBBATOM	4739	CG	ARG	B	287	20.116	-46.263	-16.687	1.00	40.54
BBBBATOM	4740	CD	ARG	B	287	21.605	-46.395	-16.906	1.00	42.34
BBBBATOM	4741	NE	ARG	B	287	22.291	-45.113	-16.802	1.00	44.33
BBBBATOM	4742	CZ	ARG	B	287	23.449	-44.842	-17.392	1.00	45.20
BBBBATOM	4743	NH1	ARG	B	287	24.045	-45.764	-18.135	1.00	45.60
BBBBATOM	4744	NH2	ARG	B	287	24.019	-43.656	-17.227	1.00	45.68
BBBBATOM	4745	C	ARG	B	287	17.449	-45.005	-19.180	1.00	33.59
BBBBATOM	4746	O	ARG	B	287	18.167	-44.255	-19.844	1.00	32.61
BBBBATOM	4747	N	GLN	B	288	16.212	-45.321	-19.533	1.00	30.94
BBBBATOM	4748	CA	GLN	B	288	15.622	-44.804	-20.755	1.00	30.77
BBBBATOM	4749	CB	GLN	B	288	14.143	-45.158	-20.810	1.00	30.59
BBBBATOM	4750	CG	GLN	B	288	13.473	-44.772	-22.109	1.00	29.73
BBBBATOM	4751	CD	GLN	B	288	11.981	-44.971	-22.044	1.00	28.04
BBBBATOM	4752	OE1	GLN	B	288	11.294	-44.295	-21.279	1.00	29.59
BBBBATOM	4753	NE2	GLN	B	288	11.468	-45.905	-22.838	1.00	26.98
BBBBATOM	4754	C	GLN	B	288	15.783	-43.291	-20.885	1.00	29.70
BBBBATOM	4755	O	GLN	B	288	16.268	-42.801	-21.902	1.00	29.79
BBBBATOM	4756	N	GLN	B	289	15.378	-42.554	-19.857	1.00	29.38
BBBBATOM	4757	CA	GLN	B	289	15.474	-41.099	-19.904	1.00	29.46
BBBBATOM	4758	CB	GLN	B	289	14.772	-40.472	-18.700	1.00	29.25
BBBBATOM	4759	CG	GLN	B	289	13.265	-40.416	-18.883	1.00	29.32
BBBBATOM	4760	CD	GLN	B	289	12.575	-39.585	-17.826	1.00	29.84
BBBBATOM	4761	OE1	GLN	B	289	13.191	-38.728	-17.188	1.00	29.52
BBBBATOM	4762	NE2	GLN	B	289	11.281	-39.821	-17.647	1.00	28.95
BBBBATOM	4763	C	GLN	B	289	16.906	-40.613	-20.005	1.00	29.36
BBBBATOM	4764	O	GLN	B	289	17.173	-39.557	-20.585	1.00	29.12
BBBBATOM	4765	N	TYR	B	290	17.835	-41.374	-19.442	1.00	28.95
BBBBATOM	4766	CA	TYR	B	290	19.228	-40.984	-19.550	1.00	29.55
BBBBATOM	4767	CB	TYR	B	290	20.136	-41.934	-18.768	1.00	31.40
BBBBATOM	4768	CG	TYR	B	290	21.587	-41.780	-19.148	1.00	33.37
BBBBATOM	4769	CD1	TYR	B	290	22.332	-40.682	-18.717	1.00	34.57
BBBBATOM	4770	CE1	TYR	B	290	23.644	-40.490	-19.148	1.00	35.97
BBBBATOM	4771	CD2	TYR	B	290	22.192	-42.684	-20.017	1.00	34.90
BBBBATOM	4772	CE2	TYR	B	290	23.497	-42.500	-20.453	1.00	36.03
BBBBATOM	4773	CZ	TYR	B	290	24.214	-41.402	-20.019	1.00	36.29
BBBBATOM	4774	OH	TYR	B	290	25.499	-41.215	-20.475	1.00	39.44
BBBBATOM	4775	C	TYR	B	290	19.593	-41.042	-21.032	1.00	28.80
BBBBATOM	4776	O	TYR	B	290	20.192	-40.113	-21.567	1.00	29.22
BBBBATOM	4777	N	TRP	B	291	19.227	-42.135	-21.697	1.00	27.57
BBBBATOM	4778	CA	TRP	B	291	19.542	-42.282	-23.116	1.00	28.07

BBBBBATOM	4779	CB	TRP	B	291	19.217	-43.705	-23.599	1.00	29.42
BBBBBATOM	4780	CG	TRP	B	291	20.070	-44.750	-22.936	1.00	31.82
BBBBBATOM	4781	CD2	TRP	B	291	21.487	-44.908	-23.069	1.00	33.22
BBBBBATOM	4782	CE2	TRP	B	291	21.873	-45.966	-22.213	1.00	33.81
BBBBBATOM	4783	CE3	TRP	B	291	22.470	-44.257	-23.826	1.00	33.13
BBBBBATOM	4784	CD1	TRP	B	291	19.663	-45.695	-22.035	1.00	32.62
BBBBBATOM	4785	NE1	TRP	B	291	20.741	-46.428	-21.595	1.00	33.43
BBBBBATOM	4786	CZ2	TRP	B	291	23.203	-46.387	-22.093	1.00	34.69
BBBBBATOM	4787	CZ3	TRP	B	291	23.794	-44.676	-23.707	1.00	35.41
BBBBBATOM	4788	CH2	TRP	B	291	24.146	-45.732	-22.845	1.00	35.26
BBBBBATOM	4789	C	TRP	B	291	18.808	-41.256	-23.978	1.00	26.84
BBBBBATOM	4790	O	TRP	B	291	19.283	-40.900	-25.058	1.00	26.55
BBBBBATOM	4791	N	ASN	B	292	17.658	-40.779	-23.508	1.00	25.52
BBBBBATOM	4792	CA	ASN	B	292	16.902	-39.784	-24.270	1.00	26.06
BBBBBATOM	4793	CB	ASN	B	292	15.484	-39.599	-23.709	1.00	24.78
BBBBBATOM	4794	CG	ASN	B	292	14.590	-40.811	-23.928	1.00	24.46
BBBBBATOM	4795	OD1	ASN	B	292	14.842	-41.641	-24.798	1.00	25.33
BBBBBATOM	4796	ND2	ASN	B	292	13.523	-40.900	-23.146	1.00	23.83
BBBBBATOM	4797	C	ASN	B	292	17.605	-38.427	-24.258	1.00	25.99
BBBBBATOM	4798	O	ASN	B	292	17.566	-37.687	-25.244	1.00	26.18
BBBBBATOM	4799	N	ALA	B	293	18.242	-38.105	-23.139	1.00	25.66
BBBBBATOM	4800	CA	ALA	B	293	18.926	-36.822	-22.979	1.00	25.69
BBBBBATOM	4801	CB	ALA	B	293	18.940	-36.422	-21.506	1.00	24.17
BBBBBATOM	4802	C	ALA	B	293	20.346	-36.800	-23.521	1.00	25.67
BBBBBATOM	4803	O	ALA	B	293	20.855	-35.743	-23.902	1.00	25.52
BBBBBATOM	4804	N	LEU	B	294	20.978	-37.969	-23.560	1.00	25.62
BBBBBATOM	4805	CA	LEU	B	294	22.354	-38.088	-24.032	1.00	25.90
BBBBBATOM	4806	CB	LEU	B	294	22.745	-39.566	-24.121	1.00	26.51
BBBBBATOM	4807	CG	LEU	B	294	24.226	-39.864	-24.350	1.00	28.12
BBBBBATOM	4808	CD1	LEU	B	294	25.085	-39.055	-23.380	1.00	28.29
BBBBBATOM	4809	CD2	LEU	B	294	24.470	-41.368	-24.169	1.00	28.15
BBBBBATOM	4810	C	LEU	B	294	22.644	-37.392	-25.359	1.00	25.66
BBBBBATOM	4811	O	LEU	B	294	23.677	-36.741	-25.507	1.00	24.79
BBBBBATOM	4812	N	PRO	B	295	21.748	-37.532	-26.351	1.00	26.24
BBBBBATOM	4813	CD	PRO	B	295	20.560	-38.400	-26.437	1.00	25.75
BBBBBATOM	4814	CA	PRO	B	295	21.998	-36.870	-27.635	1.00	26.15
BBBBBATOM	4815	CB	PRO	B	295	20.740	-37.201	-28.439	1.00	26.70
BBBBBATOM	4816	CG	PRO	B	295	20.382	-38.548	-27.932	1.00	26.84
BBBBBATOM	4817	C	PRO	B	295	22.219	-35.358	-27.480	1.00	25.78
BBBBBATOM	4818	O	PRO	B	295	23.138	-34.792	-28.069	1.00	25.05
BBBBBATOM	4819	N	LEU	B	296	21.375	-34.703	-26.688	1.00	25.66
BBBBBATOM	4820	CA	LEU	B	296	21.521	-33.265	-26.481	1.00	25.42
BBBBBATOM	4821	CB	LEU	B	296	20.283	-32.685	-25.779	1.00	24.45
BBBBBATOM	4822	CG	LEU	B	296	19.066	-32.458	-26.679	1.00	25.59
BBBBBATOM	4823	CD1	LEU	B	296	17.968	-31.718	-25.911	1.00	23.56
BBBBBATOM	4824	CD2	LEU	B	296	19.496	-31.630	-27.893	1.00	25.87
BBBBBATOM	4825	C	LEU	B	296	22.784	-32.935	-25.688	1.00	26.07
BBBBBATOM	4826	O	LEU	B	296	23.435	-31.917	-25.944	1.00	25.26
BBBBBATOM	4827	N	GLU	B	297	23.143	-33.785	-24.730	1.00	26.14
BBBBBATOM	4828	CA	GLU	B	297	24.354	-33.530	-23.953	1.00	28.78
BBBBBATOM	4829	CB	GLU	B	297	24.470	-34.483	-22.755	1.00	29.05
BBBBBATOM	4830	CG	GLU	B	297	25.716	-34.210	-21.908	1.00	30.81
BBBBBATOM	4831	CD	GLU	B	297	25.812	-35.087	-20.671	1.00	31.84
BBBBBATOM	4832	OE1	GLU	B	297	25.655	-34.555	-19.551	1.00	31.74
BBBBBATOM	4833	OE2	GLU	B	297	26.045	-36.307	-20.820	1.00	31.56
BBBBBATOM	4834	C	GLU	B	297	25.577	-33.686	-24.846	1.00	29.06
BBBBBATOM	4835	O	GLU	B	297	26.528	-32.910	-24.746	1.00	29.11
BBBBBATOM	4836	N	LYS	B	298	25.543	-34.688	-25.722	1.00	31.21
BBBBBATOM	4837	CA	LYS	B	298	26.644	-34.947	-26.648	1.00	31.90
BBBBBATOM	4838	CB	LYS	B	298	26.379	-36.216	-27.464	1.00	33.65
BBBBBATOM	4839	CG	LYS	B	298	26.519	-37.514	-26.680	1.00	36.05
BBBBBATOM	4840	CD	LYS	B	298	26.251	-38.734	-27.568	1.00	37.69
BBBBBATOM	4841	CE	LYS	B	298	26.461	-40.033	-26.801	1.00	38.51
BBBBBATOM	4842	NZ	LYS	B	298	26.094	-41.235	-27.607	1.00	39.05
BBBBBATOM	4843	C	LYS	B	298	26.829	-33.768	-27.598	1.00	31.69
BBBBBATOM	4844	O	LYS	B	298	27.945	-33.455	-27.998	1.00	30.87

BBBBATOM	4845	N	ALA	B	299	25.725	-33.116	-27.952	1.00	31.63
BBBBATOM	4846	CA	ALA	B	299	25.773	-31.965	-28.847	1.00	30.38
BBBBATOM	4847	CB	ALA	B	299	24.415	-31.778	-29.521	1.00	30.22
BBBBATOM	4848	C	ALA	B	299	26.173	-30.685	-28.106	1.00	29.94
BBBBATOM	4849	O	ALA	B	299	26.278	-29.615	-28.709	1.00	30.96
BBBBATOM	4850	N	GLY	B	300	26.398	-30.796	-26.801	1.00	27.41
BBBBATOM	4851	CA	GLY	B	300	26.777	-29.635	-26.017	1.00	26.18
BBBBATOM	4852	C	GLY	B	300	25.619	-28.665	-25.810	1.00	25.19
BBBBATOM	4853	O	GLY	B	300	25.832	-27.466	-25.644	1.00	24.70
BBBBATOM	4854	N	ALA	B	301	24.392	-29.179	-25.820	1.00	23.51
BBBBATOM	4855	CA	ALA	B	301	23.214	-28.333	-25.638	1.00	22.50
BBBBATOM	4856	CB	ALA	B	301	22.174	-28.644	-26.717	1.00	23.44
BBBBATOM	4857	C	ALA	B	301	22.591	-28.510	-24.254	1.00	22.09
BBBBATOM	4858	O	ALA	B	301	21.705	-27.746	-23.863	1.00	19.90
BBBBATOM	4859	N	ALA	B	302	23.066	-29.504	-23.507	1.00	20.94
BBBBATOM	4860	CA	ALA	B	302	22.516	-29.770	-22.186	1.00	21.78
BBBBATOM	4861	CB	ALA	B	302	21.243	-30.595	-22.327	1.00	20.10
BBBBATOM	4862	C	ALA	B	302	23.503	-30.507	-21.288	1.00	22.69
BBBBATOM	4863	O	ALA	B	302	24.561	-30.948	-21.739	1.00	22.25
BBBBATOM	4864	N	LYS	B	303	23.156	-30.613	-20.009	1.00	24.62
BBBBATOM	4865	CA	LYS	B	303	23.979	-31.340	-19.048	1.00	25.86
BBBBATOM	4866	CB	LYS	B	303	24.632	-30.401	-18.036	1.00	27.85
BBBBATOM	4867	CG	LYS	B	303	25.466	-31.146	-16.986	1.00	29.37
BBBBATOM	4868	CD	LYS	B	303	26.150	-30.186	-16.025	1.00	32.41
BBBBATOM	4869	CE	LYS	B	303	27.083	-30.912	-15.056	1.00	33.22
BBBBATOM	4870	NZ	LYS	B	303	27.827	-29.952	-14.181	1.00	33.62
BBBBATOM	4871	C	LYS	B	303	23.083	-32.319	-18.302	1.00	26.41
BBBBATOM	4872	O	LYS	B	303	22.015	-31.948	-17.802	1.00	25.76
BBBBATOM	4873	N	ILE	B	304	23.520	-33.570	-18.234	1.00	25.65
BBBBATOM	4874	CA	ILE	B	304	22.753	-34.598	-17.550	1.00	27.17
BBBBATOM	4875	CB	ILE	B	304	22.786	-35.946	-18.316	1.00	27.06
BBBBATOM	4876	CG2	ILE	B	304	21.977	-36.996	-17.555	1.00	28.49
BBBBATOM	4877	CG1	ILE	B	304	22.242	-35.769	-19.733	1.00	27.61
BBBBATOM	4878	CD1	ILE	B	304	22.380	-37.009	-20.599	1.00	27.05
BBBBATOM	4879	C	ILE	B	304	23.308	-34.855	-16.160	1.00	27.00
BBBBATOM	4880	O	ILE	B	304	24.511	-35.012	-15.986	1.00	27.46
BBBBATOM	4881	N	ILE	B	305	22.428	-34.869	-15.168	1.00	27.22
BBBBATOM	4882	CA	ILE	B	305	22.843	-35.178	-13.813	1.00	29.01
BBBBATOM	4883	CB	ILE	B	305	22.713	-33.977	-12.858	1.00	28.91
BBBBATOM	4884	CG2	ILE	B	305	23.063	-34.416	-11.432	1.00	30.98
BBBBATOM	4885	CG1	ILE	B	305	23.660	-32.855	-13.299	1.00	29.51
BBBBATOM	4886	CD1	ILE	B	305	23.674	-31.653	-12.367	1.00	29.43
BBBBATOM	4887	C	ILE	B	305	21.934	-36.302	-13.351	1.00	29.64
BBBBATOM	4888	O	ILE	B	305	20.806	-36.067	-12.932	1.00	29.25
BBBBATOM	4889	N	GLU	B	306	22.429	-37.532	-13.467	1.00	32.18
BBBBATOM	4890	CA	GLU	B	306	21.664	-38.702	-13.061	1.00	34.65
BBBBATOM	4891	CB	GLU	B	306	22.356	-39.989	-13.530	1.00	34.79
BBBBATOM	4892	CG	GLU	B	306	22.529	-40.067	-15.035	1.00	36.39
BBBBATOM	4893	CD	GLU	B	306	23.114	-41.388	-15.504	1.00	36.86
BBBBATOM	4894	OE1	GLU	B	306	22.468	-42.433	-15.289	1.00	36.59
BBBBATOM	4895	OE2	GLU	B	306	24.214	-41.378	-16.099	1.00	37.75
BBBBATOM	4896	C	GLU	B	306	21.531	-38.704	-11.552	1.00	35.50
BBBBATOM	4897	O	GLU	B	306	22.241	-37.984	-10.858	1.00	35.55
BBBBATOM	4898	N	GLN	B	307	20.612	-39.514	-11.048	1.00	38.41
BBBBATOM	4899	CA	GLN	B	307	20.377	-39.599	-9.613	1.00	40.54
BBBBATOM	4900	CB	GLN	B	307	19.397	-40.734	-9.322	1.00	40.99
BBBBATOM	4901	CG	GLN	B	307	18.896	-40.769	-7.896	1.00	42.76
BBBBATOM	4902	CD	GLN	B	307	17.879	-41.867	-7.681	1.00	44.33
BBBBATOM	4903	OE1	GLN	B	307	18.181	-43.051	-7.847	1.00	44.46
BBBBATOM	4904	NE2	GLN	B	307	16.659	-41.481	-7.318	1.00	45.30
BBBBATOM	4905	C	GLN	B	307	21.647	-39.784	-8.776	1.00	40.94
BBBBATOM	4906	O	GLN	B	307	21.796	-39.154	-7.732	1.00	41.24
BBBBATOM	4907	N	PRO	B	308	22.580	-40.648	-9.224	1.00	42.16
BBBBATOM	4908	CD	PRO	B	308	22.456	-41.593	-10.349	1.00	42.40
BBBBATOM	4909	CA	PRO	B	308	23.828	-40.891	-8.484	1.00	43.20
BBBBATOM	4910	CS	PRO	B	308	24.533	-41.954	-9.329	1.00	43.16

BBBBATOM	4911	CG	PRO	B	308	23.395	-42.708	-9.938	1.00	43.10
BBBBATOM	4912	C	PRO	B	308	24.719	-39.668	-8.250	1.00	43.82
BBBBATOM	4913	O	PRO	B	308	25.652	-39.724	-7.449	1.00	44.24
BBBBATOM	4914	N	GLN	B	309	24.442	-38.569	-8.944	1.00	44.04
BBBBATOM	4915	CA	GLN	B	309	25.247	-37.361	-8.787	1.00	43.46
BBBBATOM	4916	CB	GLN	B	309	26.071	-37.104	-10.056	1.00	44.98
BBBBATOM	4917	CG	GLN	B	309	27.183	-38.113	-10.329	1.00	46.93
BBBBATOM	4918	CD	GLN	B	309	26.683	-39.437	-10.885	1.00	47.93
BBBBATOM	4919	OE1	GLN	B	309	27.459	-40.376	-11.054	1.00	48.87
BBBBATOM	4920	NE2	GLN	B	309	25.388	-39.515	-11.179	1.00	49.17
BBBBATOM	4921	C	GLN	B	309	24.417	-36.119	-8.479	1.00	42.87
BBBBATOM	4922	O	GLN	B	309	24.955	-35.013	-8.404	1.00	43.33
BBBBATOM	4923	N	LEU	B	310	23.113	-36.297	-8.289	1.00	41.06
BBBBATOM	4924	CA	LEU	B	310	22.232	-35.166	-8.022	1.00	39.65
BBBBATOM	4925	CB	LEU	B	310	20.779	-35.549	-8.330	1.00	39.95
BBBBATOM	4926	CG	LEU	B	310	19.730	-34.437	-8.480	1.00	39.98
BBBBATOM	4927	CD1	LEU	B	310	19.545	-33.699	-7.166	1.00	41.39
BBBBATOM	4928	CD2	LEU	B	310	20.160	-33.472	-9.580	1.00	40.19
BBBBATOM	4929	C	LEU	B	310	22.342	-34.659	-6.591	1.00	38.83
BBBBATOM	4930	O	LEU	B	310	22.246	-35.428	-5.634	1.00	39.25
BBBBATOM	4931	N	SER	B	311	22.541	-33.354	-6.457	1.00	36.17
BBBBATOM	4932	CA	SER	B	311	22.660	-32.714	-5.154	1.00	34.90
BBBBATOM	4933	CB	SER	B	311	24.059	-32.928	-4.569	1.00	35.08
BBBBATOM	4934	OG	SER	B	311	25.022	-32.135	-5.248	1.00	33.92
BBBBATOM	4935	C	SER	B	311	22.434	-31.227	-5.357	1.00	33.51
BBBBATOM	4936	O	SER	B	311	22.476	-30.741	-6.485	1.00	33.60
BBBBATOM	4937	N	VAL	B	312	22.202	-30.509	-4.266	1.00	32.42
BBBBATOM	4938	CA	VAL	B	312	21.990	-29.074	-4.341	1.00	31.50
BBBBATOM	4939	CB	VAL	B	312	21.707	-28.482	-2.938	1.00	31.69
BBBBATOM	4940	CG1	VAL	B	312	21.546	-26.976	-3.023	1.00	31.54
BBBBATOM	4941	CG2	VAL	B	312	20.445	-29.106	-2.362	1.00	31.93
BBBBATOM	4942	C	VAL	B	312	23.228	-28.417	-4.946	1.00	31.40
BBBBATOM	4943	O	VAL	B	312	23.123	-27.612	-5.875	1.00	30.04
BBBBATOM	4944	N	ASP	B	313	24.406	-28.780	-4.444	1.00	30.18
BBBBATOM	4945	CA	ASP	B	313	25.642	-28.202	-4.957	1.00	29.61
BBBBATOM	4946	CB	ASP	B	313	26.840	-28.656	-4.120	1.00	32.36
BBBBATOM	4947	CG	ASP	B	313	26.817	-28.085	-2.718	1.00	34.21
BBBBATOM	4948	OD1	ASP	B	313	26.662	-26.855	-2.578	1.00	36.52
BBBBATOM	4949	OD2	ASP	B	313	26.958	-28.865	-1.751	1.00	38.92
BBBBATOM	4950	C	ASP	B	313	25.910	-28.516	-6.425	1.00	28.84
BBBBATOM	4951	O	ASP	B	313	26.442	-27.677	-7.146	1.00	28.96
BBBBATOM	4952	N	ALA	B	314	25.555	-29.719	-6.868	1.00	26.61
BBBBATOM	4953	CA	ALA	B	314	25.782	-30.099	-8.254	1.00	26.47
BBBBATOM	4954	CB	ALA	B	314	25.441	-31.575	-8.460	1.00	26.05
BBBBATOM	4955	C	ALA	B	314	24.928	-29.220	-9.174	1.00	25.78
BBBBATOM	4956	O	ALA	B	314	25.412	-28.714	-10.187	1.00	24.94
BBBBATOM	4957	N	VAL	B	315	23.661	-29.046	-8.815	1.00	25.00
BBBBATOM	4958	CA	VAL	B	315	22.755	-28.215	-9.612	1.00	25.33
BBBBATOM	4959	CB	VAL	B	315	21.305	-28.298	-9.088	1.00	24.74
BBBBATOM	4960	CG1	VAL	B	315	20.392	-27.382	-9.898	1.00	23.53
BBBBATOM	4961	CG2	VAL	B	315	20.810	-29.738	-9.172	1.00	25.69
BBBBATOM	4962	C	VAL	B	315	23.222	-26.764	-9.561	1.00	25.02
BBBBATOM	4963	O	VAL	B	315	23.398	-26.125	-10.590	1.00	25.73
BBBBATOM	4964	N	ALA	B	316	23.445	-26.251	-8.359	1.00	26.04
BBBBATOM	4965	CA	ALA	B	316	23.888	-24.872	-8.199	1.00	27.13
BBBBATOM	4966	CB	ALA	B	316	24.059	-24.545	-6.714	1.00	27.12
BBBBATOM	4967	C	ALA	B	316	25.185	-24.584	-8.955	1.00	28.17
BBBBATOM	4968	O	ALA	B	316	25.289	-23.572	-9.652	1.00	27.04
BBBBATOM	4969	N	ASN	B	317	26.178	-25.463	-8.823	1.00	28.72
BBBBATOM	4970	CA	ASN	B	317	27.444	-25.246	-9.518	1.00	28.52
BBBBATOM	4971	CB	ASN	B	317	28.493	-26.271	-9.081	1.00	31.30
BBBBATOM	4972	CG	ASN	B	317	28.940	-26.068	-7.645	1.00	34.01
BBBBATOM	4973	OD1	ASN	B	317	29.091	-24.933	-7.183	1.00	33.87
BBBBATOM	4974	ND2	ASN	B	317	29.170	-27.171	-6.933	1.00	35.63
BBBBATOM	4975	C	ASN	B	317	27.270	-25.310	-11.026	1.00	27.23
BBBBATOM	4976	O	ASN	B	317	27.887	-24.543	-11.765	1.00	26.36

BBBBATOM	4977	N	THR	B	318	26.424	-26.224	-11.482	1.00	26.95
BBBBATOM	4978	CA	THR	B	318	26.174	-26.371	-12.906	1.00	27.04
BBBBATOM	4979	CB	THR	B	318	25.203	-27.537	-13.189	1.00	27.91
BBBBATOM	4980	OG1	THR	B	318	25.843	-28.779	-12.872	1.00	30.24
BBBBATOM	4981	CG2	THR	B	318	24.784	-27.539	-14.655	1.00	27.49
BBBBATOM	4982	C	THR	B	318	25.579	-25.087	-13.480	1.00	26.50
BBBBATOM	4983	O	THR	B	318	26.085	-24.548	-14.465	1.00	26.71
BBBBATOM	4984	N	LEU	B	319	24.516	-24.588	-12.859	1.00	24.75
BBBBATOM	4985	CA	LEU	B	319	23.883	-23.370	-13.357	1.00	25.21
BBBBATOM	4986	CB	LEU	B	319	22.579	-23.090	-12.600	1.00	23.70
BBBBATOM	4987	CG	LEU	B	319	21.496	-24.153	-12.803	1.00	23.20
BBBBATOM	4988	CD1	LEU	B	319	20.384	-23.962	-11.785	1.00	22.93
BBBBATOM	4989	CD2	LEU	B	319	20.963	-24.065	-14.237	1.00	22.39
BBBBATOM	4990	C	LEU	B	319	24.814	-22.169	-13.253	1.00	25.23
BBBBATOM	4991	O	LEU	B	319	24.888	-21.368	-14.168	1.00	25.17
BBBBATOM	4992	N	ALA	B	320	25.540	-22.055	-12.147	1.00	24.41
BBBBATOM	4993	CA	ALA	B	320	26.445	-20.931	-11.957	1.00	24.59
BBBBATOM	4994	CB	ALA	B	320	27.069	-20.987	-10.547	1.00	24.46
BBBBATOM	4995	C	ALA	B	320	27.549	-20.865	-13.010	1.00	24.21
BBBBATOM	4996	O	ALA	B	320	28.091	-19.800	-13.281	1.00	24.35
BBBBATOM	4997	N	GLY	B	321	27.878	-22.005	-13.601	1.00	24.35
BBBBATOM	4998	CA	GLY	B	321	28.934	-22.031	-14.591	1.00	24.34
BBBBATOM	4999	C	GLY	B	321	28.509	-21.642	-15.993	1.00	24.34
BBBBATOM	5000	O	GLY	B	321	29.345	-21.585	-16.890	1.00	24.63
BBBBATOM	5001	N	TRP	B	322	27.225	-21.357	-16.188	1.00	22.62
BBBBATOM	5002	CA	TRP	B	322	26.738	-21.007	-17.521	1.00	21.72
BBBBATOM	5003	CB	TRP	B	322	25.499	-21.841	-17.858	1.00	20.09
BBBBATOM	5004	CG	TRP	B	322	25.763	-23.318	-17.973	1.00	19.85
BBBBATOM	5005	CD2	TRP	B	322	24.789	-24.370	-17.939	1.00	19.16
BBBBATOM	5006	CE2	TRP	B	322	25.479	-25.584	-18.164	1.00	20.31
BBBBATOM	5007	CE3	TRP	B	322	23.403	-24.406	-17.742	1.00	19.35
BBBBATOM	5008	CD1	TRP	B	322	26.973	-23.925	-18.204	1.00	19.51
BBBBATOM	5009	NE1	TRP	B	322	26.806	-25.281	-18.323	1.00	18.84
BBBBATOM	5010	CZ2	TRP	B	322	24.825	-26.825	-18.198	1.00	20.00
BBBBATOM	5011	CZ3	TRP	B	322	22.749	-25.646	-17.775	1.00	19.90
BBBBATOM	5012	CH2	TRP	B	322	23.467	-26.836	-18.003	1.00	20.26
BBBBATOM	5013	C	TRP	B	322	26.422	-19.524	-17.722	1.00	21.61
BBBBATOM	5014	O	TRP	B	322	25.390	-19.030	-17.271	1.00	21.25
BBBBATOM	5015	N	SER	B	323	27.320	-18.824	-18.409	1.00	19.53
BBBBATOM	5016	CA	SER	B	323	27.141	-17.404	-18.692	1.00	19.04
BBBBATOM	5017	CB	SER	B	323	28.456	-16.807	-19.186	1.00	18.51
BBBBATOM	5018	OG	SER	B	323	28.793	-17.374	-20.447	1.00	16.33
BBBBATOM	5019	C	SER	B	323	26.099	-17.239	-19.799	1.00	18.26
BBBBATOM	5020	O	SER	B	323	25.690	-18.216	-20.426	1.00	16.71
BBBBATOM	5021	N	ARG	B	324	25.690	-15.999	-20.053	1.00	19.12
BBBBATOM	5022	CA	ARG	B	324	24.725	-15.741	-21.112	1.00	18.09
BBBBATOM	5023	CB	ARG	B	324	24.298	-14.268	-21.108	1.00	19.15
BBBBATOM	5024	CG	ARG	B	324	23.266	-13.973	-20.031	1.00	20.58
BBBBATOM	5025	CD	ARG	B	324	22.508	-12.662	-20.220	1.00	22.13
BBBBATOM	5026	NE	ARG	B	324	21.345	-12.641	-19.331	1.00	21.36
BBBBATOM	5027	CZ	ARG	B	324	20.268	-13.403	-19.510	1.00	21.63
BBBBATOM	5028	NH1	ARG	B	324	20.206	-14.224	-20.549	1.00	20.63
BBBBATOM	5029	NH2	ARG	B	324	19.269	-13.378	-18.633	1.00	22.19
BBBBATOM	5030	C	ARG	B	324	25.288	-16.145	-22.481	1.00	17.79
BBBBATOM	5031	O	ARG	B	324	24.540	-16.611	-23.341	1.00	17.56
BBBBATOM	5032	N	GLU	B	325	26.597	-15.975	-22.686	1.00	17.74
BBBBATOM	5033	CA	GLU	B	325	27.220	-16.368	-23.954	1.00	16.96
BBBBATOM	5034	CB	GLU	B	325	28.690	-15.907	-24.028	1.00	17.92
BBBBATOM	5035	CG	GLU	B	325	29.361	-16.398	-25.319	1.00	18.50
BBBBATOM	5036	CD	GLU	B	325	30.844	-16.068	-25.454	1.00	19.03
BBBBATOM	5037	OE1	GLU	B	325	31.446	-16.562	-26.433	1.00	18.89
BBBBATOM	5038	OE2	GLU	B	325	31.408	-15.325	-24.615	1.00	20.56
BBBBATOM	5039	C	GLU	B	325	27.164	-17.894	-24.110	1.00	16.65
BBBBATOM	5040	O	GLU	B	325	26.838	-18.428	-25.172	1.00	15.39
BBBBATOM	5041	N	THR	B	326	27.500	-18.603	-23.042	1.00	16.67
BBBBATOM	5042	CA	THR	B	326	27.460	-20.055	-23.070	1.00	16.39

BBBBATOM	5043	CB	THR	B	326	27.967	-20.635	-21.725	1.00	16.62
BBBBATOM	5044	OG1	THR	B	326	29.346	-20.294	-21.561	1.00	18.31
BBBBATOM	5045	CG2	THR	B	326	27.804	-22.143	-21.690	1.00	18.20
BBBBATOM	5046	C	THR	B	326	26.034	-20.551	-23.321	1.00	17.40
BBBBATOM	5047	O	THR	B	326	25.817	-21.478	-24.107	1.00	16.65
BBBBATOM	5048	N	LEU	B	327	25.068	-19.932	-22.643	1.00	17.90
BBBBATOM	5049	CA	LEU	B	327	23.659	-20.305	-22.780	1.00	17.27
BBBBATOM	5050	CB	LEU	B	327	22.791	-19.514	-21.791	1.00	17.35
BBBBATOM	5051	CG	LEU	B	327	22.922	-19.919	-20.309	1.00	16.74
BBBBATOM	5052	CD1	LEU	B	327	22.192	-18.930	-19.416	1.00	14.82
BBBBATOM	5053	CD2	LEU	B	327	22.361	-21.312	-20.129	1.00	18.13
BBBBATOM	5054	C	LEU	B	327	23.145	-20.096	-24.198	1.00	17.58
BBBBATOM	5055	O	LEU	B	327	22.352	-20.899	-24.692	1.00	16.08
BBBBATOM	5056	N	LEU	B	328	23.584	-19.014	-24.845	1.00	17.87
BBBBATOM	5057	CA	LEU	B	328	23.175	-18.745	-26.222	1.00	17.39
BBBBATOM	5058	CB	LEU	B	328	23.706	-17.379	-26.690	1.00	17.84
BBBBATOM	5059	CG	LEU	B	328	23.475	-17.021	-28.173	1.00	18.65
BBBBATOM	5060	CD1	LEU	B	328	21.988	-17.112	-28.494	1.00	16.92
BBBBATOM	5061	CD2	LEU	B	328	23.984	-15.608	-28.460	1.00	18.47
BBBBATOM	5062	C	LEU	B	328	23.716	-19.868	-27.111	1.00	17.74
BBBBATOM	5063	O	LEU	B	328	23.003	-20.400	-27.953	1.00	17.59
BBBBATOM	5064	N	THR	B	329	24.977	-20.244	-26.910	1.00	20.12
BBBBATOM	5065	CA	THR	B	329	25.567	-21.335	-27.688	1.00	21.30
BBBBATOM	5066	CB	THR	B	329	27.069	-21.556	-27.336	1.00	22.69
BBBBATOM	5067	OG1	THR	B	329	27.866	-20.591	-28.029	1.00	25.80
BBBBATOM	5068	CG2	THR	B	329	27.533	-22.957	-27.757	1.00	24.48
BBBBATOM	5069	C	THR	B	329	24.819	-22.644	-27.457	1.00	20.40
BBBBATOM	5070	O	THR	B	329	24.552	-23.382	-28.398	1.00	20.34
BBBBATOM	5071	N	MET	B	330	24.494	-22.933	-26.200	1.00	20.31
BBBBATOM	5072	CA	MET	B	330	23.771	-24.153	-25.870	1.00	19.91
BBBBATOM	5073	CB	MET	B	330	23.642	-24.292	-24.350	1.00	20.88
BBBBATOM	5074	CG	MET	B	330	24.957	-24.571	-23.647	1.00	21.37
BBBBATOM	5075	SD	MET	B	330	24.805	-24.609	-21.855	1.00	22.76
BBBBATOM	5076	CE	MET	B	330	24.118	-26.250	-21.622	1.00	22.37
BBBBATOM	5077	C	MET	B	330	22.389	-24.149	-26.519	1.00	19.43
BBBBATOM	5078	O	MET	B	330	21.924	-25.167	-27.029	1.00	20.85
BBBBATOM	5079	N	ALA	B	331	21.737	-22.996	-26.504	1.00	18.81
BBBBATOM	5080	CA	ALA	B	331	20.412	-22.871	-27.098	1.00	18.49
BBBBATOM	5081	CB	ALA	B	331	19.868	-21.462	-26.859	1.00	17.16
BBBBATOM	5082	C	ALA	B	331	20.481	-23.162	-28.594	1.00	19.04
BBBBATOM	5083	O	ALA	B	331	19.644	-23.879	-29.130	1.00	18.16
BBBBATOM	5084	N	GLU	B	332	21.489	-22.613	-29.269	1.00	19.87
BBBBATOM	5085	CA	GLU	B	332	21.626	-22.827	-30.704	1.00	21.47
BBBBATOM	5086	CB	GLU	B	332	22.709	-21.912	-31.274	1.00	22.13
BBBBATOM	5087	CG	GLU	B	332	22.328	-20.455	-31.143	1.00	24.10
BBBBATOM	5088	CD	GLU	B	332	23.428	-19.522	-31.572	1.00	26.61
BBBBATOM	5089	OE1	GLU	B	332	24.594	-19.765	-31.197	1.00	26.92
BBBBATOM	5090	OE2	GLU	B	332	23.118	-18.542	-32.273	1.00	27.58
BBBBATOM	5091	C	GLU	B	332	21.921	-24.280	-31.025	1.00	22.44
BBBBATOM	5092	O	GLU	B	332	21.412	-24.814	-32.006	1.00	22.84
BBBBATOM	5093	N	ARG	B	333	22.739	-24.923	-30.200	1.00	22.30
BBBBATOM	5094	CA	ARG	B	333	23.040	-26.330	-30.408	1.00	23.77
BBBBATOM	5095	CB	ARG	B	333	24.117	-26.789	-29.427	1.00	25.03
BBBBATOM	5096	CG	ARG	B	333	25.503	-26.222	-29.737	1.00	26.79
BBBBATOM	5097	CD	ARG	B	333	26.443	-26.467	-28.570	1.00	28.88
BBBBATOM	5098	NE	ARG	B	333	27.810	-26.041	-28.846	1.00	29.09
BBBBATOM	5099	CZ	ARG	B	333	28.772	-26.001	-27.932	1.00	30.32
BBBBATOM	5100	NH1	ARG	B	333	28.514	-26.361	-26.678	1.00	32.07
BBBBATOM	5101	NH2	ARG	B	333	29.990	-25.596	-28.269	1.00	31.36
BBBBATOM	5102	C	ARG	B	333	21.763	-27.147	-30.218	1.00	23.13
BBBBATOM	5103	O	ARG	B	333	21.548	-28.151	-30.895	1.00	23.45
BBBBATOM	5104	N	ALA	B	334	20.907	-26.713	-29.299	1.00	22.82
BBBBATOM	5105	CA	ALA	B	334	19.648	-27.420	-29.063	1.00	22.88
BBBBATOM	5106	CB	ALA	B	334	18.915	-26.800	-27.882	1.00	22.08
BBBBATOM	5107	C	ALA	B	334	18.778	-27.333	-30.317	1.00	22.86
BBBBATOM	5108	O	ALA	B	334	18.285	-28.339	-30.827	1.00	21.38

BBBBATOM	5109	N	ARG	B	335	18.602	-26.114	-30.815	1.00	23.14
BBBBATOM	5110	CA	ARG	B	335	17.795	-25.892	-32.002	1.00	23.54
BBBBATOM	5111	CB	ARG	B	335	17.815	-24.407	-32.361	1.00	25.17
BBBBATOM	5112	CG	ARG	B	335	16.804	-23.995	-33.418	1.00	26.90
BBBBATOM	5113	CD	ARG	B	335	15.381	-24.129	-32.891	1.00	30.87
BBBBATOM	5114	NE	ARG	B	335	14.435	-23.414	-33.736	1.00	33.71
BBBBATOM	5115	CZ	ARG	B	335	13.607	-22.469	-33.301	1.00	35.57
BBBBATOM	5116	NH1	ARG	B	335	13.601	-22.123	-32.016	1.00	34.54
BBBBATOM	5117	NH2	ARG	B	335	12.791	-21.862	-34.157	1.00	35.17
BBBBATOM	5118	C	ARG	B	335	18.348	-26.724	-33.163	1.00	23.86
BBBBATOM	5119	O	ARG	B	335	17.595	-27.360	-33.902	1.00	22.38
BBBBATOM	5120	N	ALA	B	336	19.671	-26.737	-33.297	1.00	25.17
BBBBATOM	5121	CA	ALA	B	336	20.330	-27.477	-34.372	1.00	26.85
BBBBATOM	5122	CB	ALA	B	336	21.830	-27.174	-34.374	1.00	26.27
BBBBATOM	5123	C	ALA	B	336	20.101	-28.985	-34.288	1.00	27.80
BBBBATOM	5124	O	ALA	B	336	20.052	-29.665	-35.308	1.00	27.33
BBBBATOM	5125	N	ALA	B	337	19.959	-29.501	-33.072	1.00	29.45
BBBBATOM	5126	CA	ALA	B	337	19.740	-30.925	-32.865	1.00	30.89
BBBBATOM	5127	CB	ALA	B	337	20.205	-31.320	-31.467	1.00	31.47
BBBBATOM	5128	C	ALA	B	337	18.267	-31.276	-33.047	1.00	32.47
BBBBATOM	5129	O	ALA	B	337	17.887	-32.445	-33.029	1.00	34.14
BBBBATOM	5130	N	SER	B	338	17.442	-30.254	-33.229	1.00	31.76
BBBBATOM	5131	CA	SER	B	338	16.008	-30.432	-33.408	1.00	32.41
BBBBATOM	5132	CB	SER	B	338	15.286	-29.140	-33.029	1.00	31.94
BBBBATOM	5133	OG	SER	B	338	13.921	-29.196	-33.385	1.00	34.53
BBBBATOM	5134	C	SER	B	338	15.593	-30.822	-34.829	1.00	33.16
BBBBATOM	5135	O	SER	B	338	16.274	-30.503	-35.801	1.00	32.25
BBBBATOM	5136	N	ILE	B	339	14.466	-31.523	-34.921	1.00	33.44
BBBBATOM	5137	CA	ILE	B	339	13.882	-31.941	-36.187	1.00	34.35
BBBBATOM	5138	CB	ILE	B	339	13.989	-33.472	-36.384	1.00	35.51
BBBBATOM	5139	CG2	ILE	B	339	13.271	-33.880	-37.658	1.00	35.53
BBBBATOM	5140	CG1	ILE	B	339	15.463	-33.887	-36.450	1.00	36.09
BBBBATOM	5141	CD1	ILE	B	339	15.688	-35.378	-36.667	1.00	37.71
BBBBATOM	5142	C	ILE	B	339	12.416	-31.518	-36.059	1.00	34.84
BBBBATOM	5143	O	ILE	B	339	11.601	-32.229	-35.479	1.00	35.09
BBBBATOM	5144	N	PRO	B	340	12.068	-30.344	-36.611	1.00	34.93
BBBBATOM	5145	CD	PRO	B	340	12.999	-29.525	-37.409	1.00	35.06
BBBBATOM	5146	CA	PRO	B	340	10.733	-29.730	-36.600	1.00	34.94
BBBBATOM	5147	CB	PRO	B	340	10.994	-28.349	-37.194	1.00	35.58
BBBBATOM	5148	CG	PRO	B	340	12.052	-28.642	-38.205	1.00	36.27
BBBBATOM	5149	C	PRO	B	340	9.551	-30.409	-37.284	1.00	34.07
BBBBATOM	5150	O	PRO	B	340	8.410	-30.222	-36.861	1.00	34.18
BBBBATOM	5151	N	ASP	B	341	9.803	-31.180	-38.334	1.00	33.42
BBBBATOM	5152	CA	ASP	B	341	8.711	-31.820	-39.056	1.00	33.33
BBBBATOM	5153	CB	ASP	B	341	8.802	-31.448	-40.536	1.00	35.03
BBBBATOM	5154	CG	ASP	B	341	10.101	-31.886	-41.159	1.00	37.02
BBBBATOM	5155	OD1	ASP	B	341	11.125	-31.907	-40.443	1.00	37.17
BBBBATOM	5156	OD2	ASP	B	341	10.102	-32.200	-42.367	1.00	40.57
BBBBATOM	5157	C	ASP	B	341	8.655	-33.336	-38.899	1.00	32.11
BBBBATOM	5158	O	ASP	B	341	8.377	-34.066	-39.854	1.00	30.74
BBBBATOM	5159	N	ALA	B	342	8.908	-33.807	-37.683	1.00	30.63
BBBBATOM	5160	CA	ALA	B	342	8.875	-35.238	-37.411	1.00	29.09
BBBBATOM	5161	CB	ALA	B	342	9.174	-35.496	-35.927	1.00	28.28
BBBBATOM	5162	C	ALA	B	342	7.530	-35.844	-37.792	1.00	28.32
BBBBATOM	5163	O	ALA	B	342	7.475	-36.901	-38.416	1.00	29.88
BBBBATOM	5164	N	THR	B	343	6.441	-35.177	-37.427	1.00	28.28
BBBBATOM	5165	CA	THR	B	343	5.115	-35.696	-37.744	1.00	28.55
BBBBATOM	5166	CB	THR	B	343	3.998	-34.765	-37.205	1.00	29.04
BBBBATOM	5167	OG1	THR	B	343	4.119	-34.642	-35.782	1.00	28.04
BBBBATOM	5168	CG2	THR	B	343	2.628	-35.330	-37.528	1.00	28.54
BBBBATOM	5169	C	THR	B	343	4.934	-35.882	-39.254	1.00	29.50
BBBBATOM	5170	O	THR	B	343	4.533	-36.952	-39.711	1.00	28.08
BBBBATOM	5171	N	GLU	B	344	5.234	-34.843	-40.030	1.00	30.76
BBBBATOM	5172	CA	GLU	B	344	5.085	-34.933	-41.480	1.00	32.00
BBBBATOM	5173	CB	GLU	B	344	5.414	-33.589	-42.142	1.00	34.02
BBBBATOM	5174	CG	GLU	B	344	4.412	-32.483	-41.814	1.00	38.27

BBBBATOM	5175	CD	GLU	B	344	4.807	-31.661	-40.594	1.00	40.96
BBBBATOM	5176	OE1	GLU	B	344	5.252	-32.252	-39.582	1.00	41.33
BBBBATOM	5177	OE2	GLU	B	344	4.665	-30.419	-40.649	1.00	42.30
BBBBATOM	5178	C	GLU	B	344	5.970	-36.032	-42.056	1.00	31.14
BBBBATOM	5179	O	GLU	B	344	5.534	-36.805	-42.909	1.00	32.33
BBBBATOM	5180	N	ARG	B	345	7.209	-36.106	-41.587	1.00	30.66
BBBBATOM	5181	CA	ARG	B	345	8.138	-37.123	-42.067	1.00	31.44
BBBBATOM	5182	CB	ARG	B	345	9.494	-36.986	-41.376	1.00	33.54
BBBBATOM	5183	CG	ARG	B	345	10.293	-35.772	-41.793	1.00	37.73
BBBBATOM	5184	CD	ARG	B	345	11.716	-35.880	-41.284	1.00	40.70
BBBBATOM	5185	NE	ARG	B	345	12.580	-34.864	-41.873	1.00	44.36
BBBBATOM	5186	CZ	ARG	B	345	13.901	-34.841	-41.739	1.00	45.65
BBBBATOM	5187	NH1	ARG	B	345	14.514	-35.782	-41.031	1.00	46.05
BBBBATOM	5188	NH2	ARG	B	345	14.608	-33.881	-42.322	1.00	47.38
BBBBATOM	5189	C	ARG	B	345	7.626	-38.545	-41.854	1.00	30.89
BBBBATOM	5190	O	ARG	B	345	7.724	-39.387	-42.746	1.00	29.98
BBBBATOM	5191	N	VAL	B	346	7.086	-38.818	-40.670	1.00	29.72
BBBBATOM	5192	CA	VAL	B	346	6.578	-40.151	-40.384	1.00	28.61
BBBBATOM	5193	CB	VAL	B	346	6.197	-40.298	-38.885	1.00	27.90
BBBBATOM	5194	CG1	VAL	B	346	5.612	-41.680	-38.625	1.00	27.30
BBBBATOM	5195	CG2	VAL	B	346	7.419	-40.060	-38.024	1.00	27.32
BBBBATOM	5196	C	VAL	B	346	5.361	-40.435	-41.252	1.00	28.33
BBBBATOM	5197	O	VAL	B	346	5.248	-41.511	-41.847	1.00	28.30
BBBBATOM	5198	N	ALA	B	347	4.457	-39.465	-41.335	1.00	28.76
BBBBATOM	5199	CA	ALA	B	347	3.249	-39.617	-42.137	1.00	28.96
BBBBATOM	5200	CB	ALA	B	347	2.363	-38.387	-41.994	1.00	28.49
BBBBATOM	5201	C	ALA	B	347	3.596	-39.844	-43.606	1.00	30.26
BBBBATOM	5202	O	ALA	B	347	2.948	-40.641	-44.279	1.00	30.12
BBBBATOM	5203	N	ASN	B	348	4.613	-39.142	-44.098	1.00	32.77
BBBBATOM	5204	CA	ASN	B	348	5.035	-39.286	-45.493	1.00	34.56
BBBBATOM	5205	CB	ASN	B	348	6.045	-38.195	-45.868	1.00	35.68
BBBBATOM	5206	CG	ASN	B	348	5.384	-36.846	-46.123	1.00	37.21
BBBBATOM	5207	OD1	ASN	B	348	4.157	-36.719	-46.081	1.00	38.48
BBBBATOM	5208	ND2	ASN	B	348	6.199	-35.831	-46.393	1.00	38.38
BBBBATOM	5209	C	ASN	B	348	5.633	-40.668	-45.765	1.00	34.90
BBBBATOM	5210	O	ASN	B	348	5.433	-41.233	-46.841	1.00	34.59
BBBBATOM	5211	N	GLU	B	349	6.366	-41.212	-44.794	1.00	35.20
BBBBATOM	5212	CA	GLU	B	349	6.954	-42.540	-44.956	1.00	34.86
BBBBATOM	5213	CB	GLU	B	349	8.004	-42.814	-43.879	1.00	34.59
BBBBATOM	5214	CG	GLU	B	349	9.404	-42.385	-44.259	1.00	38.16
BBBBATOM	5215	CD	GLU	B	349	9.865	-42.992	-45.579	1.00	38.74
BBBBATOM	5216	OE1	GLU	B	349	9.806	-44.232	-45.735	1.00	40.12
BBBBATOM	5217	OE2	GLU	B	349	10.292	-42.225	-46.461	1.00	39.64
BBBBATOM	5218	C	GLU	B	349	5.872	-43.607	-44.895	1.00	33.96
BBBBATOM	5219	O	GLU	B	349	5.942	-44.621	-45.591	1.00	33.99
BBBBATOM	5220	N	VAL	B	350	4.875	-43.377	-44.051	1.00	33.91
BBBBATOM	5221	CA	VAL	B	350	3.767	-44.306	-43.919	1.00	33.79
BBBBATOM	5222	CB	VAL	B	350	2.848	-43.907	-42.744	1.00	33.70
BBBBATOM	5223	CG1	VAL	B	350	1.554	-44.695	-42.798	1.00	32.22
BBBBATOM	5224	CG2	VAL	B	350	3.568	-44.154	-41.425	1.00	32.24
BBBBATOM	5225	C	VAL	B	350	2.969	-44.274	-45.217	1.00	34.78
BBBBATOM	5226	O	VAL	B	350	2.411	-45.285	-45.645	1.00	34.85
BBBBATOM	5227	N	SER	B	351	2.925	-43.102	-45.844	1.00	35.34
BBBBATOM	5228	CA	SER	B	351	2.196	-42.946	-47.095	1.00	36.67
BBBBATOM	5229	CB	SER	B	351	2.024	-41.462	-47.425	1.00	37.32
BBBBATOM	5230	OG	SER	B	351	1.241	-41.292	-48.590	1.00	37.74
BBBBATOM	5231	C	SER	B	351	2.958	-43.639	-48.222	1.00	37.35
BBBBATOM	5232	O	SER	B	351	2.365	-44.309	-49.064	1.00	36.85
BBBBATOM	5233	N	ARG	B	352	4.277	-43.482	-48.223	1.00	37.89
BBBBATOM	5234	CA	ARG	B	352	5.114	-44.088	-49.251	1.00	40.03
BBBBATOM	5235	CB	ARG	B	352	6.557	-43.600	-49.114	1.00	41.58
BBBBATOM	5236	CG	ARG	B	352	7.470	-44.069	-50.232	1.00	44.46
BBBBATOM	5237	CD	ARG	B	352	8.906	-44.157	-49.759	1.00	47.36
BBBBATOM	5238	NE	ARG	B	352	9.097	-45.271	-48.832	1.00	49.57
BBBBATOM	5239	CZ	ARG	B	352	10.234	-45.524	-48.191	1.00	50.54
BBBBATOM	5240	NH1	ARG	B	352	11.287	-44.738	-48.372	1.00	50.88

BBBBATOM	5241	NH2	ARG	B	352	10.321	-46.566	-47.373	1.00	50.24
BBBBATOM	5242	C	ARG	B	352	5.098	-45.613	-49.176	1.00	40.60
BBBBATOM	5243	O	ARG	B	352	5.101	-46.292	-50.204	1.00	39.84
BBBBATOM	5244	N	VAL	B	353	5.096	-46.143	-47.955	1.00	41.33
BBBBATOM	5245	CA	VAL	B	353	5.089	-47.587	-47.737	1.00	42.78
BBBBATOM	5246	CB	VAL	B	353	5.446	-47.927	-46.271	1.00	42.54
BBBBATOM	5247	CG1	VAL	B	353	5.279	-49.420	-46.014	1.00	42.05
BBBBATOM	5248	CG2	VAL	B	353	6.879	-47.509	-45.987	1.00	41.86
BBBBATOM	5249	C	VAL	B	353	3.742	-48.206	-48.095	1.00	43.85
BBBBATOM	5250	O	VAL	B	353	3.679	-49.343	-48.556	1.00	44.43
BBBBATOM	5251	N	ALA	B	354	2.664	-47.465	-47.871	1.00	45.85
BBBBATOM	5252	CA	ALA	B	354	1.336	-47.957	-48.212	1.00	47.24
BBBBATOM	5253	CB	ALA	B	354	0.264	-47.043	-47.628	1.00	46.79
BBBBATOM	5254	C	ALA	B	354	1.250	-47.971	-49.737	1.00	48.54
BBBBATOM	5255	O	ALA	B	354	0.531	-48.780	-50.324	1.00	48.48
BBBBATOM	5256	N	ARG	B	355	1.998	-47.068	-50.366	1.00	50.49
BBBBATOM	5257	CA	ARG	B	355	2.035	-46.964	-51.824	1.00	52.71
BBBBATOM	5258	CB	ARG	B	355	2.658	-45.633	-52.264	1.00	53.58
BBBBATOM	5259	CG	ARG	B	355	1.998	-44.372	-51.730	1.00	55.08
BBBBATOM	5260	CD	ARG	B	355	0.716	-44.014	-52.461	1.00	56.64
BBBBATOM	5261	NE	ARG	B	355	0.112	-42.802	-51.907	1.00	57.43
BBBBATOM	5262	CZ	ARG	B	355	-1.054	-42.296	-52.299	1.00	58.24
BBBBATOM	5263	NH1	ARG	B	355	-1.758	-42.896	-53.252	1.00	58.53
BBBBATOM	5264	NH2	ARG	B	355	-1.519	-41.186	-51.738	1.00	58.87
BBBBATOM	5265	C	ARG	B	355	2.899	-48.099	-52.366	1.00	53.41
BBBBATOM	5266	O	ARG	B	355	2.966	-48.319	-53.575	1.00	53.50
BBBBATOM	5267	N	ALA	B	356	3.569	-48.805	-51.456	1.00	54.15
BBBBATOM	5268	CA	ALA	B	356	4.453	-49.913	-51.809	1.00	54.93
BBBBATOM	5269	CB	ALA	B	356	3.669	-51.004	-52.546	1.00	54.86
BBBBATOM	5270	C	ALA	B	356	5.611	-49.417	-52.671	1.00	55.63
BBBBATOM	5271	O	ALA	B	356	6.193	-50.178	-53.442	1.00	55.95
BBBBATOM	5272	N	LEU	B	357	5.942	-48.136	-52.526	1.00	56.45
BBBBATOM	5273	CA	LEU	B	357	7.023	-47.522	-53.289	1.00	57.81
BBBBATOM	5274	CB	LEU	B	357	6.871	-45.997	-53.290	1.00	58.04
BBBBATOM	5275	CG	LEU	B	357	5.595	-45.422	-53.915	1.00	58.29
BBBBATOM	5276	CD1	LEU	B	357	5.624	-43.903	-53.820	1.00	58.36
BBBBATOM	5277	CD2	LEU	B	357	5.485	-45.859	-55.370	1.00	58.62
BBBBATOM	5278	C	LEU	B	357	8.391	-47.895	-52.729	1.00	58.46
BBBBATOM	5279	OT1	LEU	B	357	9.244	-48.359	-53.514	1.00	58.97
BBBBATOM	5280	OT2	LEU	B	357	8.601	-47.710	-51.512	1.00	58.97
BBBB										
ATOM	5281	OH2	WAT	W	1	-20.568	11.549	41.653	1.00	24.11
WATR										
ATOM	5282	OH2	WAT	W	4	-7.219	-67.275	-41.843	1.00	35.35
WATR										
ATOM	5283	OH2	WAT	W	5	20.119	-17.520	-22.473	1.00	21.13
WATR										
ATOM	5284	OH2	WAT	W	6	18.858	-19.701	-23.468	1.00	18.31
WATR										
ATOM	5285	OH2	WAT	W	7	2.329	-28.724	-15.978	1.00	27.32
WATR										
ATOM	5286	OH2	WAT	W	8	9.484	-48.435	-27.938	1.00	23.67
WATR										
ATOM	5287	OH2	WAT	W	9	7.645	-57.693	-27.177	1.00	21.03
WATR										
ATOM	5288	OH2	WAT	W	10	-1.542	-8.422	1.824	1.00	29.71
WATR										
ATOM	5289	OH2	WAT	W	11	5.875	-50.793	-32.396	1.00	20.21
WATR										
ATOM	5290	OH2	WAT	W	12	27.592	-18.174	-27.779	1.00	22.52
WATR										
ATOM	5291	OH2	WAT	W	13	7.842	-13.432	-21.178	1.00	25.85
WATR										
ATOM	5292	OH2	WAT	W	14	4.845	-57.924	-27.444	1.00	24.35
WATR										

ATOM	5293	OH2	WAT	W	15	0.473	-58.751	-17.746	1.00	35.49
WATR										
ATOM	5294	OH2	WAT	W	16	7.998	-52.522	-25.785	1.00	22.34
WATR										
ATOM	5295	OH2	WAT	W	17	-8.656	11.300	18.872	1.00	23.81
WATR										
ATOM	5296	OH2	WAT	W	18	8.711	-45.913	-29.121	1.00	21.55
WATR										
ATOM	5297	OH2	WAT	W	19	2.957	-68.158	-38.242	1.00	29.43
WATR										
ATOM	5298	OH2	WAT	W	20	16.486	-11.742	-16.567	1.00	22.13
WATR										
ATOM	5299	OH2	WAT	W	21	-6.251	17.702	28.534	1.00	24.24
WATR										
ATOM	5300	OH2	WAT	W	22	12.670	-47.636	-24.808	1.00	25.87
WATR										
ATOM	5301	OH2	WAT	W	23	6.513	-15.597	-22.517	1.00	26.31
WATR										
ATOM	5302	OH2	WAT	W	24	7.536	-66.906	-21.753	1.00	21.48
WATR										
ATOM	5303	OH2	WAT	W	25	-29.060	13.621	26.406	1.00	21.08
WATR										
ATOM	5304	OH2	WAT	W	26	-5.240	10.154	13.527	1.00	29.62
WATR										
ATOM	5305	OH2	WAT	W	27	29.942	-20.139	-19.237	1.00	20.38
WATR										
ATOM	5306	OH2	WAT	W	28	18.996	-28.763	-24.427	1.00	20.28
WATR										
ATOM	5307	OH2	WAT	W	29	8.755	-51.080	-27.990	1.00	20.66
WATR										
ATOM	5308	OH2	WAT	W	30	4.215	-64.684	-43.328	1.00	39.67
WATR										
ATOM	5309	OH2	WAT	W	31	14.708	-11.936	-1.749	1.00	24.57
WATR										
ATOM	5310	OH2	WAT	W	32	28.140	-13.870	-21.266	1.00	18.93
WATR										
ATOM	5311	OH2	WAT	W	33	4.057	-1.221	9.809	1.00	32.30
WATR										
ATOM	5312	OH2	WAT	W	34	4.784	-56.759	-43.904	1.00	25.99
WATR										
ATOM	5313	OH2	WAT	W	35	-22.733	10.283	33.238	1.00	24.60
WATR										
ATOM	5314	OH2	WAT	W	36	0.540	14.225	10.932	1.00	26.89
WATR										
ATOM	5315	OH2	WAT	W	37	-7.560	11.931	12.593	1.00	27.76
WATR										
ATOM	5316	OH2	WAT	W	38	-7.966	17.043	30.555	1.00	20.04
WATR										
ATOM	5317	OH2	WAT	W	39	6.716	-55.314	-42.959	1.00	25.72
WATR										
ATOM	5318	OH2	WAT	W	40	6.833	-32.402	-3.845	1.00	32.49
WATR										
ATOM	5319	OH2	WAT	W	41	30.445	-20.104	-25.459	1.00	27.97
WATR										
ATOM	5320	OH2	WAT	W	42	1.475	-15.304	-22.128	1.00	30.57
WATR										
ATOM	5321	OH2	WAT	W	43	15.703	-42.835	-31.237	1.00	26.74
WATR										
ATOM	5322	OH2	WAT	W	44	7.131	-6.595	-18.003	1.00	29.47
WATR										
ATOM	5323	OH2	WAT	W	45	30.256	-23.202	-11.163	1.00	33.81
WATR										
ATOM	5324	OH2	WAT	W	46	-6.107	-66.004	-38.690	1.00	30.45
WATR										
ATOM	5325	OH2	WAT	W	47	17.631	-17.241	-5.864	1.00	28.69
WATR										

ATOM	5326	OH2	WAT	W	48	13.436	-59.821	-27.855	1.00	28.71
WATR										
ATOM	5327	OH2	WAT	W	49	11.395	-15.293	2.925	1.00	29.36
WATR										
ATOM	5328	OH2	WAT	W	50	19.218	-21.377	-34.248	1.00	31.41
WATR										
ATOM	5329	OH2	WAT	W	51	11.973	-11.890	-15.788	1.00	35.59
WATR										
ATOM	5330	OH2	WAT	W	52	9.140	-8.260	-23.371	1.00	40.29
WATR										
ATOM	5331	OH2	WAT	W	53	-19.061	14.438	38.966	1.00	38.01
WATR										
ATOM	5332	OH2	WAT	W	54	-3.895	-70.510	-28.249	1.00	25.56
WATR										
ATOM	5333	OH2	WAT	W	55	20.909	-23.456	-34.213	1.00	26.74
WATR										
ATOM	5334	OH2	WAT	W	56	-8.505	11.136	10.323	1.00	30.97
WATR										
ATOM	5335	OH2	WAT	W	57	22.022	-15.529	-23.223	1.00	26.74
WATR										
ATOM	5336	OH2	WAT	W	58	13.860	-49.304	-42.490	1.00	27.91
WATR										
ATOM	5337	OH2	WAT	W	59	-9.455	-6.552	-9.720	1.00	41.70
WATR										
ATOM	5338	OH2	WAT	W	60	13.798	-49.732	-23.016	1.00	41.60
WATR										
ATOM	5339	OH2	WAT	W	61	15.881	-60.461	-31.910	1.00	48.66
WATR										
ATOM	5340	OH2	WAT	W	62	-9.797	12.718	13.997	1.00	29.14
WATR										
ATOM	5341	OH2	WAT	W	63	16.793	0.356	-6.115	1.00	26.17
WATR										
ATOM	5342	OH2	WAT	W	64	3.173	18.778	20.793	1.00	31.13
WATR										
ATOM	5343	OH2	WAT	W	65	13.433	-11.079	0.672	1.00	27.40
WATR										
ATOM	5344	OH2	WAT	W	66	3.118	-0.813	0.729	1.00	24.68
WATR										
ATOM	5345	OH2	WAT	W	67	-22.179	3.583	26.978	1.00	32.28
WATR										
ATOM	5346	OH2	WAT	W	68	24.433	-30.481	-1.783	1.00	41.91
WATR										
ATOM	5347	OH2	WAT	W	69	4.384	-66.131	-41.203	1.00	34.75
WATR										
ATOM	5348	OH2	WAT	W	70	20.398	-7.386	-4.280	1.00	30.85
WATR										
ATOM	5349	OH2	WAT	W	71	-2.444	-70.752	-22.067	1.00	25.46
WATR										
ATOM	5350	OH2	WAT	W	72	-3.963	-4.914	-5.711	1.00	29.67
WATR										
ATOM	5351	OH2	WAT	W	73	17.663	-11.040	-34.488	1.00	30.24
WATR										
ATOM	5352	OH2	WAT	W	74	21.404	-42.041	-26.621	1.00	31.41
WATRATOM	5353	OH2	WAT	W	75	-1.110	-15.319	-1.089	1.00	31.51
WATRATOM	5354	OH2	WAT	W	76	0.688	19.730	22.519	1.00	26.71
WATRATOM	5355	OH2	WAT	W	77	12.113	-69.335	-26.593	1.00	27.11
WATRATOM	5356	OH2	WAT	W	78	11.725	-25.065	-33.817	1.00	43.79
WATRATOM	5357	OH2	WAT	W	79	-25.519	9.450	22.092	1.00	28.18
WATRATOM	5358	OH2	WAT	W	80	-14.673	6.584	16.023	1.00	31.37
WATRATOM	5359	OH2	WAT	W	81	-2.250	-0.253	-1.741	1.00	29.99
WATRATOM	5360	OH2	WAT	W	82	-7.300	12.943	8.415	1.00	32.39
WATRATOM	5361	OH2	WAT	W	83	1.712	-13.629	-13.904	1.00	34.08
WATRATOM	5362	OH2	WAT	W	84	4.709	-17.478	-6.557	1.00	29.67
WATRATOM	5363	OH2	WAT	W	85	10.070	-57.496	-44.450	1.00	48.39
WATRATOM	5364	OH2	WAT	W	86	8.040	-30.281	-10.117	1.00	28.59
WATRATOM	5365	OH2	WAT	W	87	-1.967	-32.372	-38.643	1.00	31.55

WATRATOM	5366	OH2	WAT	W	88	-3.178	-64.576	-25.506	1.00	33.66
WATRATOM	5367	OH2	WAT	W	89	15.762	-9.860	-10.400	1.00	34.29
WATRATOM	5368	OH2	WAT	W	90	5.654	-30.990	-27.758	1.00	35.84
WATRATOM	5369	OH2	WAT	W	91	14.959	-46.096	-42.270	1.00	35.21
WATRATOM	5370	OH2	WAT	W	92	10.137	-13.308	-9.753	1.00	32.65
WATRATOM	5371	OH2	WAT	W	93	-4.480	6.624	6.614	1.00	27.37
WATRATOM	5372	OH2	WAT	W	94	-14.574	22.522	18.870	1.00	49.48
WATRATOM	5373	OH2	WAT	W	95	-11.031	-42.768	-39.637	1.00	37.63
WATRATOM	5374	OH2	WAT	W	96	9.906	-35.479	-19.203	1.00	29.59
WATRATOM	5375	OH2	WAT	W	97	-0.990	-0.781	36.951	1.00	37.27
WATRATOM	5376	OH2	WAT	W	98	-11.422	9.059	11.252	1.00	30.43
WATRATOM	5377	OH2	WAT	W	99	8.118	-36.710	-22.371	1.00	34.85
WATRATOM	5378	OH2	WAT	W	100	12.414	-67.326	-22.791	1.00	31.24
WATRATOM	5379	OH2	WAT	W	101	28.541	-24.603	-31.049	1.00	40.14
WATRATOM	5380	OH2	WAT	W	102	16.276	-10.934	-3.673	1.00	33.80
WATRATOM	5381	OH2	WAT	W	103	30.979	-13.264	-22.953	1.00	24.73
WATRATOM	5382	OH2	WAT	W	104	12.759	-31.636	-31.838	1.00	26.40
WATRATOM	5383	OH2	WAT	W	105	23.507	-29.661	-32.187	1.00	29.62
WATRATOM	5384	OH2	WAT	W	106	21.292	-13.141	-24.874	1.00	37.83
WATRATOM	5385	OH2	WAT	W	107	10.171	-32.960	-15.580	1.00	26.59
WATRATOM	5386	OH2	WAT	W	108	-2.207	2.376	2.034	1.00	27.55
WATRATOM	5387	OH2	WAT	W	109	-6.984	22.588	16.082	1.00	39.01
WATRATOM	5388	OH2	WAT	W	110	14.308	-11.038	-15.406	1.00	26.48
WATRATOM	5389	OH2	WAT	W	111	10.612	9.749	24.161	1.00	40.18
WATRATOM	5390	OH2	WAT	W	112	2.406	-15.823	-10.196	1.00	27.61
WATRATOM	5391	OH2	WAT	W	113	6.310	-68.984	-20.661	1.00	40.25
WATRATOM	5392	OH2	WAT	W	114	14.379	-10.930	-8.565	1.00	35.86
WATRATOM	5393	OH2	WAT	W	115	24.183	-35.475	-30.338	1.00	35.17
WATRATOM	5394	OH2	WAT	W	116	21.897	-31.717	-1.243	1.00	47.61
WATRATOM	5395	OH2	WAT	W	117	24.065	-17.545	-13.707	1.00	32.24
WATRATOM	5396	OH2	WAT	W	118	16.772	-51.926	-25.940	1.00	38.66
WATRATOM	5397	OH2	WAT	W	119	-5.862	6.629	4.446	1.00	39.57
WATRATOM	5398	OH2	WAT	W	120	14.133	-57.303	-28.159	1.00	30.19
WATRATOM	5399	OH2	WAT	W	121	-16.538	-6.724	21.638	1.00	40.50
WATRATOM	5400	OH2	WAT	W	122	19.669	-18.487	-33.216	1.00	38.38
WATRATOM	5401	OH2	WAT	W	123	15.481	1.078	-4.048	1.00	32.28
WATRATOM	5402	OH2	WAT	W	124	20.395	-13.033	-2.072	1.00	49.69
WATRATOM	5403	OH2	WAT	W	125	15.526	-1.437	-15.842	1.00	36.06
WATRATOM	5404	OH2	WAT	W	126	7.297	-29.419	-1.509	1.00	34.75
WATRATOM	5405	OH2	WAT	W	127	9.994	-12.069	-21.013	1.00	32.21
WATRATOM	5406	OH2	WAT	W	128	17.433	-42.825	-16.713	1.00	31.02
WATRATOM	5407	OH2	WAT	W	129	-15.855	20.882	21.019	1.00	44.11
WATRATOM	5408	OH2	WAT	W	130	-6.351	-7.687	-14.067	1.00	35.04
WATRATOM	5409	OH2	WAT	W	131	7.954	-17.872	-1.475	1.00	28.45
WATRATOM	5410	OH2	WAT	W	132	13.526	-34.593	-31.844	1.00	31.12
WATRATOM	5411	OH2	WAT	W	133	9.992	-41.228	-23.098	1.00	26.45
WATRATOM	5412	OH2	WAT	W	134	8.434	18.132	16.019	1.00	32.97
WATRATOM	5413	OH2	WAT	W	135	-1.208	-33.658	-36.216	1.00	38.33
WATRATOM	5414	OH2	WAT	W	136	-14.502	9.100	12.433	1.00	43.21
WATRATOM	5415	OH2	WAT	W	137	14.394	-43.675	-17.325	1.00	32.32
WATRATOM	5416	OH2	WAT	W	138	-4.809	-30.333	-46.416	1.00	42.65
WATRATOM	5417	OH2	WAT	W	139	18.861	-35.072	-35.671	1.00	43.56
WATRATOM	5418	OH2	WAT	W	140	-10.162	-60.139	-32.862	1.00	35.41
WATRATOM	5419	OH2	WAT	W	141	6.740	-32.411	-35.303	1.00	38.57
WATRATOM	5420	OH2	WAT	W	142	-12.257	-60.854	-39.307	1.00	32.90
WATRATOM	5421	OH2	WAT	W	143	18.910	-40.984	-13.084	1.00	43.43
WATRATOM	5422	OH2	WAT	W	144	18.857	-49.375	-28.645	1.00	31.34
WATRATOM	5423	OH2	WAT	W	145	0.235	-17.424	-16.608	1.00	38.85
WATRATOM	5424	OH2	WAT	W	146	14.236	-11.252	-24.086	1.00	27.79
WATRATOM	5425	OH2	WAT	W	147	31.513	-22.336	-22.128	1.00	43.18
WATRATOM	5426	OH2	WAT	W	148	-5.314	-70.396	-26.090	1.00	43.91
WATRATOM	5427	OH2	WAT	W	149	-7.717	-64.969	-36.808	1.00	26.30
WATRATOM	5428	OH2	WAT	W	150	22.584	-12.594	-4.179	1.00	46.91
WATRATOM	5429	OH2	WAT	W	151	-12.388	9.493	36.619	1.00	32.82
WATRATOM	5430	OH2	WAT	W	152	-14.517	16.479	37.760	1.00	39.52
WATRATOM	5431	OH2	WAT	W	153	-10.095	-34.647	-29.068	1.00	41.08

WATRATOM	5432	OH2	WAT	W	154	-5.233	-4.134	31.160	1.00	35.31
WATRATOM	5433	OH2	WAT	W	155	-6.322	11.278	-1.883	1.00	35.75
WATRATOM	5434	OH2	WAT	W	156	10.262	-9.572	-16.736	1.00	42.40
WATRATOM	5435	OH2	WAT	W	157	22.929	-10.414	-23.566	1.00	36.66
WATRATOM	5436	OH2	WAT	W	158	-15.987	3.994	16.559	1.00	37.22
WATRATOM	5437	OH2	WAT	W	159	13.385	-44.923	-46.826	1.00	41.55
WATRATOM	5438	OH2	WAT	W	160	26.508	-13.616	-18.049	1.00	25.93
WATRATOM	5439	OH2	WAT	W	161	4.671	-66.907	-17.861	1.00	31.54
WATRATOM	5440	OH2	WAT	W	162	-12.589	12.262	11.825	1.00	32.71
WATRATOM	5441	OH2	WAT	W	163	13.899	-62.269	-25.144	1.00	30.71
WATRATOM	5442	OH2	WAT	W	164	-31.053	15.663	19.272	1.00	30.19
WATRATOM	5443	OH2	WAT	W	165	9.797	-47.899	-25.140	1.00	26.79
WATRATOM	5444	OH2	WAT	W	166	0.877	-51.774	-25.619	1.00	30.02
WATRATOM	5445	OH2	WAT	W	167	-17.088	16.246	37.180	1.00	25.63
WATRATOM	5446	OH2	WAT	W	168	0.855	-52.086	-22.078	1.00	40.99
WATRATOM	5447	OH2	WAT	W	169	-14.873	18.295	21.203	1.00	40.28
WATRATOM	5448	OH2	WAT	W	170	11.913	-62.134	-35.641	1.00	41.33
WATRATOM	5449	OH2	WAT	W	171	25.783	-23.984	-33.162	1.00	44.03
WATRATOM	5450	OH2	WAT	W	172	7.169	-50.047	-23.737	1.00	47.85
WATRATOM	5451	OH2	WAT	W	173	20.074	-42.845	-14.939	1.00	32.87
WATRATOM	5452	OH2	WAT	W	174	8.765	5.909	9.193	1.00	34.30
WATRATOM	5453	OH2	WAT	W	175	-4.953	-64.494	-45.351	1.00	47.11
WATRATOM	5454	OH2	WAT	W	176	11.889	-61.263	-22.531	1.00	36.63
WATRATOM	5455	OH2	WAT	W	177	2.149	-49.169	-24.836	1.00	39.21
WATRATOM	5456	OH2	WAT	W	178	-14.051	6.399	13.353	1.00	39.89
WATRATOM	5457	OH2	WAT	W	179	8.488	-46.760	-23.118	1.00	45.24
WATRATOM	5458	OH2	WAT	W	180	-1.152	-23.348	-11.975	1.00	30.36
WATRATOM	5459	OH2	WAT	W	181	-7.002	3.531	7.051	1.00	44.50
WATRATOM	5460	OH2	WAT	W	182	-12.320	-54.772	-29.990	1.00	38.61
WATRATOM	5461	OH2	WAT	W	183	6.790	-54.559	-47.733	1.00	44.05
WATRATOM	5462	OH2	WAT	W	184	26.305	-38.240	-19.177	1.00	39.53
WATRATOM	5463	OH2	WAT	W	185	20.402	-58.179	-34.391	1.00	46.11
WATRATOM	5464	OH2	WAT	W	186	8.061	-31.341	-19.653	1.00	41.37
WATRATOM	5465	OH2	WAT	W	187	-7.549	-15.619	-5.482	1.00	40.60
WATRATOM	5466	OH2	WAT	W	188	-31.099	11.941	25.471	1.00	38.80
WATRATOM	5467	OH2	WAT	W	189	28.566	-25.441	-15.103	1.00	34.75
WATRATOM	5468	OH2	WAT	W	190	-5.613	-40.109	-50.158	1.00	49.21
WATRATOM	5469	OH2	WAT	W	191	17.024	-13.428	1.709	1.00	39.93
WATRATOM	5470	OH2	WAT	W	192	-22.114	10.176	37.673	1.00	32.53
WATRATOM	5471	OH2	WAT	W	193	10.204	-29.330	-20.066	1.00	27.24
WATRATOM	5472	OH2	WAT	W	194	27.893	-25.793	-21.862	1.00	38.97
WATRATOM	5473	OH2	WAT	W	195	-5.582	17.681	32.898	1.00	43.64
WATRATOM	5474	OH2	WAT	W	196	23.004	-45.224	-27.870	1.00	43.04
WATRATOM	5475	OH2	WAT	W	197	5.189	-58.857	-25.016	1.00	28.15
WATRATOM	5476	OH2	WAT	W	198	-7.740	-56.165	-24.052	1.00	35.98
WATRATOM	5477	OH2	WAT	W	199	-8.156	24.723	26.733	1.00	45.54
WATRATOM	5478	OH2	WAT	W	200	23.286	-32.333	-33.400	1.00	38.12
WATRATOM	5479	OH2	WAT	W	201	30.646	-14.180	-20.528	1.00	31.01
WATRATOM	5480	OH2	WAT	W	202	-8.238	-4.609	29.299	1.00	39.76
WATRATOM	5481	OH2	WAT	W	203	19.370	0.814	-7.532	1.00	35.83
WATRATOM	5482	OH2	WAT	W	204	0.885	-27.619	-1.442	1.00	47.04
WATRATOM	5483	OH2	WAT	W	205	16.084	-56.649	-26.382	1.00	45.97
WATRATOM	5484	OH2	WAT	W	206	-0.698	-19.360	-9.869	1.00	37.53
WATRATOM	5485	OH2	WAT	W	207	0.682	-14.985	-15.794	1.00	33.35
WATRATOM	5486	OH2	WAT	W	208	1.646	17.427	31.991	1.00	40.39
WATRATOM	5487	OH2	WAT	W	209	-21.611	1.533	20.359	1.00	31.04
WATRATOM	5488	OH2	WAT	W	210	-5.143	-55.137	-45.825	1.00	30.17
WATRATOM	5489	OH2	WAT	W	211	-9.645	13.045	37.660	1.00	42.93
WATRATOM	5490	OH2	WAT	W	212	22.096	-11.242	-30.224	1.00	48.12
WATRATOM	5491	OH2	WAT	W	213	-5.759	2.610	-15.984	1.00	41.67
WATRATOM	5492	OH2	WAT	W	214	-4.323	7.731	-7.331	1.00	37.92
WATRATOM	5493	OH2	WAT	W	215	-5.450	7.197	10.632	1.00	33.99
WATRATOM	5494	OH2	WAT	W	216	2.330	-32.635	-34.500	1.00	38.85
WATRATOM	5495	OH2	WAT	W	217	-26.827	16.219	13.451	1.00	38.12
WATRATOM	5496	OH2	WAT	W	218	10.887	-51.427	-23.191	1.00	39.81
WATRATOM	5497	OH2	WAT	W	219	-9.020	19.746	-3.698	1.00	46.58

WATRATOM	5498	OH2	WAT	W	220	9.054	6.622	-0.709	1.00	34.14
WATRATOM	5499	OH2	WAT	W	221	4.173	-7.985	-23.786	1.00	32.75
WATRATOM	5500	OH2	WAT	W	222	0.983	16.806	3.910	1.00	40.83
WATRATOM	5501	OH2	WAT	W	223	2.222	-16.848	-6.783	1.00	33.50
WATRATOM	5502	OH2	WAT	W	224	13.627	1.072	-15.114	1.00	37.51
WATRATOM	5503	OH2	WAT	W	225	12.533	-14.212	-9.007	1.00	38.40
WATRATOM	5504	OH2	WAT	W	226	1.404	-7.852	5.396	1.00	38.55
WATRATOM	5505	OH2	WAT	W	227	31.159	-24.354	-31.143	1.00	37.67
WATRATOM	5506	OH2	WAT	W	228	-13.047	-60.728	-42.282	1.00	42.18
WATRATOM	5507	OH2	WAT	W	229	8.956	-37.681	-16.765	1.00	41.45
WATRATOM	5508	OH2	WAT	W	230	28.749	-13.637	-16.860	1.00	42.34
WATRATOM	5509	OH2	WAT	W	231	-4.461	19.451	8.684	1.00	36.17
WATRATOM	5510	OH2	WAT	W	232	-9.785	-66.504	-35.701	1.00	44.07
WATRATOM	5511	OH2	WAT	W	233	10.673	-41.619	-20.678	1.00	36.58
WATRATOM	5512	OH2	WAT	W	234	-15.694	1.684	32.613	1.00	44.04
WATRATOM	5513	OH2	WAT	W	235	3.345	1.229	9.738	1.00	35.70
WATRATOM	5514	OH2	WAT	W	236	-6.256	-68.913	-30.401	1.00	36.72
WATRATOM	5515	OH2	WAT	W	237	28.344	-21.326	-30.399	1.00	36.45
WATRATOM	5516	OH2	WAT	W	238	2.876	-34.368	-17.344	1.00	42.48
WATRATOM	5517	OH2	WAT	W	239	15.355	-11.202	2.371	1.00	38.84
WATRATOM	5518	OH2	WAT	W	240	27.066	-22.336	-6.437	1.00	37.37
WATRATOM	5519	OH2	WAT	W	241	2.222	18.464	26.994	1.00	35.75
WATRATOM	5520	OH2	WAT	W	242	15.052	-9.829	-31.019	1.00	44.31
WATRATOM	5521	OH2	WAT	W	243	10.351	-67.649	-21.184	1.00	35.79
WATRATOM	5522	OH2	WAT	W	244	-13.173	14.269	38.605	1.00	41.50
WATRATOM	5523	OH2	WAT	W	245	-7.569	9.658	0.793	1.00	37.62
WATRATOM	5524	OH2	WAT	W	246	-2.167	-47.395	-19.605	1.00	45.90
WATRATOM	5525	OH2	WAT	W	247	7.166	2.400	15.830	1.00	42.90
WATRATOM	5526	OH2	WAT	W	248	-11.231	-10.901	-10.057	1.00	45.28
WATRATOM	5527	OH2	WAT	W	249	5.684	-16.094	-26.796	1.00	44.76
WATRATOM	5528	OH2	WAT	W	250	-4.745	3.667	-18.932	1.00	46.20
WATRATOM	5529	OH2	WAT	W	251	-0.505	-22.136	-9.079	1.00	42.89
WATRATOM	5530	OH2	WAT	W	252	16.668	-37.987	-7.767	1.00	35.76
WATRATOM	5531	OH2	WAT	W	253	2.454	-18.256	-26.130	1.00	43.33
WATRATOM	5532	OH2	WAT	W	254	-8.367	-39.960	-21.638	1.00	43.07
WATRATOM	5533	OH2	WAT	W	255	15.642	7.805	9.633	1.00	47.78
WATRATOM	5534	OH2	WAT	W	256	13.660	-24.331	1.932	1.00	42.50
WATRATOM	5535	OH2	WAT	W	257	11.567	-6.104	-23.359	1.00	37.10
WATRATOM	5536	OH2	WAT	W	258	18.941	-16.698	0.528	1.00	40.97
WATRATOM	5537	OH2	WAT	W	259	-11.441	-63.514	-39.126	1.00	43.17
WATRATOM	5538	OH2	WAT	W	260	28.664	-39.605	-22.853	1.00	42.65
WATRATOM	5539	OH2	WAT	W	261	6.795	-6.961	31.114	1.00	38.28
WATRATOM	5540	OH2	WAT	W	262	7.077	-14.349	-24.858	1.00	41.00
WATRATOM	5541	OH2	WAT	W	263	-2.259	-48.991	-29.099	1.00	34.96
WATRATOM	5542	OH2	WAT	W	264	21.812	-44.128	-35.641	1.00	44.51
WATRATOM	5543	OH2	WAT	W	265	-27.570	4.389	13.296	1.00	48.63
WATRATOM	5544	OH2	WAT	W	266	13.573	-27.185	0.220	1.00	43.56
WATRATOM	5545	OH2	WAT	W	267	16.549	8.451	-13.582	1.00	44.84
WATRATOM	5546	OH2	WAT	W	268	-9.142	9.107	36.872	1.00	37.66
WATRATOM	5547	OH2	WAT	W	269	5.648	-11.797	-24.893	1.00	45.79
WATRATOM	5548	OH2	WAT	W	270	3.619	-14.850	-23.652	1.00	34.09
WATRATOM	5549	OH2	WAT	W	271	-8.129	-11.098	-16.064	1.00	39.37
WATRATOM	5550	OH2	WAT	W	272	-17.342	8.563	9.979	1.00	46.38
WATRATOM	5551	OH2	WAT	W	273	8.798	-36.348	-46.119	1.00	37.71
WATRATOM	5552	OH2	WAT	W	274	9.190	-10.509	-35.865	1.00	45.80
WATRATOM	5553	OH2	WAT	W	275	13.545	-13.441	3.898	1.00	42.83
WATRATOM	5554	OH2	WAT	W	276	-7.844	0.944	-2.560	1.00	46.27
WATRATOM	5555	OH2	WAT	W	277	0.478	-47.721	-55.170	1.00	46.25
WATRATOM	5556	OH2	WAT	W	278	24.658	-18.359	-11.005	1.00	36.33
WATRATOM	5557	OH2	WAT	W	279	-4.675	21.561	12.155	1.00	37.17
WATRATOM	5558	OH2	WAT	W	280	0.382	20.486	4.930	1.00	41.40
WATRATOM	5559	OH2	WAT	W	281	5.919	18.010	25.033	1.00	41.72
WATRATOM	5560	OH2	WAT	W	282	-2.987	-63.751	-22.983	1.00	43.76
WATRATOM	5561	OH2	WAT	W	283	8.990	-33.134	-17.898	1.00	40.17
WATRATOM	5562	OH2	WAT	W	284	0.155	-61.872	-48.384	1.00	49.87
WATRATOM	5563	OH2	WAT	W	285	-10.443	-56.965	-24.681	1.00	48.02

WATRATOM	5564	OH2	WAT	W	286	18.915	-33.048	-3.930	1.00	37.81
WATRATOM	5565	OH2	WAT	W	287	-16.181	11.706	12.277	1.00	41.77
WATRATOM	5566	OH2	WAT	W	288	7.197	7.180	10.953	1.00	46.19
WATRATOM	5567	OH2	WAT	W	289	31.934	-26.155	-26.053	1.00	38.77
WATRATOM	5568	OH2	WAT	W	290	-15.232	-0.248	11.315	1.00	40.14
WATRATOM	5569	OH2	WAT	W	291	9.450	-27.963	-1.396	1.00	41.29
WATRATOM	5570	OH2	WAT	W	292	-1.800	13.139	-9.983	1.00	41.60
WATRATOM	5571	OH2	WAT	W	293	-7.766	5.988	9.798	1.00	40.11
WATRATOM	5572	OH2	WAT	W	294	7.973	4.338	14.321	1.00	39.97
WATRATOM	5573	OH2	WAT	W	295	23.449	-40.563	-27.347	1.00	40.59
WATRATOM	5574	OH2	WAT	W	296	-3.537	-28.260	-15.925	1.00	42.10
WATRATOM	5575	OH2	WAT	W	297	28.052	-32.620	-12.168	1.00	48.03
WATRATOM	5576	OH2	WAT	W	298	20.655	-43.315	-28.829	1.00	40.17
WATR										
ATOM	5577	S	SO4	S	1	1.273	-70.953	-23.009	1.00	22.99
SO4										
ATOM	5578	O1	SO4	S	1	1.720	-71.882	-24.053	1.00	21.18
SO4										
ATOM	5579	O2	SO4	S	1	0.908	-69.659	-23.626	1.00	22.47
SO4										
ATOM	5580	O3	SO4	S	1	2.337	-70.752	-22.018	1.00	23.88
SO4										
ATOM	5581	O4	SO4	S	1	0.088	-71.522	-22.328	1.00	22.50
SO4										
TEREND										

TABLE 2 ATOMIC COORDINATES OF E.COLI MURG C-ALPHA

BACKBONE ATOMS

ATOM	2649	CA	LYS	B	7	-6.512	-45.403	-47.519	1.00	45.28	BBBB
ATOM	2651	CA	ARG	B	8	-6.682	-47.303	-44.240	1.00	38.63	BBBB
ATOM	2662	CA	LEU	B	9	-4.094	-47.039	-41.477	1.00	30.88	BBBB
ATOM	2670	CA	MET	B	10	-4.048	-49.055	-38.275	1.00	26.66	BBBB
ATOM	2678	CA	VAL	B	11	-1.982	-47.605	-35.449	1.00	23.16	BBBB
ATOM	2685	CA	MET	B	12	-0.523	-49.707	-32.613	1.00	24.54	BBBB
ATOM	2693	CA	ALA	B	13	0.508	-47.410	-29.752	1.00	29.43	BBBB
ATOM	2698	CA	GLY	B	14	-0.513	-47.804	-26.120	1.00	33.82	BBBB
ATOM	2702	CA	GLY	B	15	-0.700	-45.047	-23.536	1.00	36.08	BBBB
ATOM	2706	CA	THR	B	16	1.920	-46.787	-21.421	1.00	38.51	BBBB
ATOM	2713	CA	GLY	B	17	5.367	-45.567	-22.392	1.00	36.57	BBBB
ATOM	2717	CA	GLY	B	18	3.631	-42.529	-23.872	1.00	33.48	BBBB
ATOM	2721	CA	HIS	B	19	3.548	-43.865	-27.435	1.00	28.22	BBBB
ATOM	2731	CA	VAL	B	20	-0.098	-42.894	-27.965	1.00	27.77	BBBB
ATOM	2738	CA	PHE	B	21	0.517	-39.136	-28.160	1.00	29.00	BBBB
ATOM	2750	CA	PRO	B	22	2.986	-39.252	-31.086	1.00	26.12	BBBB
ATOM	2756	CA	GLY	B	23	0.787	-41.864	-32.752	1.00	25.07	BBBB
ATOM	2760	CA	LEU	B	24	-2.201	-39.551	-32.401	1.00	25.32	BBBB
ATOM	2768	CA	ALA	B	25	-0.197	-36.754	-34.013	1.00	25.94	BBBB
ATOM	2773	CA	VAL	B	26	0.466	-38.955	-37.056	1.00	25.70	BBBB
ATOM	2780	CA	ALA	B	27	-3.116	-40.222	-37.199	1.00	26.15	BBBB
ATOM	2785	CA	HIS	B	28	-4.574	-36.702	-37.190	1.00	29.32	BBBB
ATOM	2795	CA	HIS	B	29	-2.070	-35.623	-39.806	1.00	32.38	BBBB
ATOM	2805	CA	LEU	B	30	-3.136	-38.417	-42.162	1.00	32.00	BBBB
ATOM	2813	CA	MET	B	31	-6.849	-38.064	-41.424	1.00	34.91	BBBB
ATOM	2821	CA	ALA	B	32	-6.510	-34.511	-42.722	1.00	37.55	BBBB
ATOM	2826	CA	GLN	B	33	-5.182	-36.070	-45.938	1.00	38.24	BBBB
ATOM	2835	CA	GLY	B	34	-8.305	-38.169	-46.353	1.00	35.75	BBBB
ATOM	2839	CA	TRP	B	35	-7.016	-41.246	-44.508	1.00	34.58	BBBB
ATOM	2853	CA	GLN	B	36	-9.175	-43.535	-42.402	1.00	35.40	BBBB
ATOM	2862	CA	VAL	B	37	-7.417	-44.516	-39.184	1.00	34.16	BBBB
ATOM	2869	CA	ARG	B	38	-8.219	-47.286	-36.730	1.00	31.56	BBBB
ATOM	2880	CA	TRP	B	39	-6.456	-48.070	-33.471	1.00	27.41	BBBB
ATOM	2894	CA	LEU	B	40	-5.200	-51.364	-32.026	1.00	24.71	BBBB
ATOM	2902	CA	GLY	B	41	-4.691	-51.450	-28.257	1.00	23.47	BBBB
ATOM	2906	CA	THR	B	42	-5.787	-53.141	-25.027	1.00	29.84	BBBB
ATOM	2913	CA	ALA	B	43	-9.000	-52.595	-23.047	1.00	38.81	BBBB
ATOM	2918	CA	ASP	B	44	-7.455	-51.942	-19.632	1.00	44.47	BBBB
ATOM	2926	CA	ARG	B	45	-4.887	-49.367	-20.763	1.00	40.44	BBBB
ATOM	2937	CA	MET	B	46	-4.881	-45.581	-21.249	1.00	36.33	BBBB
ATOM	2945	CA	GLU	B	47	-5.458	-45.655	-25.029	1.00	31.79	BBBB
ATOM	2954	CA	ALA	B	48	-8.821	-47.344	-24.414	1.00	32.58	BBBB
ATOM	2959	CA	ASP	B	49	-10.143	-44.065	-23.009	1.00	35.60	BBBB
ATOM	2967	CA	LEU	B	50	-8.026	-41.484	-24.840	1.00	33.49	BBBB
ATOM	2975	CA	VAL	B	51	-8.299	-42.641	-28.449	1.00	32.68	BBBB
ATOM	2983	CA	PRO	B	52	-12.111	-42.601	-28.453	1.00	34.43	BBBB
ATOM	2989	CA	LYS	B	53	-11.998	-39.054	-27.064	1.00	36.73	BBBB
ATOM	2998	CA	HIS	B	54	-10.116	-38.212	-30.259	1.00	34.62	BBBB
ATOM	3008	CA	GLY	B	55	-12.938	-39.481	-32.447	1.00	35.34	BBBB
ATOM	3012	CA	ILE	B	56	-10.909	-42.517	-33.514	1.00	33.81	BBBB
ATOM	3020	CA	GLU	B	57	-12.228	-46.083	-33.467	1.00	34.16	BBBB
ATOM	3029	CA	ILE	B	58	-10.217	-48.658	-31.553	1.00	31.38	BBBB
ATOM	3037	CA	ASP	B	59	-10.039	-52.442	-31.720	1.00	31.09	BBBB
ATOM	3045	CA	PHE	B	60	-8.809	-54.410	-28.713	1.00	30.32	BBBB
ATOM	3056	CA	ILE	B	61	-6.832	-57.616	-28.269	1.00	28.55	BBBB
ATOM	3064	CA	ARG	B	62	-5.709	-59.416	-25.133	1.00	30.76	BBBB
ATOM	3075	CA	ILE	B	63	-2.036	-59.770	-24.231	1.00	31.38	BBBB
ATOM	3083	CA	SER	B	64	-2.356	-60.520	-20.505	1.00	37.51	BBBB
ATOM	3089	CA	GLY	B	65	0.679	-62.355	-19.199	1.00	37.13	BBBB
ATOM	3093	CA	LEU	B	66	2.591	-61.413	-22.355	1.00	33.17	BBBB
ATOM	3101	CA	ARG	B	67	3.671	-57.928	-21.277	1.00	30.90	BBBB

ATOM	3112	CA	GLY	B	68	7.380	-57.427	-20.685	1.00	26.79	BBBB
ATOM	3116	CA	LYS	B	69	8.238	-60.463	-22.796	1.00	23.93	BBBB
ATOM	3125	CA	GLY	B	70	10.755	-60.229	-25.636	1.00	22.26	BBBB
ATOM	3129	CA	ILE	B	71	10.357	-62.386	-28.762	1.00	23.55	BBBB
ATOM	3137	CA	LYS	B	72	12.038	-65.491	-27.343	1.00	24.92	BBBB
ATOM	3146	CA	ALA	B	73	9.839	-65.306	-24.233	1.00	21.18	BBBB
ATOM	3151	CA	LEU	B	74	6.745	-64.762	-26.387	1.00	19.36	BBBB
ATOM	3159	CA	ILE	B	75	7.434	-67.768	-28.601	1.00	21.18	BBBB
ATOM	3167	CA	ALA	B	76	7.996	-69.726	-25.374	1.00	21.72	BBBB
ATOM	3172	CA	ALA	B	77	4.289	-69.121	-24.655	1.00	21.07	BBBB
ATOM	3178	CA	PRO	B	78	2.772	-70.846	-27.771	1.00	20.95	BBBB
ATOM	3184	CA	LEU	B	79	-0.896	-70.728	-26.783	1.00	21.32	BBBB
ATOM	3192	CA	ARG	B	80	-0.980	-67.115	-25.637	1.00	21.30	BBBB
ATOM	3203	CA	ILE	B	81	1.113	-65.621	-28.421	1.00	19.47	BBBB
ATOM	3211	CA	PHE	B	82	-0.875	-67.582	-31.038	1.00	19.15	BBBB
ATOM	3222	CA	ASN	B	83	-4.150	-66.332	-29.577	1.00	20.90	BBBB
ATOM	3230	CA	ALA	B	84	-3.177	-62.647	-29.484	1.00	19.30	BBBB
ATOM	3235	CA	TRP	B	85	-1.820	-63.111	-33.032	1.00	20.56	BBBB
ATOM	3249	CA	ARG	B	86	-5.140	-64.660	-34.166	1.00	23.28	BBBB
ATOM	3260	CA	GLN	B	87	-7.101	-61.802	-32.567	1.00	24.07	BBBB
ATOM	3269	CA	ALA	B	88	-4.996	-59.183	-34.355	1.00	23.78	BBBB
ATOM	3274	CA	ARG	B	89	-5.285	-61.111	-37.636	1.00	24.94	BBBB
ATOM	3285	CA	ALA	B	90	-9.088	-61.151	-37.383	1.00	26.16	BBBB
ATOM	3290	CA	ILE	B	91	-9.108	-57.400	-36.733	1.00	26.97	BBBB
ATOM	3298	CA	MET	B	92	-6.872	-56.693	-39.717	1.00	29.03	BBBB
ATOM	3306	CA	LYS	B	93	-8.735	-59.038	-42.050	1.00	33.20	BBBB
ATOM	3315	CA	ALA	B	94	-11.943	-57.157	-41.183	1.00	33.62	BBBB
ATOM	3320	CA	TYR	B	95	-10.504	-53.620	-41.224	1.00	33.83	BBBB
ATOM	3332	CA	LYS	B	96	-8.104	-54.327	-44.122	1.00	33.85	BBBB
ATOM	3342	CA	PRO	B	97	-5.490	-51.623	-43.419	1.00	31.82	BBBB
ATOM	3348	CA	ASP	B	98	-3.049	-50.685	-46.188	1.00	29.78	BBBB
ATOM	3356	CA	VAL	B	99	-0.296	-50.214	-43.660	1.00	26.75	BBBB
ATOM	3363	CA	VAL	B	100	0.227	-50.613	-39.936	1.00	23.59	BBBB
ATOM	3370	CA	LEU	B	101	2.214	-48.199	-37.797	1.00	21.59	BBBB
ATOM	3378	CA	GLY	B	102	3.796	-49.357	-34.549	1.00	19.23	BBBB
ATOM	3382	CA	MET	B	103	4.892	-46.597	-32.191	1.00	18.93	BBBB
ATOM	3390	CA	GLY	B	104	6.275	-49.080	-29.686	1.00	21.89	BBBB
ATOM	3394	CA	GLY	B	105	4.593	-50.905	-26.827	1.00	23.54	BBBB
ATOM	3398	CA	TYR	B	106	3.818	-54.554	-26.159	1.00	22.37	BBBB
ATOM	3410	CA	VAL	B	107	0.557	-54.694	-28.099	1.00	18.06	BBBB
ATOM	3417	CA	SER	B	108	2.488	-53.892	-31.290	1.00	19.67	BBBB
ATOM	3423	CA	GLY	B	109	4.251	-57.256	-31.023	1.00	20.03	BBBB
ATOM	3428	CA	PRO	B	110	1.251	-59.478	-31.855	1.00	18.99	BBBB
ATOM	3434	CA	GLY	B	111	-0.160	-56.702	-34.025	1.00	19.60	BBBB
ATOM	3438	CA	GLY	B	112	3.014	-56.417	-36.074	1.00	19.97	BBBB
ATOM	3442	CA	LEU	B	113	3.265	-60.184	-36.429	1.00	19.49	BBBB
ATOM	3450	CA	ALA	B	114	-0.334	-60.292	-37.661	1.00	18.70	BBBB
ATOM	3455	CA	ALA	B	115	0.167	-57.516	-40.229	1.00	21.84	BBBB
ATOM	3460	CA	TRP	B	116	3.365	-59.126	-41.478	1.00	23.22	BBBB
ATOM	3474	CA	SER	B	117	1.735	-62.573	-41.873	1.00	22.61	BBBB
ATOM	3480	CA	LEU	B	118	-1.069	-60.957	-43.882	1.00	25.70	BBBB
ATOM	3488	CA	GLY	B	119	1.354	-59.174	-46.192	1.00	27.80	BBBB
ATOM	3492	CA	ILE	B	120	0.568	-55.744	-44.731	1.00	24.85	BBBB
ATOM	3501	CA	PRO	B	121	3.625	-53.477	-44.591	1.00	22.63	BBBB
ATOM	3507	CA	VAL	B	122	4.743	-52.594	-41.083	1.00	22.03	BBBB
ATOM	3514	CA	VAL	B	123	6.200	-49.184	-40.310	1.00	20.82	BBBB
ATOM	3521	CA	LEU	B	124	7.749	-48.485	-36.915	1.00	22.10	BBBB
ATOM	3529	CA	HIS	B	125	8.814	-45.413	-34.981	1.00	21.42	BBBB
ATOM	3539	CA	GLU	B	126	10.947	-45.452	-31.817	1.00	22.15	BBBB
ATOM	3548	CA	GLN	B	127	10.682	-42.270	-29.735	1.00	22.81	BBBB
ATOM	3557	CA	ASN	B	128	13.406	-43.097	-27.216	1.00	22.96	BBBB
ATOM	3565	CA	GLY	B	129	17.203	-43.019	-27.294	1.00	25.36	BBBB
ATOM	3569	CA	ILE	B	130	17.160	-46.716	-26.488	1.00	28.00	BBBB
ATOM	3577	CA	ALA	B	131	14.978	-49.139	-28.461	1.00	25.88	BBBB
ATOM	3582	CA	GLY	B	132	12.007	-50.532	-26.568	1.00	24.05	BBBB
ATOM	3586	CA	LEU	B	133	11.903	-54.293	-26.020	1.00	24.54	BBBB

ATOM	3594	CA	THR	B	134	9.202	-54.860	-28.639	1.00	21.22	BBBB
ATOM	3601	CA	ASN	B	135	10.407	-52.419	-31.324	1.00	20.50	BBBB
ATOM	3609	CA	LYS	B	136	13.886	-53.949	-31.144	1.00	22.79	BBBB
ATOM	3618	CA	TRP	B	137	12.753	-57.345	-32.424	1.00	22.06	BBBB
ATOM	3632	CA	LEU	B	138	9.744	-56.188	-34.431	1.00	23.15	BBBB
ATOM	3640	CA	ALA	B	139	12.128	-54.092	-36.542	1.00	25.29	BBBB
ATOM	3645	CA	LYS	B	140	13.279	-57.337	-38.182	1.00	28.05	BBBB
ATOM	3654	CA	ILE	B	141	9.963	-57.818	-40.016	1.00	26.09	BBBB
ATOM	3662	CA	ALA	B	142	9.331	-54.107	-40.498	1.00	25.03	BBBB
ATOM	3667	CA	THR	B	143	9.262	-52.595	-43.984	1.00	26.10	BBBB
ATOM	3674	CA	LYS	B	144	10.436	-49.238	-42.618	1.00	24.73	BBBB
ATOM	3683	CA	VAL	B	145	11.947	-48.311	-39.252	1.00	23.62	BBBB
ATOM	3690	CA	MET	B	146	12.338	-44.736	-37.993	1.00	23.15	BBBB
ATOM	3698	CA	GLN	B	147	13.762	-43.418	-34.712	1.00	25.05	BBBB
ATOM	3707	CA	ALA	B	148	13.559	-40.032	-33.009	1.00	26.88	BBBB
ATOM	3712	CA	PHE	B	149	17.239	-39.820	-32.098	1.00	29.39	BBBB
ATOM	3724	CA	PRO	B	150	20.310	-41.541	-33.535	1.00	31.87	BBBB
ATOM	3730	CA	GLY	B	151	21.629	-44.537	-31.595	1.00	32.62	BBBB
ATOM	3734	CA	ALA	B	152	18.447	-46.476	-30.753	1.00	32.71	BBBB
ATOM	3739	CA	PHE	B	153	18.925	-48.506	-33.937	1.00	34.83	BBBB
ATOM	3751	CA	PRO	B	154	22.158	-48.751	-35.993	1.00	38.97	BBBB
ATOM	3757	CA	ASN	B	155	20.765	-47.568	-39.346	1.00	41.08	BBBB
ATOM	3765	CA	ALA	B	156	17.170	-46.407	-38.843	1.00	37.55	BBBB
ATOM	3770	CA	GLU	B	157	16.367	-43.044	-40.460	1.00	34.40	BBBB
ATOM	3779	CA	VAL	B	158	16.337	-40.344	-37.764	1.00	31.16	BBBB
ATOM	3786	CA	VAL	B	159	13.155	-38.265	-37.889	1.00	28.10	BBBB
ATOM	3793	CA	GLY	B	160	12.724	-36.921	-34.355	1.00	26.93	BBBB
ATOM	3797	CA	ASN	B	161	9.456	-36.807	-32.375	1.00	25.27	BBBB
ATOM	3806	CA	PRO	B	162	6.315	-34.747	-33.004	1.00	26.14	BBBB
ATOM	3812	CA	VAL	B	163	6.456	-31.379	-31.216	1.00	27.75	BBBB
ATOM	3819	CA	ARG	B	164	3.667	-28.953	-30.246	1.00	32.36	BBBB
ATOM	3830	CA	THR	B	165	3.038	-26.307	-32.924	1.00	31.74	BBBB
ATOM	3837	CA	ASP	B	166	3.252	-23.404	-30.466	1.00	30.64	BBBB
ATOM	3845	CA	VAL	B	167	6.746	-24.503	-29.440	1.00	25.91	BBBB
ATOM	3852	CA	LEU	B	168	7.780	-25.002	-33.075	1.00	28.46	BBBB
ATOM	3860	CA	ALA	B	169	6.580	-21.455	-33.756	1.00	31.43	BBBB
ATOM	3865	CA	LEU	B	170	9.002	-19.905	-31.268	1.00	29.60	BBBB
ATOM	3874	CA	PRO	B	171	11.611	-17.457	-32.642	1.00	30.11	BBBB
ATOM	3880	CA	LEU	B	172	15.157	-18.780	-33.062	1.00	28.33	BBBB
ATOM	3889	CA	PRO	B	173	17.450	-18.550	-29.977	1.00	25.25	BBBB
ATOM	3895	CA	GLN	B	174	19.526	-15.527	-31.049	1.00	25.46	BBBB
ATOM	3904	CA	GLN	B	175	16.365	-13.525	-31.718	1.00	28.47	BBBB
ATOM	3913	CA	ARG	B	176	14.611	-14.635	-28.525	1.00	29.01	BBBB
ATOM	3924	CA	LEU	B	177	17.673	-13.970	-26.331	1.00	29.90	BBBB
ATOM	3932	CA	ALA	B	178	18.766	-10.776	-28.131	1.00	30.78	BBBB
ATOM	3937	CA	GLY	B	179	19.846	-7.993	-25.784	1.00	30.10	BBBB
ATOM	3941	CA	ARG	B	180	18.676	-9.965	-22.787	1.00	28.97	BBBB
ATOM	3952	CA	GLU	B	181	20.545	-9.027	-19.621	1.00	31.79	BBBB
ATOM	3961	CA	GLY	B	182	19.871	-9.586	-15.943	1.00	27.75	BBBB
ATOM	3966	CA	PRO	B	183	19.450	-12.832	-13.913	1.00	22.93	BBBB
ATOM	3972	CA	VAL	B	184	19.524	-16.146	-15.729	1.00	18.01	BBBB
ATOM	3979	CA	ARG	B	185	15.873	-17.216	-16.011	1.00	17.62	BBBB
ATOM	3990	CA	VAL	B	186	15.508	-20.771	-14.741	1.00	16.47	BBBB
ATOM	3997	CA	LEU	B	187	12.361	-22.710	-15.604	1.00	16.75	BBBB
ATOM	4005	CA	VAL	B	188	11.774	-25.775	-13.381	1.00	18.41	BBBB
ATOM	4012	CA	VAL	B	189	9.298	-28.234	-14.948	1.00	22.11	BBBB
ATOM	4019	CA	GLY	B	190	7.914	-31.188	-12.994	1.00	27.28	BBBB
ATOM	4023	CA	GLY	B	191	4.935	-32.163	-15.115	1.00	31.94	BBBB
ATOM	4027	CA	SER	B	192	1.313	-32.665	-14.064	1.00	35.91	BBBB
ATOM	4033	CA	GLN	B	193	2.292	-34.763	-11.033	1.00	38.53	BBBB
ATOM	4042	CA	GLY	B	194	5.398	-32.711	-10.350	1.00	35.02	BBBB
ATOM	4046	CA	ALA	B	195	8.977	-33.819	-9.709	1.00	33.12	BBBB
ATOM	4051	CA	ARG	B	196	9.538	-34.512	-6.010	1.00	32.63	BBBB
ATOM	4062	CA	ILE	B	197	13.329	-34.168	-6.164	1.00	28.10	BBBB
ATOM	4070	CA	LEU	B	198	13.069	-30.833	-8.003	1.00	26.58	BBBB
ATOM	4078	CA	ASN	B	199	10.497	-29.447	-5.563	1.00	27.07	BBBB

ATOM	4086	CA	GLN	B	200	12.955	-30.326	-2.794	1.00	30.10	BBBB
ATOM	4095	CA	THR	B	201	16.215	-29.345	-4.474	1.00	27.34	BBBB
ATOM	4102	CA	MET	B	202	15.567	-26.048	-6.268	1.00	23.68	BBBB
ATOM	4111	CA	PRO	B	203	14.608	-23.963	-3.220	1.00	23.84	BBBB
ATOM	4117	CA	GLN	B	204	18.033	-24.708	-1.684	1.00	26.34	BBBB
ATOM	4126	CA	VAL	B	205	19.672	-24.033	-5.043	1.00	24.44	BBBB
ATOM	4133	CA	ALA	B	206	17.980	-20.610	-5.013	1.00	22.84	BBBB
ATOM	4138	CA	ALA	B	207	19.442	-19.857	-1.576	1.00	26.65	BBBB
ATOM	4143	CA	LYS	B	208	22.915	-20.595	-2.919	1.00	28.31	BBBB
ATOM	4152	CA	LEU	B	209	22.577	-18.640	-6.171	1.00	25.68	BBBB
ATOM	4160	CA	GLY	B	210	20.675	-15.628	-4.804	1.00	26.56	BBBB
ATOM	4164	CA	ASP	B	211	20.370	-12.647	-7.190	1.00	28.28	BBBB
ATOM	4172	CA	SER	B	212	22.098	-14.474	-10.067	1.00	25.73	BBBB
ATOM	4178	CA	VAL	B	213	18.925	-16.308	-11.116	1.00	20.76	BBBB
ATOM	4185	CA	THR	B	214	15.204	-15.726	-11.337	1.00	19.60	BBBB
ATOM	4192	CA	ILE	B	215	13.076	-18.850	-11.169	1.00	18.75	BBBB
ATOM	4200	CA	TRP	B	216	9.661	-19.973	-12.378	1.00	19.34	BBBB
ATOM	4214	CA	HIS	B	217	9.015	-23.303	-10.680	1.00	21.06	BBBB
ATOM	4224	CA	GLN	B	218	6.149	-25.594	-11.735	1.00	24.30	BBBB
ATOM	4233	CA	SER	B	219	5.463	-27.800	-8.684	1.00	26.73	BBBB
ATOM	4239	CA	GLY	B	220	2.855	-30.242	-9.961	1.00	30.53	BBBB
ATOM	4243	CA	LYS	B	221	-0.657	-30.914	-8.628	1.00	35.12	BBBB
ATOM	4252	CA	GLY	B	222	-1.195	-29.899	-5.011	1.00	35.34	BBBB
ATOM	4256	CA	SER	B	223	2.451	-28.934	-4.418	1.00	33.98	BBBB
ATOM	4262	CA	GLN	B	224	2.187	-25.208	-5.186	1.00	33.71	BBBB
ATOM	4271	CA	GLN	B	225	1.823	-24.239	-1.519	1.00	32.32	BBBB
ATOM	4280	CA	SER	B	226	4.701	-26.309	-0.122	1.00	28.30	BBBB
ATOM	4286	CA	VAL	B	227	7.214	-25.247	-2.791	1.00	24.28	BBBB
ATOM	4293	CA	GLU	B	228	6.178	-21.592	-2.387	1.00	27.23	BBBB
ATOM	4302	CA	GLN	B	229	6.853	-22.046	1.329	1.00	28.38	BBBB
ATOM	4311	CA	ALA	B	230	10.185	-23.754	0.682	1.00	26.18	BBBB
ATOM	4316	CA	TYR	B	231	11.371	-20.766	-1.366	1.00	25.47	BBBB
ATOM	4328	CA	ALA	B	232	10.342	-18.322	1.368	1.00	27.51	BBBB
ATOM	4333	CA	GLU	B	233	12.145	-20.441	3.966	1.00	30.87	BBBB
ATOM	4342	CA	ALA	B	234	15.215	-20.417	1.714	1.00	28.48	BBBB
ATOM	4347	CA	GLY	B	235	15.033	-16.627	1.815	1.00	26.23	BBBB
ATOM	4351	CA	GLN	B	236	14.121	-16.198	-1.870	1.00	25.53	BBBB
ATOM	4361	CA	PRO	B	237	10.336	-15.587	-1.720	1.00	24.65	BBBB
ATOM	4367	CA	GLN	B	238	10.277	-13.558	-4.945	1.00	24.29	BBBB
ATOM	4376	CA	HIS	B	239	10.526	-16.608	-7.201	1.00	22.08	BBBB
ATOM	4386	CA	LYS	B	240	7.375	-17.589	-9.105	1.00	23.26	BBBB
ATOM	4395	CA	VAL	B	241	5.740	-20.911	-8.277	1.00	23.78	BBBB
ATOM	4402	CA	THR	B	242	2.758	-22.301	-10.177	1.00	25.93	BBBB
ATOM	4409	CA	GLU	B	243	0.999	-25.651	-9.837	1.00	27.03	BBBB
ATOM	4418	CA	PHE	B	244	0.964	-26.068	-13.620	1.00	26.54	BBBB
ATOM	4429	CA	ILE	B	245	1.932	-24.242	-16.802	1.00	28.48	BBBB
ATOM	4437	CA	ASP	B	246	-0.754	-24.396	-19.457	1.00	36.00	BBBB
ATOM	4445	CA	ASP	B	247	1.245	-22.392	-21.999	1.00	30.74	BBBB
ATOM	4453	CA	MET	B	248	4.625	-24.136	-22.138	1.00	28.41	BBBB
ATOM	4461	CA	ALA	B	249	5.512	-22.216	-25.290	1.00	24.67	BBBB
ATOM	4466	CA	ALA	B	250	5.188	-18.933	-23.390	1.00	21.78	BBBB
ATOM	4471	CA	ALA	B	251	7.301	-20.259	-20.501	1.00	20.85	BBBB
ATOM	4476	CA	TYR	B	252	9.972	-21.616	-22.886	1.00	22.78	BBBB
ATOM	4488	CA	ALA	B	253	10.131	-18.224	-24.636	1.00	23.54	BBBB
ATOM	4493	CA	TRP	B	254	10.829	-16.534	-21.303	1.00	19.76	BBBB
ATOM	4507	CA	ALA	B	255	13.399	-19.025	-20.003	1.00	19.51	BBBB
ATOM	4512	CA	ASP	B	256	17.176	-19.026	-20.434	1.00	17.58	BBBB
ATOM	4520	CA	VAL	B	257	17.535	-22.603	-19.194	1.00	18.53	BBBB
ATOM	4527	CA	VAL	B	258	15.208	-25.456	-18.234	1.00	19.32	BBBB
ATOM	4534	CA	VAL	B	259	15.581	-27.957	-15.374	1.00	19.85	BBBB
ATOM	4541	CA	CYS	B	260	13.454	-31.055	-15.946	1.00	22.00	BBBB
ATOM	4547	CA	ARG	B	261	13.170	-34.800	-16.515	1.00	23.75	BBBB
ATOM	4558	CA	SER	B	262	13.975	-36.189	-19.948	1.00	23.18	BBBB
ATOM	4564	CA	GLY	B	263	11.026	-38.079	-21.361	1.00	22.85	BBBB
ATOM	4568	CA	ALA	B	264	11.482	-38.564	-25.115	1.00	24.25	BBBB
ATOM	4573	CA	LEU	B	265	8.846	-36.037	-26.205	1.00	24.66	BBBB

ATOM	4581	CA	THR	B	266	10.194	-33.557	-23.657	1.00	22.34	BBBB
ATOM	4588	CA	VAL	B	267	13.730	-33.762	-25.023	1.00	21.11	BBBB
ATOM	4595	CA	SER	B	268	12.411	-33.191	-28.567	1.00	21.96	BBBB
ATOM	4601	CA	GLU	B	269	10.282	-30.272	-27.378	1.00	21.95	BBBB
ATOM	4610	CA	ILE	B	270	13.295	-28.698	-25.638	1.00	20.62	BBBB
ATOM	4618	CA	ALA	B	271	15.440	-29.058	-28.776	1.00	22.45	BBBB
ATOM	4623	CA	ALA	B	272	12.719	-27.451	-30.898	1.00	22.17	BBBB
ATOM	4628	CA	ALA	B	273	12.361	-24.596	-28.407	1.00	21.97	BBBB
ATOM	4633	CA	GLY	B	274	16.093	-24.023	-28.709	1.00	21.07	BBBB
ATOM	4637	CA	LEU	B	275	16.666	-24.057	-24.966	1.00	19.78	BBBB
ATOM	4646	CA	PRO	B	276	19.651	-25.199	-22.875	1.00	16.62	BBBB
ATOM	4652	CA	ALA	B	277	18.638	-27.807	-20.321	1.00	15.80	BBBB
ATOM	4657	CA	LEU	B	278	19.896	-29.429	-17.145	1.00	18.48	BBBB
ATOM	4665	CA	PHE	B	279	18.266	-32.838	-17.392	1.00	21.59	BBBB
ATOM	4676	CA	VAL	B	280	17.502	-34.902	-14.281	1.00	25.67	BBBB
ATOM	4684	CA	PRO	B	281	16.698	-38.320	-15.824	1.00	29.05	BBBB
ATOM	4690	CA	PHE	B	282	14.246	-40.496	-13.926	1.00	37.13	BBBB
ATOM	4701	CA	GLN	B	283	16.319	-43.395	-12.591	1.00	41.11	BBBB
ATOM	4710	CA	HIS	B	284	15.641	-46.917	-13.843	1.00	43.69	BBBB
ATOM	4720	CA	LYS	B	285	17.767	-49.993	-14.571	1.00	45.34	BBBB
ATOM	4729	CA	ASP	B	286	16.949	-49.299	-18.222	1.00	43.26	BBBB
ATOM	4737	CA	ARG	B	287	17.951	-45.623	-17.883	1.00	36.28	BBBB
ATOM	4748	CA	GLN	B	288	15.622	-44.804	-20.755	1.00	30.77	BBBB
ATOM	4757	CA	GLN	B	289	15.474	-41.099	-19.904	1.00	29.46	BBBB
ATOM	4766	CA	TYR	B	290	19.228	-40.984	-19.550	1.00	29.55	BBBB
ATOM	4778	CA	TRP	B	291	19.542	-42.282	-23.116	1.00	28.07	BBBB
ATOM	4792	CA	ASN	B	292	16.902	-39.784	-24.270	1.00	26.06	BBBB
ATOM	4800	CA	ALA	B	293	18.926	-36.822	-22.979	1.00	25.69	BBBB
ATOM	4805	CA	LEU	B	294	22.354	-38.088	-24.032	1.00	25.90	BBBB
ATOM	4814	CA	PRO	B	295	21.998	-36.870	-27.635	1.00	26.15	BBBB
ATOM	4820	CA	LEU	B	296	21.521	-33.265	-26.481	1.00	25.42	BBBB
ATOM	4828	CA	GLU	B	297	24.354	-33.530	-23.953	1.00	28.78	BBBB
ATOM	4837	CA	LYS	B	298	26.644	-34.947	-26.648	1.00	31.90	BBBB
ATOM	4846	CA	ALA	B	299	25.773	-31.965	-28.847	1.00	30.38	BBBB
ATOM	4851	CA	GLY	B	300	26.777	-29.635	-26.017	1.00	26.18	BBBB
ATOM	4855	CA	ALA	B	301	23.214	-28.333	-25.638	1.00	22.50	BBBB
ATOM	4860	CA	ALA	B	302	22.516	-29.770	-22.186	1.00	21.78	BBBB
ATOM	4865	CA	LYS	B	303	23.979	-31.340	-19.048	1.00	25.86	BBBB
ATOM	4874	CA	ILE	B	304	22.753	-34.598	-17.550	1.00	27.17	BBBB
ATOM	4882	CA	ILE	B	305	22.843	-35.178	-13.813	1.00	29.01	BBBB
ATOM	4890	CA	GLU	B	306	21.664	-38.702	-13.061	1.00	34.65	BBBB
ATOM	4899	CA	GLN	B	307	20.377	-39.599	-9.613	1.00	40.54	BBBB
ATOM	4909	CA	PRO	B	308	23.828	-40.891	-8.484	1.00	43.20	BBBB
ATOM	4915	CA	GLN	B	309	25.247	-37.361	-8.787	1.00	43.46	BBBB
ATOM	4924	CA	LEU	B	310	22.232	-35.166	-8.022	1.00	39.65	BBBB
ATOM	4932	CA	SER	B	311	22.660	-32.714	-5.154	1.00	34.90	BBBB
ATOM	4938	CA	VAL	B	312	21.990	-29.074	-4.341	1.00	31.50	BBBB
ATOM	4945	CA	ASP	B	313	25.642	-28.202	-4.957	1.00	29.61	BBBB
ATOM	4953	CA	ALA	B	314	25.782	-30.099	-8.254	1.00	26.47	BBBB
ATOM	4958	CA	VAL	B	315	22.755	-28.215	-9.612	1.00	25.33	BBBB
ATOM	4965	CA	ALA	B	316	23.888	-24.872	-8.199	1.00	27.13	BBBB
ATOM	4970	CA	ASN	B	317	27.444	-25.246	-9.518	1.00	28.52	BBBB
ATOM	4978	CA	THR	B	318	26.174	-26.371	-12.906	1.00	27.04	BBBB
ATOM	4985	CA	LEU	B	319	23.883	-23.370	-13.357	1.00	25.21	BBBB
ATOM	4993	CA	ALA	B	320	26.445	-20.931	-11.957	1.00	24.59	BBBB
ATOM	4998	CA	GLY	B	321	28.934	-22.031	-14.591	1.00	24.34	BBBB
ATOM	5002	CA	TRP	B	322	26.738	-21.007	-17.521	1.00	21.72	BBBB
ATOM	5016	CA	SER	B	323	27.141	-17.404	-18.692	1.00	19.04	BBBB
ATOM	5022	CA	ARG	B	324	24.725	-15.741	-21.112	1.00	18.09	BBBB
ATOM	5033	CA	GLU	B	325	27.220	-16.368	-23.954	1.00	16.96	BBBB
ATOM	5042	CA	THR	B	326	27.460	-20.055	-23.070	1.00	16.39	BBBB
ATOM	5049	CA	LEU	B	327	23.659	-20.305	-22.780	1.00	17.27	BBBB
ATOM	5057	CA	LEU	B	328	23.175	-18.745	-26.222	1.00	17.39	BBBB
ATOM	5065	CA	THR	B	329	25.567	-21.335	-27.688	1.00	21.30	BBBB
ATOM	5072	CA	MET	B	330	23.771	-24.153	-25.870	1.00	19.91	BBBB
ATOM	5080	CA	ALA	B	331	20.412	-22.871	-27.098	1.00	18.49	BBBB

ATOM	5085	CA	GLU	B	332	21.626	-22.827	-30.704	1.00	21.47	BBBB
ATOM	5094	CA	ARG	B	333	23.040	-26.330	-30.408	1.00	23.77	BBBB
ATOM	5105	CA	ALA	B	334	19.648	-27.420	-29.063	1.00	22.88	BBBB
ATOM	5110	CA	ARG	B	335	17.795	-25.892	-32.002	1.00	23.54	BBBB
ATOM	5121	CA	ALA	B	336	20.330	-27.477	-34.372	1.00	26.85	BBBB
ATOM	5126	CA	ALA	B	337	19.740	-30.925	-32.865	1.00	30.89	BBBB
ATOM	5131	CA	SER	B	338	16.008	-30.432	-33.408	1.00	32.41	BBBB
ATOM	5137	CA	ILE	B	339	13.882	-31.941	-36.187	1.00	34.35	BBBB
ATOM	5146	CA	PRO	B	340	10.733	-29.730	-36.600	1.00	34.94	BBBB
ATOM	5152	CA	ASP	B	341	8.711	-31.820	-39.056	1.00	33.33	BBBB
ATOM	5160	CA	ALA	B	342	8.875	-35.238	-37.411	1.00	29.09	BBBB
ATOM	5165	CA	THR	B	343	5.115	-35.696	-37.744	1.00	28.55	BBBB
ATOM	5172	CA	GLU	B	344	5.085	-34.933	-41.480	1.00	32.00	BBBB
ATOM	5181	CA	ARG	B	345	8.138	-37.123	-42.067	1.00	31.44	BBBB
ATOM	5192	CA	VAL	B	346	6.578	-40.151	-40.384	1.00	28.61	BBBB
ATOM	5199	CA	ALA	B	347	3.249	-39.617	-42.137	1.00	28.96	BBBB
ATOM	5204	CA	ASN	B	348	5.035	-39.286	-45.493	1.00	34.56	BBBB
ATOM	5212	CA	GLU	B	349	6.954	-42.540	-44.956	1.00	34.86	BBBB
ATOM	5221	CA	VAL	B	350	3.767	-44.306	-43.919	1.00	33.79	BBBB
ATOM	5228	CA	SER	B	351	2.196	-42.946	-47.095	1.00	36.67	BBBB
ATOM	5234	CA	ARG	B	352	5.114	-44.088	-49.251	1.00	40.03	BBBB
ATOM	5245	CA	VAL	B	353	5.089	-47.587	-47.737	1.00	42.78	BBBB
ATOM	5252	CA	ALA	B	354	1.336	-47.957	-48.212	1.00	47.24	BBBB
ATOM	5257	CA	ARG	B	355	2.035	-46.964	-51.824	1.00	52.71	BBBB
ATOM	5268	CA	ALA	B	356	4.453	-49.913	-51.809	1.00	54.93	BBBB
ATOM	5273	CA	LEU	B	357	7.023	-47.522	-53.289	1.00	57.81	BBBB

END

TABLE 3 ATOMIC COORDINATES OF E.COLI MURG C-ALPHA
BACKBONE AND CONSERVED AMINO ACID RESIDUES

ATOM	2649	CA	LYS	B	7	-6.512	-45.403	-47.519	1.00	45.28	BBBB
ATOM	2651	CA	ARG	B	8	-6.682	-47.303	-44.240	1.00	38.63	BBBB
ATOM	2662	CA	LEU	B	9	-4.094	-47.039	-41.477	1.00	30.88	BBBB
ATOM	2670	CA	MET	B	10	-4.048	-49.055	-38.275	1.00	26.66	BBBB
ATOM	2678	CA	VAL	B	11	-1.982	-47.605	-35.449	1.00	23.16	BBBB
ATOM	2685	CA	MET	B	12	-0.523	-49.707	-32.613	1.00	24.54	BBBB
ATOM	2693	CA	ALA	B	13	0.508	-47.410	-29.752	1.00	29.43	BBBB
ATOM	2697	N	GLY	B	14	0.150	-47.934	-27.405	1.00	32.46	BBBB
ATOM	2698	CA	GLY	B	14	-0.513	-47.804	-26.120	1.00	33.82	BBBB
ATOM	2699	C	GLY	B	14	-0.107	-46.595	-25.299	1.00	34.82	BBBB
ATOM	2700	O	GLY	B	14	0.975	-46.040	-25.479	1.00	35.47	BBBB
ATOM	2701	N	GLY	B	15	-0.986	-46.188	-24.385	1.00	35.56	BBBB
ATOM	2702	CA	GLY	B	15	-0.700	-45.047	-23.536	1.00	36.08	BBBB
ATOM	2703	C	GLY	B	15	0.539	-45.254	-22.683	1.00	36.84	BBBB
ATOM	2704	O	GLY	B	15	1.293	-44.311	-22.426	1.00	36.03	BBBB
ATOM	2706	CA	THR	B	16	1.920	-46.787	-21.421	1.00	38.51	BBBB
ATOM	2713	CA	GLY	B	17	5.367	-45.567	-22.392	1.00	36.57	BBBB
ATOM	2716	N	GLY	B	18	3.949	-43.752	-23.150	1.00	33.83	BBBB
ATOM	2717	CA	GLY	B	18	3.631	-42.529	-23.872	1.00	33.48	BBBB
ATOM	2718	C	GLY	B	18	3.825	-42.593	-25.378	1.00	33.12	BBBB
ATOM	2719	O	GLY	B	18	4.345	-41.650	-25.984	1.00	35.38	BBBB
ATOM	2720	N	HIS	B	19	3.416	-43.699	-25.988	1.00	30.26	BBBB
ATOM	2721	CA	HIS	B	19	3.548	-43.865	-27.435	1.00	28.22	BBBB
ATOM	2722	CB	HIS	B	19	3.772	-45.349	-27.779	1.00	25.81	BBBB
ATOM	2723	CG	HIS	B	19	4.957	-45.966	-27.094	1.00	25.35	BBBB
ATOM	2724	CD2	HIS	B	19	6.281	-45.694	-27.184	1.00	24.18	BBBB
ATOM	2725	ND1	HIS	B	19	4.845	-47.025	-26.217	1.00	24.57	BBBB
ATOM	2726	CE1	HIS	B	19	6.046	-47.380	-25.798	1.00	23.08	BBBB
ATOM	2727	NE2	HIS	B	19	6.936	-46.589	-26.369	1.00	25.51	BBBB
ATOM	2728	C	HIS	B	19	2.280	-43.370	-28.144	1.00	27.91	BBBB
ATOM	2729	O	HIS	B	19	2.300	-43.049	-29.337	1.00	26.91	BBBB
ATOM	2731	CA	VAL	B	20	-0.098	-42.894	-27.965	1.00	27.77	BBBB
ATOM	2738	CA	PHE	B	21	0.517	-39.136	-28.160	1.00	29.00	BBBB
ATOM	2750	CA	PRO	B	22	2.986	-39.252	-31.086	1.00	26.12	BBBB
ATOM	2756	CA	GLY	B	23	0.787	-41.864	-32.752	1.00	25.07	BBBB
ATOM	2760	CA	LEU	B	24	-2.201	-39.551	-32.401	1.00	25.32	BBBB
ATOM	2768	CA	ALA	B	25	-0.197	-36.754	-34.013	1.00	25.94	BBBB
ATOM	2773	CA	VAL	B	26	0.466	-38.955	-37.056	1.00	25.70	BBBB
ATOM	2780	CA	ALA	B	27	-3.116	-40.222	-37.199	1.00	26.15	BBBB
ATOM	2785	CA	HIS	B	28	-4.574	-36.702	-37.190	1.00	29.32	BBBB
ATOM	2795	CA	HIS	B	29	-2.070	-35.623	-39.806	1.00	32.38	BBBB
ATOM	2805	CA	LEU	B	30	-3.136	-38.417	-42.162	1.00	32.00	BBBB
ATOM	2813	CA	MET	B	31	-6.849	-38.064	-41.424	1.00	34.91	BBBB
ATOM	2821	CA	ALA	B	32	-6.510	-34.511	-42.722	1.00	37.55	BBBB
ATOM	2826	CA	GLN	B	33	-5.182	-36.070	-45.938	1.00	38.24	BBBB
ATOM	2835	CA	GLY	B	34	-8.305	-38.169	-46.353	1.00	35.75	BBBB
ATOM	2839	CA	TRP	B	35	-7.016	-41.246	-44.508	1.00	34.58	BBBB
ATOM	2853	CA	GLN	B	36	-9.175	-43.535	-42.402	1.00	35.40	BBBB
ATOM	2862	CA	VAL	B	37	-7.417	-44.516	-39.184	1.00	34.16	BBBB
ATOM	2869	CA	ARG	B	38	-8.219	-47.286	-36.730	1.00	31.56	BBBB
ATOM	2880	CA	TRP	B	39	-6.456	-48.070	-33.471	1.00	27.41	BBBB
ATOM	2894	CA	LEU	B	40	-5.200	-51.364	-32.026	1.00	24.71	BBBB
ATOM	2902	CA	GLY	B	41	-4.691	-51.450	-28.257	1.00	23.47	BBBB
ATOM	2906	CA	THR	B	42	-5.787	-53.141	-25.027	1.00	29.84	BBBB
ATOM	2913	CA	ALA	B	43	-9.000	-52.595	-23.047	1.00	38.81	BBBB
ATOM	2918	CA	ASP	B	44	-7.455	-51.942	-19.632	1.00	44.47	BBBB
ATOM	2926	CA	ARG	B	45	-4.887	-49.367	-20.763	1.00	40.44	BBBB
ATOM	2937	CA	MET	B	46	-4.881	-45.581	-21.249	1.00	36.33	BBBB
ATOM	2945	CA	GLU	B	47	-5.458	-45.655	-25.029	1.00	31.79	BBBB
ATOM	2954	CA	ALA	B	48	-8.821	-47.344	-24.414	1.00	32.58	BBBB
ATOM	2959	CA	ASP	B	49	-10.143	-44.065	-23.009	1.00	35.60	BBBB

ATOM	2967	CA	LEU	B	50	-8.026	-41.484	-24.840	1.00	33.49	BBBB
ATOM	2975	CA	VAL	B	51	-8.299	-42.641	-28.449	1.00	32.68	BBBB
ATOM	2983	CA	PRO	B	52	-12.111	-42.601	-28.453	1.00	34.43	BBBB
ATOM	2989	CA	LYS	B	53	-11.998	-39.054	-27.064	1.00	36.73	BBBB
ATOM	2998	CA	HIS	B	54	-10.116	-38.212	-30.259	1.00	34.62	BBBB
ATOM	3008	CA	GLY	B	55	-12.938	-39.481	-32.447	1.00	35.34	BBBB
ATOM	3012	CA	ILE	B	56	-10.909	-42.517	-33.514	1.00	33.81	BBBB
ATOM	3020	CA	GLU	B	57	-12.228	-46.083	-33.467	1.00	34.16	BBBB
ATOM	3029	CA	ILE	B	58	-10.217	-48.658	-31.553	1.00	31.38	BBBB
ATOM	3037	CA	ASP	B	59	-10.039	-52.442	-31.720	1.00	31.09	BBBB
ATOM	3045	CA	PHE	B	60	-8.809	-54.410	-28.713	1.00	30.32	BBBB
ATOM	3056	CA	ILE	B	61	-6.832	-57.616	-28.269	1.00	28.55	BBBB
ATOM	3064	CA	ARG	B	62	-5.709	-59.416	-25.133	1.00	30.76	BBBB
ATOM	3075	CA	ILE	B	63	-2.036	-59.770	-24.231	1.00	31.38	BBBB
ATOM	3083	CA	SER	B	64	-2.356	-60.520	-20.505	1.00	37.51	BBBB
ATOM	3089	CA	GLY	B	65	0.679	-62.355	-19.199	1.00	37.13	BBBB
ATOM	3093	CA	LEU	B	66	2.591	-61.413	-22.355	1.00	33.17	BBBB
ATOM	3101	CA	ARG	B	67	3.671	-57.928	-21.277	1.00	30.90	BBBB
ATOM	3112	CA	GLY	B	68	7.380	-57.427	-20.685	1.00	26.79	BBBB
ATOM	3116	CA	LYS	B	69	8.238	-60.463	-22.796	1.00	23.93	BBBB
ATOM	3125	CA	GLY	B	70	10.755	-60.229	-25.636	1.00	22.26	BBBB
ATOM	3129	CA	ILE	B	71	10.357	-62.386	-28.762	1.00	23.55	BBBB
ATOM	3137	CA	LYS	B	72	12.038	-65.491	-27.343	1.00	24.92	BBBB
ATOM	3146	CA	ALA	B	73	9.839	-65.306	-24.233	1.00	21.18	BBBB
ATOM	3151	CA	LEU	B	74	6.745	-64.762	-26.387	1.00	19.36	BBBB
ATOM	3159	CA	ILE	B	75	7.434	-67.768	-28.601	1.00	21.18	BBBB
ATOM	3167	CA	ALA	B	76	7.996	-69.726	-25.374	1.00	21.72	BBBB
ATOM	3172	CA	ALA	B	77	4.289	-69.121	-24.655	1.00	21.07	BBBB
ATOM	3178	CA	PRO	B	78	2.772	-70.846	-27.771	1.00	20.95	BBBB
ATOM	3184	CA	LEU	B	79	-0.896	-70.728	-26.783	1.00	21.32	BBBB
ATOM	3192	CA	ARG	B	80	-0.980	-67.115	-25.637	1.00	21.30	BBBB
ATOM	3203	CA	ILE	B	81	1.113	-65.621	-28.421	1.00	19.47	BBBB
ATOM	3211	CA	PHE	B	82	-0.875	-67.582	-31.038	1.00	19.15	BBBB
ATOM	3222	CA	ASN	B	83	-4.150	-66.332	-29.577	1.00	20.90	BBBB
ATOM	3230	CA	ALA	B	84	-3.177	-62.647	-29.484	1.00	19.30	BBBB
ATOM	3235	CA	TRP	B	85	-1.820	-63.111	-33.032	1.00	20.56	BBBB
ATOM	3249	CA	ARG	B	86	-5.140	-64.660	-34.166	1.00	23.28	BBBB
ATOM	3260	CA	GLN	B	87	-7.101	-61.802	-32.567	1.00	24.07	BBBB
ATOM	3269	CA	ALA	B	88	-4.996	-59.183	-34.355	1.00	23.78	BBBB
ATOM	3274	CA	ARG	B	89	-5.285	-61.111	-37.636	1.00	24.94	BBBB
ATOM	3285	CA	ALA	B	90	-9.088	-61.151	-37.383	1.00	26.16	BBBB
ATOM	3290	CA	ILE	B	91	-9.108	-57.400	-36.733	1.00	26.97	BBBB
ATOM	3298	CA	MET	B	92	-6.872	-56.693	-39.717	1.00	29.03	BBBB
ATOM	3306	CA	LYS	B	93	-8.735	-59.038	-42.050	1.00	33.20	BBBB
ATOM	3315	CA	ALA	B	94	-11.943	-57.157	-41.183	1.00	33.62	BBBB
ATOM	3320	CA	TYR	B	95	-10.504	-53.620	-41.224	1.00	33.83	BBBB
ATOM	3332	CA	LYS	B	96	-8.104	-54.327	-44.122	1.00	33.85	BBBB
ATOM	3342	CA	PRO	B	97	-5.490	-51.623	-43.419	1.00	31.82	BBBB
ATOM	3348	CA	ASP	B	98	-3.049	-50.685	-46.188	1.00	29.78	BBBB
ATOM	3356	CA	VAL	B	99	-0.296	-50.214	-43.660	1.00	26.75	BBBB
ATOM	3363	CA	VAL	B	100	0.227	-50.613	-39.936	1.00	23.59	BBBB
ATOM	3370	CA	LEU	B	101	2.214	-48.199	-37.797	1.00	21.59	BBBB
ATOM	3378	CA	GLY	B	102	3.796	-49.357	-34.549	1.00	19.23	BBBB
ATOM	3382	CA	MET	B	103	4.892	-46.597	-32.191	1.00	18.93	BBBB
ATOM	3389	N	GLY	B	104	5.640	-48.450	-30.827	1.00	21.56	BBBB
ATOM	3390	CA	GLY	B	104	6.275	-49.080	-29.686	1.00	21.89	BBBB
ATOM	3391	C	GLY	B	104	5.192	-49.614	-28.764	1.00	23.28	BBBB
ATOM	3392	O	GLY	B	104	4.009	-49.353	-28.980	1.00	22.50	BBBB
ATOM	3394	CA	GLY	B	105	4.593	-50.905	-26.827	1.00	23.54	BBBB
ATOM	3398	CA	TYR	B	106	3.818	-54.554	-26.159	1.00	22.37	BBBB
ATOM	3410	CA	VAL	B	107	0.557	-54.694	-28.099	1.00	18.06	BBBB
ATOM	3417	CA	SER	B	108	2.488	-53.892	-31.290	1.00	19.67	BBBB
ATOM	3423	CA	GLY	B	109	4.251	-57.256	-31.023	1.00	20.03	BBBB
ATOM	3428	CA	PRO	B	110	1.251	-59.478	-31.855	1.00	18.99	BBBB
ATOM	3434	CA	GLY	B	111	-0.160	-56.702	-34.025	1.00	19.60	BBBB
ATOM	3438	CA	GLY	B	112	3.014	-56.417	-36.074	1.00	19.97	BBBB

ATOM	3442	CA	LEU	B	113	3.265	-60.184	-36.429	1.00	19.49	BBBB
ATOM	3450	CA	ALA	B	114	-0.334	-60.292	-37.661	1.00	18.70	BBBB
ATOM	3455	CA	ALA	B	115	0.167	-57.516	-40.229	1.00	21.84	BBBB
ATOM	3460	CA	TRP	B	116	3.365	-59.126	-41.478	1.00	23.22	BBBB
ATOM	3474	CA	SER	B	117	1.735	-62.573	-41.873	1.00	22.61	BBBB
ATOM	3480	CA	LEU	B	118	-1.069	-60.957	-43.882	1.00	25.70	BBBB
ATOM	3488	CA	GLY	B	119	1.354	-59.174	-46.192	1.00	27.80	BBBB
ATOM	3492	CA	ILE	B	120	0.568	-55.744	-44.731	1.00	24.85	BBBB
ATOM	3501	CA	PRO	B	121	3.625	-53.477	-44.591	1.00	22.63	BBBB
ATOM	3507	CA	VAL	B	122	4.743	-52.594	-41.083	1.00	22.03	BBBB
ATOM	3514	CA	VAL	B	123	6.200	-49.184	-40.310	1.00	20.82	BBBB
ATOM	3521	CA	LEU	B	124	7.749	-48.485	-36.915	1.00	22.10	BBBB
ATOM	3528	N	HIS	B	125	8.182	-46.638	-35.447	1.00	21.40	BBBB
ATOM	3529	CA	HIS	B	125	8.814	-45.413	-34.981	1.00	21.42	BBBB
ATOM	3530	CB	HIS	B	125	7.858	-44.218	-35.067	1.00	21.57	BBBB
ATOM	3531	CG	HIS	B	125	8.432	-42.948	-34.511	1.00	23.73	BBBB
ATOM	3532	CD2	HIS	B	125	8.300	-42.368	-33.295	1.00	22.15	BBBB
ATOM	3533	ND1	HIS	B	125	9.274	-42.127	-35.236	1.00	26.23	BBBB
ATOM	3534	CE1	HIS	B	125	9.631	-41.095	-34.490	1.00	24.20	BBBB
ATOM	3535	NE2	HIS	B	125	9.054	-41.218	-33.307	1.00	26.07	BBBB
ATOM	3536	C	HIS	B	125	9.196	-45.642	-33.519	1.00	21.70	BBBB
ATOM	3537	O	HIS	B	125	8.378	-46.117	-32.725	1.00	19.81	BBBB
ATOM	3538	N	GLU	B	126	10.444	-45.332	-33.186	1.00	21.20	BBBB
ATOM	3539	CA	GLU	B	126	10.947	-45.452	-31.817	1.00	22.15	BBBB
ATOM	3540	CB	GLU	B	126	12.252	-46.246	-31.790	1.00	21.99	BBBB
ATOM	3541	CG	GLU	B	126	12.958	-46.206	-30.439	1.00	22.04	BBBB
ATOM	3542	CD	GLU	B	126	12.119	-46.824	-29.338	1.00	21.43	BBBB
ATOM	3543	OE1	GLU	B	126	11.767	-48.014	-29.471	1.00	21.92	BBBB
ATOM	3544	OE2	GLU	B	126	11.807	-46.124	-28.349	1.00	21.08	BBBB
ATOM	3545	C	GLU	B	126	11.205	-44.027	-31.326	1.00	21.93	BBBB
ATOM	3546	O	GLU	B	126	12.016	-43.300	-31.908	1.00	21.33	BBBB
ATOM	3548	CA	GLN	B	127	10.682	-42.270	-29.735	1.00	22.81	BBBB
ATOM	3557	CA	ASN	B	128	13.406	-43.097	-27.216	1.00	22.96	BBBB
ATOM	3565	CA	GLY	B	129	17.203	-43.019	-27.294	1.00	25.36	BBBB
ATOM	3569	CA	ILE	B	130	17.160	-46.716	-26.488	1.00	28.00	BBBB
ATOM	3577	CA	ALA	B	131	14.978	-49.139	-28.461	1.00	25.88	BBBB
ATOM	3582	CA	GLY	B	132	12.007	-50.532	-26.568	1.00	24.05	BBBB
ATOM	3586	CA	LEU	B	133	11.903	-54.293	-26.020	1.00	24.54	BBBB
ATOM	3594	CA	THR	B	134	9.202	-54.860	-28.639	1.00	21.22	BBBB
ATOM	3601	CA	ASN	B	135	10.407	-52.419	-31.324	1.00	20.50	BBBB
ATOM	3609	CA	LYS	B	136	13.886	-53.949	-31.144	1.00	22.79	BBBB
ATOM	3618	CA	TRP	B	137	12.753	-57.345	-32.424	1.00	22.06	BBBB
ATOM	3632	CA	LEU	B	138	9.744	-56.188	-34.431	1.00	23.15	BBBB
ATOM	3640	CA	ALA	B	139	12.128	-54.092	-36.542	1.00	25.29	BBBB
ATOM	3645	CA	LYS	B	140	13.279	-57.337	-38.182	1.00	28.05	BBBB
ATOM	3654	CA	ILE	B	141	9.963	-57.818	-40.016	1.00	26.09	BBBB
ATOM	3662	CA	ALA	B	142	9.331	-54.107	-40.498	1.00	25.03	BBBB
ATOM	3667	CA	THR	B	143	9.262	-52.595	-43.984	1.00	26.10	BBBB
ATOM	3674	CA	LYS	B	144	10.436	-49.238	-42.618	1.00	24.73	BBBB
ATOM	3683	CA	VAL	B	145	11.947	-48.311	-39.252	1.00	23.62	BBBB
ATOM	3690	CA	MET	B	146	12.338	-44.736	-37.993	1.00	23.15	BBBB
ATOM	3698	CA	GLN	B	147	13.762	-43.418	-34.712	1.00	25.05	BBBB
ATOM	3707	CA	ALA	B	148	13.559	-40.032	-33.009	1.00	26.88	BBBB
ATOM	3712	CA	PHE	B	149	17.239	-39.820	-32.098	1.00	29.39	BBBB
ATOM	3724	CA	PRO	B	150	20.310	-41.541	-33.535	1.00	31.87	BBBB
ATOM	3730	CA	GLY	B	151	21.629	-44.537	-31.595	1.00	32.62	BBBB
ATOM	3734	CA	ALA	B	152	18.447	-46.476	-30.753	1.00	32.71	BBBB
ATOM	3739	CA	PHE	B	153	18.925	-48.506	-33.937	1.00	34.83	BBBB
ATOM	3751	CA	PRO	B	154	22.158	-48.751	-35.993	1.00	38.97	BBBB
ATOM	3757	CA	ASN	B	155	20.765	-47.568	-39.346	1.00	41.08	BBBB
ATOM	3765	CA	ALA	B	156	17.170	-46.407	-38.843	1.00	37.55	BBBB
ATOM	3770	CA	GLU	B	157	16.367	-43.044	-40.460	1.00	34.40	BBBB
ATOM	3779	CA	VAL	B	158	16.337	-40.344	-37.764	1.00	31.16	BBBB
ATOM	3786	CA	VAL	B	159	13.155	-38.265	-37.889	1.00	28.10	BBBB
ATOM	3793	CA	GLY	B	160	12.724	-36.921	-34.355	1.00	26.93	BBBB
ATOM	3797	CA	ASN	B	161	9.456	-36.807	-32.375	1.00	25.27	BBBB

ATOM	3806	CA	PRO	B	162	6.315	-34.747	-33.004	1.00	26.14	BBBB
ATOM	3812	CA	VAL	B	163	6.456	-31.379	-31.216	1.00	27.75	BBBB
ATOM	3819	CA	ARG	B	164	3.667	-28.953	-30.246	1.00	32.36	BBBB
ATOM	3830	CA	THR	B	165	3.038	-26.307	-32.924	1.00	31.74	BBBB
ATOM	3837	CA	ASP	B	166	3.252	-23.404	-30.466	1.00	30.64	BBBB
ATOM	3845	CA	VAL	B	167	6.746	-24.503	-29.440	1.00	25.91	BBBB
ATOM	3852	CA	LEU	B	168	7.780	-25.002	-33.075	1.00	28.46	BBBB
ATOM	3860	CA	ALA	B	169	6.580	-21.455	-33.756	1.00	31.43	BBBB
ATOM	3865	CA	LEU	B	170	9.002	-19.905	-31.268	1.00	29.60	BBBB
ATOM	3874	CA	PRO	B	171	11.611	-17.457	-32.642	1.00	30.11	BBBB
ATOM	3880	CA	LEU	B	172	15.157	-18.780	-33.062	1.00	28.33	BBBB
ATOM	3889	CA	PRO	B	173	17.450	-18.550	-29.977	1.00	25.25	BBBB
ATOM	3895	CA	GLN	B	174	19.526	-15.527	-31.049	1.00	25.46	BBBB
ATOM	3904	CA	GLN	B	175	16.365	-13.525	-31.718	1.00	28.47	BBBB
ATOM	3913	CA	ARG	B	176	14.611	-14.635	-28.525	1.00	29.01	BBBB
ATOM	3924	CA	LEU	B	177	17.673	-13.970	-26.331	1.00	29.90	BBBB
ATOM	3932	CA	ALA	B	178	18.766	-10.776	-28.131	1.00	30.78	BBBB
ATOM	3937	CA	GLY	B	179	19.846	-7.993	-25.784	1.00	30.10	BBBB
ATOM	3941	CA	ARG	B	180	18.676	-9.965	-22.787	1.00	28.97	BBBB
ATOM	3952	CA	GLU	B	181	20.545	-9.027	-19.621	1.00	31.79	BBBB
ATOM	3961	CA	GLY	B	182	19.871	-9.586	-15.943	1.00	27.75	BBBB
ATOM	3966	CA	PRO	B	183	19.450	-12.832	-13.913	1.00	22.93	BBBB
ATOM	3972	CA	VAL	B	184	19.524	-16.146	-15.729	1.00	18.01	BBBB
ATOM	3979	CA	ARG	B	185	15.873	-17.216	-16.011	1.00	17.62	BBBB
ATOM	3990	CA	VAL	B	186	15.508	-20.771	-14.741	1.00	16.47	BBBB
ATOM	3997	CA	LEU	B	187	12.361	-22.710	-15.604	1.00	16.75	BBBB
ATOM	4005	CA	VAL	B	188	11.774	-25.775	-13.381	1.00	18.41	BBBB
ATOM	4012	CA	VAL	B	189	9.298	-28.234	-14.948	1.00	22.11	BBBB
ATOM	4018	N	GLY	B	190	8.111	-29.887	-13.615	1.00	25.60	BBBB
ATOM	4019	CA	GLY	B	190	7.914	-31.188	-12.994	1.00	27.28	BBBB
ATOM	4020	C	GLY	B	190	6.808	-32.026	-13.604	1.00	29.67	BBBB
ATOM	4021	O	GLY	B	190	6.668	-33.208	-13.283	1.00	29.86	BBBB
ATOM	4022	N	GLY	B	191	6.025	-31.430	-14.497	1.00	30.56	BBBB
ATOM	4023	CA	GLY	B	191	4.935	-32.163	-15.115	1.00	31.94	BBBB
ATOM	4024	C	GLY	B	191	3.676	-32.104	-14.269	1.00	33.11	BBBB
ATOM	4025	O	GLY	B	191	3.691	-31.556	-13.165	1.00	32.14	BBBB
ATOM	4026	N	SER	B	192	2.587	-32.673	-14.779	1.00	34.23	BBBB
ATOM	4027	CA	SER	B	192	1.313	-32.665	-14.064	1.00	35.91	BBBB
ATOM	4028	CB	SER	B	192	0.283	-33.532	-14.801	1.00	36.87	BBBB
ATOM	4029	OG	SER	B	192	0.702	-34.887	-14.877	1.00	39.58	BBBB
ATOM	4030	C	SER	B	192	1.419	-33.128	-12.609	1.00	36.41	BBBB
ATOM	4031	O	SER	B	192	0.862	-32.499	-11.714	1.00	35.78	BBBB
ATOM	4033	CA	GLN	B	193	2.292	-34.763	-11.033	1.00	38.53	BBBB
ATOM	4041	N	GLY	B	194	4.291	-33.398	-10.986	1.00	36.47	BBBB
ATOM	4042	CA	GLY	B	194	5.398	-32.711	-10.350	1.00	35.02	BBBB
ATOM	4043	C	GLY	B	194	6.584	-33.630	-10.146	1.00	34.51	BBBB
ATOM	4044	O	GLY	B	194	6.442	-34.851	-10.191	1.00	34.26	BBBB
ATOM	4045	N	ALA	B	195	7.761	-33.045	-9.938	1.00	33.54	BBBB
ATOM	4046	CA	ALA	B	195	8.977	-33.819	-9.709	1.00	33.12	BBBB
ATOM	4047	CB	ALA	B	195	10.073	-33.387	-10.679	1.00	33.17	BBBB
ATOM	4048	C	ALA	B	195	9.423	-33.590	-8.267	1.00	32.87	BBBB
ATOM	4049	O	ALA	B	195	9.955	-32.533	-7.923	1.00	31.47	BBBB
ATOM	4051	CA	ARG	B	196	9.538	-34.512	-6.010	1.00	32.63	BBBB
ATOM	4062	CA	ILE	B	197	13.329	-34.168	-6.164	1.00	28.10	BBBB
ATOM	4070	CA	LEU	B	198	13.069	-30.833	-8.003	1.00	26.58	BBBB
ATOM	4078	CA	ASN	B	199	10.497	-29.447	-5.563	1.00	27.07	BBBB
ATOM	4086	CA	GLN	B	200	12.955	-30.326	-2.794	1.00	30.10	BBBB
ATOM	4095	CA	THR	B	201	16.215	-29.345	-4.474	1.00	27.34	BBBB
ATOM	4102	CA	MET	B	202	15.567	-26.048	-6.268	1.00	23.68	BBBB
ATOM	4111	CA	PRO	B	203	14.608	-23.963	-3.220	1.00	23.84	BBBB
ATOM	4117	CA	GLN	B	204	18.033	-24.708	-1.684	1.00	26.34	BBBB
ATOM	4126	CA	VAL	B	205	19.672	-24.033	-5.043	1.00	24.44	BBBB
ATOM	4133	CA	ALA	B	206	17.980	-20.610	-5.013	1.00	22.84	BBBB
ATOM	4138	CA	ALA	B	207	19.442	-19.857	-1.576	1.00	26.65	BBBB
ATOM	4143	CA	LYS	B	208	22.915	-20.595	-2.919	1.00	28.31	BBBB
ATOM	4152	CA	LEU	B	209	22.577	-18.640	-6.171	1.00	25.68	BBBB

ATOM	4160	CA	GLY	B	210	20.675	-15.628	-4.804	1.00	26.56	BBBB
ATOM	4164	CA	ASP	B	211	20.370	-12.647	-7.190	1.00	28.28	BBBB
ATOM	4172	CA	SER	B	212	22.098	-14.474	-10.067	1.00	25.73	BBBB
ATOM	4178	CA	VAL	B	213	18.925	-16.308	-11.116	1.00	20.76	BBBB
ATOM	4185	CA	THR	B	214	15.204	-15.726	-11.337	1.00	19.60	BBBB
ATOM	4192	CA	ILE	B	215	13.076	-18.850	-11.169	1.00	18.75	BBBB
ATOM	4200	CA	TRP	B	216	9.661	-19.973	-12.378	1.00	19.34	BBBB
ATOM	4214	CA	HIS	B	217	9.015	-23.303	-10.680	1.00	21.06	BBBB
ATOM	4224	CA	GLN	B	218	6.149	-25.594	-11.735	1.00	24.30	BBBB
ATOM	4233	CA	SER	B	219	5.463	-27.800	-8.684	1.00	26.73	BBBB
ATOM	4239	CA	GLY	B	220	2.855	-30.242	-9.961	1.00	30.53	BBBB
ATOM	4243	CA	LYS	B	221	-0.657	-30.914	-8.628	1.00	35.12	BBBB
ATOM	4252	CA	GLY	B	222	-1.195	-29.899	-5.011	1.00	35.34	BBBB
ATOM	4256	CA	SER	B	223	2.451	-28.934	-4.418	1.00	33.98	BBBB
ATOM	4262	CA	GLN	B	224	2.187	-25.208	-5.186	1.00	33.71	BBBB
ATOM	4271	CA	GLN	B	225	1.823	-24.239	-1.519	1.00	32.32	BBBB
ATOM	4280	CA	SER	B	226	4.701	-26.309	-0.122	1.00	28.30	BBBB
ATOM	4286	CA	VAL	B	227	7.214	-25.247	-2.791	1.00	24.28	BBBB
ATOM	4293	CA	GLU	B	228	6.178	-21.592	-2.387	1.00	27.23	BBBB
ATOM	4302	CA	GLN	B	229	6.853	-22.046	1.329	1.00	28.38	BBBB
ATOM	4311	CA	ALA	B	230	10.185	-23.754	0.682	1.00	26.18	BBBB
ATOM	4316	CA	TYR	B	231	11.371	-20.766	-1.366	1.00	25.47	BBBB
ATOM	4328	CA	ALA	B	232	10.342	-18.322	1.368	1.00	27.51	BBBB
ATOM	4333	CA	GLU	B	233	12.145	-20.441	3.966	1.00	30.87	BBBB
ATOM	4342	CA	ALA	B	234	15.215	-20.417	1.714	1.00	28.48	BBBB
ATOM	4347	CA	GLY	B	235	15.033	-16.627	1.815	1.00	26.23	BBBB
ATOM	4351	CA	GLN	B	236	14.121	-16.198	-1.870	1.00	25.53	BBBB
ATOM	4361	CA	PRO	B	237	10.336	-15.587	-1.720	1.00	24.65	BBBB
ATOM	4367	CA	GLN	B	238	10.277	-13.558	-4.945	1.00	24.29	BBBB
ATOM	4376	CA	HIS	B	239	10.526	-16.608	-7.201	1.00	22.08	BBBB
ATOM	4386	CA	LYS	B	240	7.375	-17.589	-9.105	1.00	23.26	BBBB
ATOM	4395	CA	VAL	B	241	5.740	-20.911	-8.277	1.00	23.78	BBBB
ATOM	4402	CA	THR	B	242	2.758	-22.301	-10.177	1.00	25.93	BBBB
ATOM	4409	CA	GLU	B	243	0.999	-25.651	-9.837	1.00	27.03	BBBB
ATOM	4418	CA	PHE	B	244	0.964	-26.068	-13.620	1.00	26.54	BBBB
ATOM	4429	CA	ILE	B	245	1.932	-24.242	-16.802	1.00	28.48	BBBB
ATOM	4437	CA	ASP	B	246	-0.754	-24.396	-19.457	1.00	36.00	BBBB
ATOM	4445	CA	ASP	B	247	1.245	-22.392	-21.999	1.00	30.74	BBBB
ATOM	4453	CA	MET	B	248	4.625	-24.136	-22.138	1.00	28.41	BBBB
ATOM	4461	CA	ALA	B	249	5.512	-22.216	-25.290	1.00	24.67	BBBB
ATOM	4466	CA	ALA	B	250	5.188	-18.933	-23.390	1.00	21.78	BBBB
ATOM	4471	CA	ALA	B	251	7.301	-20.259	-20.501	1.00	20.85	BBBB
ATOM	4476	CA	TYR	B	252	9.972	-21.616	-22.886	1.00	22.78	BBBB
ATOM	4488	CA	ALA	B	253	10.131	-18.224	-24.636	1.00	23.54	BBBB
ATOM	4493	CA	TRP	B	254	10.829	-16.534	-21.303	1.00	19.76	BBBB
ATOM	4507	CA	ALA	B	255	13.399	-19.025	-20.003	1.00	19.51	BBBB
ATOM	4512	CA	ASP	B	256	17.176	-19.026	-20.434	1.00	17.58	BBBB
ATOM	4520	CA	VAL	B	257	17.535	-22.603	-19.194	1.00	18.53	BBBB
ATOM	4527	CA	VAL	B	258	15.208	-25.456	-18.234	1.00	19.32	BBBB
ATOM	4534	CA	VAL	B	259	15.581	-27.957	-15.374	1.00	19.85	BBBB
ATOM	4541	CA	CYS	B	260	13.454	-31.055	-15.946	1.00	22.00	BBBB
ATOM	4546	N	ARG	B	261	12.937	-33.397	-16.212	1.00	22.34	BBBB
ATOM	4547	CA	ARG	B	261	13.170	-34.800	-16.515	1.00	23.75	BBBB
ATOM	4548	CB	ARG	B	261	11.964	-35.663	-16.104	1.00	27.16	BBBB
ATOM	4549	CG	ARG	B	261	11.376	-35.337	-14.738	1.00	31.82	BBBB
ATOM	4550	CD	ARG	B	261	11.490	-36.473	-13.732	1.00	36.33	BBBB
ATOM	4551	NE	ARG	B	261	12.865	-36.721	-13.323	1.00	38.48	BBBB
ATOM	4552	CZ	ARG	B	261	13.218	-37.176	-12.125	1.00	37.25	BBBB
ATOM	4553	NH1	ARG	B	261	12.295	-37.433	-11.204	1.00	38.46	BBBB
ATOM	4554	NH2	ARG	B	261	14.499	-37.370	-11.848	1.00	36.79	BBBB
ATOM	4555	C	ARG	B	261	13.351	-34.871	-18.032	1.00	23.98	BBBB
ATOM	4556	O	ARG	B	261	13.117	-33.983	-18.746	1.00	22.44	BBBB
ATOM	4558	CA	SER	B	262	13.975	-36.189	-19.948	1.00	23.18	BBBB
ATOM	4563	N	GLY	B	263	11.850	-37.151	-20.619	1.00	22.74	BBBB
ATOM	4564	CA	GLY	B	263	11.026	-38.079	-21.361	1.00	22.85	BBBB
ATOM	4565	C	GLY	B	263	11.392	-37.793	-22.813	1.00	24.06	BBBB

ATOM	4566	O	GLY	B	263	11.908	-36.705	-23.121	1.00	22.75	BBBB
ATOM	4567	N	ALA	B	264	11.130	-38.739	-23.708	1.00	23.37	BBBB
ATOM	4568	CA	ALA	B	264	11.482	-38.564	-25.115	1.00	24.25	BBBB
ATOM	4569	CB	ALA	B	264	11.133	-39.829	-25.894	1.00	24.58	BBBB
ATOM	4570	C	ALA	B	264	10.843	-37.343	-25.783	1.00	24.29	BBBB
ATOM	4571	O	ALA	B	264	11.523	-36.572	-26.470	1.00	24.33	BBBB
ATOM	4573	CA	LEU	B	265	8.846	-36.037	-26.205	1.00	24.66	BBBB
ATOM	4581	CA	THR	B	266	10.194	-33.557	-23.657	1.00	22.34	BBBB
ATOM	4588	CA	VAL	B	267	13.730	-33.762	-25.023	1.00	21.11	BBBB
ATOM	4595	CA	SER	B	268	12.411	-33.191	-28.567	1.00	21.96	BBBB
ATOM	4600	N	GLU	B	269	10.928	-31.563	-27.557	1.00	21.64	BBBB
ATOM	4601	CA	GLU	B	269	10.282	-30.272	-27.378	1.00	21.95	BBBB
ATOM	4602	CB	GLU	B	269	9.213	-30.399	-26.292	1.00	24.72	BBBB
ATOM	4603	CG	GLU	B	269	8.480	-29.128	-25.940	1.00	27.67	BBBB
ATOM	4604	CD	GLU	B	269	7.385	-29.380	-24.908	1.00	30.05	BBBB
ATOM	4605	OE1	GLU	B	269	6.325	-29.915	-25.287	1.00	31.50	BBBB
ATOM	4606	OE2	GLU	B	269	7.591	-29.057	-23.719	1.00	29.84	BBBB
ATOM	4607	C	GLU	B	269	11.321	-29.214	-26.999	1.00	21.68	BBBB
ATOM	4608	O	GLU	B	269	11.301	-28.095	-27.518	1.00	18.12	BBBB
ATOM	4610	CA	ILE	B	270	13.295	-28.698	-25.638	1.00	20.62	BBBB
ATOM	4618	CA	ALA	B	271	15.440	-29.058	-28.776	1.00	22.45	BBBB
ATOM	4623	CA	ALA	B	272	12.719	-27.451	-30.898	1.00	22.17	BBBB
ATOM	4628	CA	ALA	B	273	12.361	-24.596	-28.407	1.00	21.97	BBBB
ATOM	4633	CA	GLY	B	274	16.093	-24.023	-28.709	1.00	21.07	BBBB
ATOM	4637	CA	LEU	B	275	16.666	-24.057	-24.966	1.00	19.78	BBBB
ATOM	4646	CA	PRO	B	276	19.651	-25.199	-22.875	1.00	16.62	BBBB
ATOM	4652	CA	ALA	B	277	18.638	-27.807	-20.321	1.00	15.80	BBBB
ATOM	4657	CA	LEU	B	278	19.896	-29.429	-17.145	1.00	18.48	BBBB
ATOM	4665	CA	PHE	B	279	18.266	-32.838	-17.392	1.00	21.59	BBBB
ATOM	4676	CA	VAL	B	280	17.502	-34.902	-14.281	1.00	25.67	BBBB
ATOM	4682	N	PRO	B	281	17.324	-37.080	-15.370	1.00	27.08	BBBB
ATOM	4683	CD	PRO	B	281	18.750	-37.057	-15.726	1.00	27.31	BBBB
ATOM	4684	CA	PRO	B	281	16.698	-38.320	-15.824	1.00	29.05	BBBB
ATOM	4685	CB	PRO	B	281	17.851	-39.071	-16.492	1.00	29.44	BBBB
ATOM	4686	CG	PRO	B	281	18.791	-37.992	-16.895	1.00	29.67	BBBB
ATOM	4687	C	PRO	B	281	16.092	-39.121	-14.684	1.00	31.51	BBBB
ATOM	4688	O	PRO	B	281	16.675	-39.223	-13.603	1.00	32.26	BBBB
ATOM	4690	CA	PHE	B	282	14.246	-40.496	-13.926	1.00	37.13	BBBB
ATOM	4701	CA	GLN	B	283	16.319	-43.395	-12.591	1.00	41.11	BBBB
ATOM	4710	CA	HIS	B	284	15.641	-46.917	-13.843	1.00	43.69	BBBB
ATOM	4720	CA	LYS	B	285	17.767	-49.993	-14.571	1.00	45.34	BBBB
ATOM	4729	CA	ASP	B	286	16.949	-49.299	-18.222	1.00	43.26	BBBB
ATOM	4737	CA	ARG	B	287	17.951	-45.623	-17.883	1.00	36.28	BBBB
ATOM	4748	CA	GLN	B	288	15.622	-44.804	-20.755	1.00	30.77	BBBB
ATOM	4756	N	GLN	B	289	15.378	-42.554	-19.857	1.00	29.38	BBBB
ATOM	4757	CA	GLN	B	289	15.474	-41.099	-19.904	1.00	29.46	BBBB
ATOM	4758	CB	GLN	B	289	14.772	-40.472	-18.700	1.00	29.25	BBBB
ATOM	4759	CG	GLN	B	289	13.265	-40.416	-18.883	1.00	29.32	BBBB
ATOM	4760	CD	GLN	B	289	12.575	-39.585	-17.826	1.00	29.84	BBBB
ATOM	4761	OE1	GLN	B	289	13.191	-38.728	-17.188	1.00	29.52	BBBB
ATOM	4762	NE2	GLN	B	289	11.281	-39.821	-17.647	1.00	28.95	BBBB
ATOM	4763	C	GLN	B	289	16.906	-40.613	-20.005	1.00	29.36	BBBB
ATOM	4764	O	GLN	B	289	17.173	-39.557	-20.585	1.00	29.12	BBBB
ATOM	4766	CA	TYR	B	290	19.228	-40.984	-19.550	1.00	29.55	BBBB
ATOM	4778	CA	TRP	B	291	19.542	-42.282	-23.116	1.00	28.07	BBBB
ATOM	4791	N	ASN	B	292	17.658	-40.779	-23.508	1.00	25.52	BBBB
ATOM	4792	CA	ASN	B	292	16.902	-39.784	-24.270	1.00	26.06	BBBB
ATOM	4793	CB	ASN	B	292	15.484	-39.599	-23.709	1.00	24.78	BBBB
ATOM	4794	CG	ASN	B	292	14.590	-40.811	-23.928	1.00	24.46	BBBB
ATOM	4795	OD1	ASN	B	292	14.842	-41.641	-24.798	1.00	25.33	BBBB
ATOM	4796	ND2	ASN	B	292	13.523	-40.900	-23.146	1.00	23.83	BBBB
ATOM	4797	C	ASN	B	292	17.605	-38.427	-24.258	1.00	25.99	BBBB
ATOM	4798	O	ASN	B	292	17.566	-37.687	-25.244	1.00	26.18	BBBB
ATOM	4799	N	ALA	B	293	18.242	-38.105	-23.139	1.00	25.66	BBBB
ATOM	4800	CA	ALA	B	293	18.926	-36.822	-22.979	1.00	25.69	BBBB
ATOM	4801	CB	ALA	B	293	18.940	-36.422	-21.506	1.00	24.17	BBBB

ATOM	4802	C	ALA B 293	20.346	-36.800	-23.521	1.00	25.67	BBBB
ATOM	4803	O	ALA B 293	20.855	-35.743	-23.902	1.00	25.52	BBBB
ATOM	4805	CA	LEU B 294	22.354	-38.088	-24.032	1.00	25.90	BBBB
ATOM	4814	CA	PRO B 295	21.998	-36.870	-27.635	1.00	26.15	BBBB
ATOM	4820	CA	LEU B 296	21.521	-33.265	-26.481	1.00	25.42	BBBB
ATOM	4828	CA	GLU B 297	24.354	-33.530	-23.953	1.00	28.78	BBBB
ATOM	4837	CA	LYS B 298	26.644	-34.947	-26.648	1.00	31.90	BBBB
ATOM	4846	CA	ALA B 299	25.773	-31.965	-28.847	1.00	30.38	BBBB
ATOM	4851	CA	GLY B 300	26.777	-29.635	-26.017	1.00	26.18	BBBB
ATOM	4855	CA	ALA B 301	23.214	-28.333	-25.638	1.00	22.50	BBBB
ATOM	4860	CA	ALA B 302	22.516	-29.770	-22.186	1.00	21.78	BBBB
ATOM	4865	CA	LYS B 303	23.979	-31.340	-19.048	1.00	25.86	BBBB
ATOM	4874	CA	ILE B 304	22.753	-34.598	-17.550	1.00	27.17	BBBB
ATOM	4882	CA	ILE B 305	22.843	-35.178	-13.813	1.00	29.01	BBBB
ATOM	4890	CA	GLU B 306	21.664	-38.702	-13.061	1.00	34.65	BBBB
ATOM	4899	CA	GLN B 307	20.377	-39.599	-9.613	1.00	40.54	BBBB
ATOM	4909	CA	PRO B 308	23.828	-40.891	-8.484	1.00	43.20	BBBB
ATOM	4915	CA	GLN B 309	25.247	-37.361	-8.787	1.00	43.46	BBBB
ATOM	4924	CA	LEU B 310	22.232	-35.166	-8.022	1.00	39.65	BBBB
ATOM	4932	CA	SER B 311	22.660	-32.714	-5.154	1.00	34.90	BBBB
ATOM	4938	CA	VAL B 312	21.990	-29.074	-4.341	1.00	31.50	BBBB
ATOM	4945	CA	ASP B 313	25.642	-28.202	-4.957	1.00	29.61	BBBB
ATOM	4953	CA	ALA B 314	25.782	-30.099	-8.254	1.00	26.47	BBBB
ATOM	4958	CA	VAL B 315	22.755	-28.215	-9.612	1.00	25.33	BBBB
ATOM	4965	CA	ALA B 316	23.888	-24.872	-8.199	1.00	27.13	BBBB
ATOM	4970	CA	ASN B 317	27.444	-25.246	-9.518	1.00	28.52	BBBB
ATOM	4978	CA	THR B 318	26.174	-26.371	-12.906	1.00	27.04	BBBB
ATOM	4985	CA	LEU B 319	23.883	-23.370	-13.357	1.00	25.21	BBBB
ATOM	4993	CA	ALA B 320	26.445	-20.931	-11.957	1.00	24.59	BBBB
ATOM	4998	CA	GLY B 321	28.934	-22.031	-14.591	1.00	24.34	BBBB
ATOM	5002	CA	TRP B 322	26.738	-21.007	-17.521	1.00	21.72	BBBB
ATOM	5016	CA	SER B 323	27.141	-17.404	-18.692	1.00	19.04	BBBB
ATOM	5022	CA	ARG B 324	24.725	-15.741	-21.112	1.00	18.09	BBBB
ATOM	5033	CA	GLU B 325	27.220	-16.368	-23.954	1.00	16.96	BBBB
ATOM	5042	CA	THR B 326	27.460	-20.055	-23.070	1.00	16.39	BBBB
ATOM	5049	CA	LEU B 327	23.659	-20.305	-22.780	1.00	17.27	BBBB
ATOM	5057	CA	LEU B 328	23.175	-18.745	-26.222	1.00	17.39	BBBB
ATOM	5065	CA	THR B 329	25.567	-21.335	-27.688	1.00	21.30	BBBB
ATOM	5072	CA	MET B 330	23.771	-24.153	-25.870	1.00	19.91	BBBB
ATOM	5080	CA	ALA B 331	20.412	-22.871	-27.098	1.00	18.49	BBBB
ATOM	5085	CA	GLU B 332	21.626	-22.827	-30.704	1.00	21.47	BBBB
ATOM	5094	CA	ARG B 333	23.040	-26.330	-30.408	1.00	23.77	BBBB
ATOM	5105	CA	ALA B 334	19.648	-27.420	-29.063	1.00	22.88	BBBB
ATOM	5110	CA	ARG B 335	17.795	-25.892	-32.002	1.00	23.54	BBBB
ATOM	5121	CA	ALA B 336	20.330	-27.477	-34.372	1.00	26.85	BBBB
ATOM	5126	CA	ALA B 337	19.740	-30.925	-32.865	1.00	30.89	BBBB
ATOM	5131	CA	SER B 338	16.008	-30.432	-33.408	1.00	32.41	BBBB
ATOM	5137	CA	ILE B 339	13.882	-31.941	-36.187	1.00	34.35	BBBB
ATOM	5146	CA	PRO B 340	10.733	-29.730	-36.600	1.00	34.94	BBBB
ATOM	5152	CA	ASP B 341	8.711	-31.820	-39.056	1.00	33.33	BBBB
ATOM	5160	CA	ALA B 342	8.875	-35.238	-37.411	1.00	29.09	BBBB
ATOM	5165	CA	THR B 343	5.115	-35.696	-37.744	1.00	28.55	BBBB
ATOM	5172	CA	GLU B 344	5.085	-34.933	-41.480	1.00	32.00	BBBB
ATOM	5181	CA	ARG B 345	8.138	-37.123	-42.067	1.00	31.44	BBBB
ATOM	5192	CA	VAL B 346	6.578	-40.151	-40.384	1.00	28.61	BBBB
ATOM	5199	CA	ALA B 347	3.249	-39.617	-42.137	1.00	28.96	BBBB
ATOM	5204	CA	ASN B 348	5.035	-39.286	-45.493	1.00	34.56	BBBB
ATOM	5212	CA	GLU B 349	6.954	-42.540	-44.956	1.00	34.86	BBBB
ATOM	5221	CA	VAL B 350	3.767	-44.306	-43.919	1.00	33.79	BBBB
ATOM	5228	CA	SER B 351	2.196	-42.946	-47.095	1.00	36.67	BBBB
ATOM	5234	CA	ARG B 352	5.114	-44.088	-49.251	1.00	40.03	BBBB
ATOM	5245	CA	VAL B 353	5.089	-47.587	-47.737	1.00	42.78	BBBB
ATOM	5252	CA	ALA B 354	1.336	-47.957	-48.212	1.00	47.24	BBBB
ATOM	5257	CA	ARG B 355	2.035	-46.964	-51.824	1.00	52.71	BBBB
ATOM	5268	CA	ALA B 356	4.453	-49.913	-51.809	1.00	54.93	BBBB
ATOM	5273	CA	LEU B 357	7.023	-47.522	-53.289	1.00	57.81	BBBB

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END

TABLE 4 ATOMIC COORDINATES OF THE
DONOR NUCLEOTIDE BINDING SITE

REMARK	4	1MUR	COMPLIES	WITH	FORMAT	V. 2.0,	11-MAY-2000		
ATOM	1	N	LEU	B	187	13.695	-22.128	-15.588	1.00 15.92 N
ATOM	2	CA	LEU	B	187	12.361	-22.710	-15.604	1.00 16.75 C
ATOM	3	C	LEU	B	187	12.450	-24.146	-15.085	1.00 16.85 C
ATOM	4	O	LEU	B	187	13.115	-24.982	-15.688	1.00 17.18 O
ATOM	5	CB	LEU	B	187	11.813	-22.701	-17.035	1.00 16.85 C
ATOM	6	CG	LEU	B	187	10.445	-23.340	-17.276	1.00 18.63 C
ATOM	7	CD1	LEU	B	187	9.368	-22.478	-16.625	1.00 19.42 C
ATOM	8	CD2	LEU	B	187	10.198	-23.449	-18.783	1.00 19.11 C
ATOM	9	N	VAL	B	188	11.788	-24.426	-13.964	1.00 18.20 N
ATOM	10	CA	VAL	B	188	11.774	-25.775	-13.381	1.00 18.41 C
ATOM	11	C	VAL	B	188	10.434	-26.440	-13.739	1.00 19.88 C
ATOM	12	O	VAL	B	188	9.371	-25.967	-13.336	1.00 20.39 O
ATOM	13	CB	VAL	B	188	11.902	-25.714	-11.842	1.00 18.98 C
ATOM	14	CG1	VAL	B	188	12.088	-27.126	-11.270	1.00 18.50 C
ATOM	15	CG2	VAL	B	188	13.061	-24.818	-11.449	1.00 18.83 C
ATOM	16	N	VAL	B	189	10.493	-27.532	-14.496	1.00 21.55 N
ATOM	17	CA	VAL	B	189	9.298	-28.234	-14.948	1.00 22.11 C
ATOM	18	C	VAL	B	189	9.191	-29.639	-14.351	1.00 23.90 C
ATOM	19	O	VAL	B	189	10.067	-30.478	-14.559	1.00 23.61 O
ATOM	20	CB	VAL	B	189	9.299	-28.342	-16.488	1.00 22.50 C
ATOM	21	CG1	VAL	B	189	8.009	-29.013	-16.981	1.00 22.70 C
ATOM	22	CG2	VAL	B	189	9.470	-26.943	-17.101	1.00 21.26 C
ATOM	23	N	GLY	B	190	8.111	-29.887	-13.615	1.00 25.60 N
ATOM	24	CA	GLY	B	190	7.914	-31.188	-12.994	1.00 27.28 C
ATOM	25	C	GLY	B	190	6.808	-32.026	-13.604	1.00 29.67 C
ATOM	26	O	GLY	B	190	6.668	-33.208	-13.283	1.00 29.86 O
ATOM	27	N	GLY	B	191	6.025	-31.430	-14.497	1.00 30.56 N
ATOM	28	CA	GLY	B	191	4.935	-32.163	-15.115	1.00 31.94 C
ATOM	29	C	GLY	B	191	3.676	-32.104	-14.269	1.00 33.11 C
ATOM	30	O	GLY	B	191	3.691	-31.556	-13.165	1.00 32.14 O
ATOM	31	N	ALA	B	195	7.761	-33.045	-9.938	1.00 33.54 N
ATOM	32	CA	ALA	B	195	8.977	-33.819	-9.709	1.00 33.12 C
ATOM	33	C	ALA	B	195	9.423	-33.590	-8.267	1.00 32.87 C
ATOM	34	O	ALA	B	195	9.955	-32.533	-7.923	1.00 31.47 O
ATOM	35	CB	ALA	B	195	10.073	-33.387	-10.679	1.00 33.17 C
ATOM	36	N	LEU	B	198	12.897	-32.223	-7.590	1.00 27.07 N
ATOM	37	CA	LEU	B	198	13.069	-30.833	-8.003	1.00 26.58 C
ATOM	38	C	LEU	B	198	12.388	-29.893	-7.006	1.00 26.41 C
ATOM	39	O	LEU	B	198	12.930	-28.835	-6.667	1.00 26.35 O
ATOM	40	CB	LEU	B	198	12.504	-30.616	-9.412	1.00 25.88 C
ATOM	41	CG	LEU	B	198	13.196	-31.408	-10.524	1.00 25.40 C
ATOM	42	CD1	LEU	B	198	12.625	-31.007	-11.874	1.00 26.54 C
ATOM	43	CD2	LEU	B	198	14.692	-31.146	-10.493	1.00 25.94 C
ATOM	44	N	TYR	B	252	8.723	-21.314	-22.184	1.00 21.27 N
ATOM	45	CA	TYR	B	252	9.972	-21.616	-22.886	1.00 22.78 C
ATOM	46	C	TYR	B	252	10.566	-20.354	-23.516	1.00 23.57 C
ATOM	47	O	TYR	B	252	11.784	-20.180	-23.550	1.00 23.91 O
ATOM	48	CB	TYR	B	252	9.726	-22.661	-23.980	1.00 21.62 C
ATOM	49	CG	TYR	B	252	9.662	-24.100	-23.505	1.00 23.34 C
ATOM	50	CD1	TYR	B	252	9.003	-25.065	-24.261	1.00 22.88 C
ATOM	51	CD2	TYR	B	252	10.288	-24.505	-22.319	1.00 22.30 C
ATOM	52	CE1	TYR	B	252	8.961	-26.392	-23.861	1.00 24.81 C
ATOM	53	CE2	TYR	B	252	10.253	-25.838	-21.912	1.00 23.56 C
ATOM	54	CZ	TYR	B	252	9.590	-26.772	-22.687	1.00 24.26 C
ATOM	55	OH	TYR	B	252	9.554	-28.088	-22.305	1.00 25.57 O
ATOM	56	N	VAL	B	258	16.263	-24.643	-18.818	1.00 18.74 N
ATOM	57	CA	VAL	B	258	15.208	-25.456	-18.234	1.00 19.32 C
ATOM	58	C	VAL	B	258	15.799	-26.585	-17.389	1.00 19.70 C

ATOM	59	O	VAL	B	258	16.808	-27.175	-17.758	1.00	18.96	O
ATOM	60	CB	VAL	B	258	14.328	-26.100	-19.337	1.00	19.89	C
ATOM	61	CG1	VAL	B	258	13.101	-26.754	-18.714	1.00	19.81	C
ATOM	62	CG2	VAL	B	258	13.907	-25.041	-20.364	1.00	21.59	C
ATOM	63	N	VAL	B	259	15.167	-26.861	-16.253	1.00	20.24	N
ATOM	64	CA	VAL	B	259	15.581	-27.957	-15.374	1.00	19.85	C
ATOM	65	C	VAL	B	259	14.382	-28.890	-15.371	1.00	20.02	C
ATOM	66	O	VAL	B	259	13.301	-28.500	-14.942	1.00	21.88	O
ATOM	67	CB	VAL	B	259	15.850	-27.483	-13.936	1.00	20.08	C
ATOM	68	CG1	VAL	B	259	16.222	-28.689	-13.059	1.00	20.22	C
ATOM	69	CG2	VAL	B	259	16.966	-26.453	-13.930	1.00	17.86	C
ATOM	70	N	CYS	B	260	14.562	-30.111	-15.867	1.00	21.70	N
ATOM	71	CA	CYS	B	260	13.454	-31.055	-15.946	1.00	22.00	C
ATOM	72	C	CYS	B	260	13.903	-32.478	-16.242	1.00	21.86	C
ATOM	73	O	CYS	B	260	15.087	-32.730	-16.496	1.00	21.34	O
ATOM	74	CB	CYS	B	260	12.494	-30.618	-17.057	1.00	22.77	C
ATOM	75	SG	CYS	B	260	13.297	-30.506	-18.711	1.00	22.15	S
ATOM	76	N	ARG	B	261	12.937	-33.397	-16.212	1.00	22.34	N
ATOM	77	CA	ARG	B	261	13.170	-34.800	-16.515	1.00	23.75	C
ATOM	78	C	ARG	B	261	13.351	-34.871	-18.032	1.00	23.98	C
ATOM	79	O	ARG	B	261	13.117	-33.883	-18.746	1.00	22.44	O
ATOM	80	CB	ARG	B	261	11.964	-35.663	-16.104	1.00	27.16	C
ATOM	81	CG	ARG	B	261	11.376	-35.337	-14.738	1.00	31.82	C
ATOM	82	CD	ARG	B	261	11.490	-36.473	-13.732	1.00	36.33	C
ATOM	83	NE	ARG	B	261	12.865	-36.721	-13.323	1.00	38.48	N
ATOM	84	CZ	ARG	B	261	13.218	-37.176	-12.125	1.00	37.25	C
ATOM	85	NH1	ARG	B	261	12.295	-37.433	-11.204	1.00	38.46	N
ATOM	86	NH2	ARG	B	261	14.499	-37.370	-11.848	1.00	36.79	N
ATOM	87	N	SER	B	262	13.740	-36.038	-18.527	1.00	22.00	N
ATOM	88	CA	SER	B	262	13.975	-36.189	-19.948	1.00	23.18	C
ATOM	89	C	SER	B	262	13.173	-37.263	-20.676	1.00	22.90	C
ATOM	90	O	SER	B	262	13.738	-38.179	-21.274	1.00	23.25	O
ATOM	91	CB	SER	B	262	15.481	-36.377	-20.203	1.00	24.45	C
ATOM	92	OG	SER	B	262	16.043	-37.326	-19.311	1.00	25.79	O
ATOM	93	N	GLY	B	263	11.850	-37.151	-20.619	1.00	22.74	N
ATOM	94	CA	GLY	B	263	11.026	-38.079	-21.361	1.00	22.85	C
ATOM	95	C	GLY	B	263	11.392	-37.793	-22.813	1.00	24.06	C
ATOM	96	O	GLY	B	263	11.908	-36.705	-23.121	1.00	22.75	O
ATOM	97	N	ALA	B	264	11.130	-38.739	-23.708	1.00	23.37	N
ATOM	98	CA	ALA	B	264	11.482	-38.564	-25.115	1.00	24.25	C
ATOM	99	C	ALA	B	264	10.843	-37.343	-25.783	1.00	24.29	C
ATOM	100	O	ALA	B	264	11.523	-36.572	-26.470	1.00	24.33	O
ATOM	101	CB	ALA	B	264	11.133	-39.829	-25.894	1.00	24.58	C
ATOM	102	N	LEU	B	265	9.541	-37.167	-25.596	1.00	24.44	N
ATOM	103	CA	LEU	B	265	8.846	-36.037	-26.205	1.00	24.66	C
ATOM	104	C	LEU	B	265	9.331	-34.717	-25.613	1.00	24.47	C
ATOM	105	O	LEU	B	265	9.374	-33.693	-26.301	1.00	23.85	O
ATOM	106	CB	LEU	B	265	7.332	-36.183	-26.011	1.00	25.33	C
ATOM	107	CG	LEU	B	265	6.760	-37.544	-26.426	1.00	27.97	C
ATOM	108	CD1	LEU	B	265	5.242	-37.541	-26.258	1.00	28.21	C
ATOM	109	CD2	LEU	B	265	7.146	-37.856	-27.878	1.00	27.40	C
ATOM	110	N	THR	B	266	9.702	-34.747	-24.338	1.00	22.12	N
ATOM	111	CA	THR	B	266	10.194	-33.557	-23.657	1.00	22.34	C
ATOM	112	C	THR	B	266	11.535	-33.117	-24.226	1.00	21.15	C
ATOM	113	O	THR	B	266	11.761	-31.926	-24.442	1.00	20.35	O
ATOM	114	CB	THR	B	266	10.348	-33.803	-22.140	1.00	22.35	C
ATOM	115	OG1	THR	B	266	9.061	-34.087	-21.583	1.00	24.46	O
ATOM	116	CG2	THR	B	266	10.945	-32.573	-21.444	1.00	24.00	C
ATOM	117	N	VAL	B	267	12.427	-34.075	-24.461	1.00	20.46	N
ATOM	118	CA	VAL	B	267	13.730	-33.762	-25.023	1.00	21.11	C
ATOM	119	C	VAL	B	267	13.548	-33.138	-26.416	1.00	21.34	C
ATOM	120	O	VAL	B	267	14.188	-32.135	-26.747	1.00	19.99	O
ATOM	121	CB	VAL	B	267	14.614	-35.039	-25.114	1.00	21.54	C
ATOM	122	CG1	VAL	B	267	15.903	-34.740	-25.865	1.00	20.72	C
ATOM	123	CG2	VAL	B	267	14.938	-35.541	-23.708	1.00	20.45	C
ATOM	124	N	SER	B	268	12.663	-33.717	-27.222	1.00	21.61	N

ATOM	125	CA	SER	B	268	12.411	-33.191	-28.567	1.00	21.96	C
ATOM	126	C	SER	B	268	11.817	-31.790	-28.519	1.00	21.81	C
ATOM	127	O	SER	B	268	12.158	-30.933	-29.336	1.00	22.60	O
ATOM	128	CB	SER	B	268	11.474	-34.121	-29.344	1.00	21.57	C
ATOM	129	OG	SER	B	268	12.141	-35.316	-29.721	1.00	24.06	O
ATOM	130	N	GLU	B	269	10.928	-31.563	-27.557	1.00	21.64	N
ATOM	131	CA	GLU	B	269	10.282	-30.272	-27.378	1.00	21.95	C
ATOM	132	C	GLU	B	269	11.321	-29.214	-26.999	1.00	21.68	C
ATOM	133	O	GLU	B	269	11.301	-28.095	-27.518	1.00	18.12	O
ATOM	134	CB	GLU	B	269	9.213	-30.399	-26.292	1.00	24.72	C
ATOM	135	CG	GLU	B	269	8.480	-29.128	-25.940	1.00	27.67	C
ATOM	136	CD	GLU	B	269	7.385	-29.380	-24.908	1.00	30.05	C
ATOM	137	OE1	GLU	B	269	6.325	-29.915	-25.287	1.00	31.50	O
ATOM	138	OE2	GLU	B	269	7.591	-29.057	-23.719	1.00	29.84	O
ATOM	139	N	ILE	B	270	12.224	-29.581	-26.092	1.00	19.43	N
ATOM	140	CA	ILE	B	270	13.295	-28.698	-25.638	1.00	20.62	C
ATOM	141	C	ILE	B	270	14.214	-28.314	-26.806	1.00	20.58	C
ATOM	142	O	ILE	B	270	14.595	-27.151	-26.954	1.00	20.50	O
ATOM	143	CB	ILE	B	270	14.157	-29.391	-24.533	1.00	20.30	C
ATOM	144	CG1	ILE	B	270	13.337	-29.574	-23.254	1.00	21.32	C
ATOM	145	CG2	ILE	B	270	15.415	-28.595	-24.266	1.00	19.17	C
ATOM	146	CD1	ILE	B	270	12.926	-28.291	-22.583	1.00	23.40	C
ATOM	147	N	ALA	B	277	19.316	-27.110	-21.396	1.00	17.01	N
ATOM	148	CA	ALA	B	277	18.638	-27.807	-20.321	1.00	15.80	C
ATOM	149	C	ALA	B	277	19.591	-28.526	-19.382	1.00	17.37	C
ATOM	150	O	ALA	B	277	20.710	-28.891	-19.755	1.00	17.09	O
ATOM	151	CB	ALA	B	277	17.641	-28.805	-20.895	1.00	17.01	C
ATOM	152	N	LEU	B	278	19.147	-28.673	-18.138	1.00	17.14	N
ATOM	153	CA	LEU	B	278	19.896	-29.429	-17.145	1.00	18.48	C
ATOM	154	C	LEU	B	278	18.884	-30.535	-16.898	1.00	19.62	C
ATOM	155	O	LEU	B	278	17.870	-30.330	-16.218	1.00	20.77	O
ATOM	156	CB	LEU	B	278	20.140	-28.619	-15.869	1.00	19.19	C
ATOM	157	CG	LEU	B	278	21.084	-29.308	-14.868	1.00	20.85	C
ATOM	158	CD1	LEU	B	278	21.283	-28.411	-13.668	1.00	21.11	C
ATOM	159	CD2	LEU	B	278	20.497	-30.647	-14.433	1.00	19.16	C
ATOM	160	N	PHE	B	279	19.149	-31.691	-17.495	1.00	19.50	N
ATOM	161	CA	PHE	B	279	18.266	-32.838	-17.392	1.00	21.59	C
ATOM	162	C	PHE	B	279	18.525	-33.709	-16.167	1.00	22.86	C
ATOM	163	O	PHE	B	279	19.671	-34.065	-15.871	1.00	23.32	O
ATOM	164	CB	PHE	B	279	18.385	-33.700	-18.651	1.00	21.07	C
ATOM	165	CG	PHE	B	279	17.740	-33.099	-19.876	1.00	19.35	C
ATOM	166	CD1	PHE	B	279	18.481	-32.898	-21.035	1.00	19.42	C
ATOM	167	CD2	PHE	B	279	16.379	-32.794	-19.888	1.00	18.16	C
ATOM	168	CE1	PHE	B	279	17.874	-32.405	-22.203	1.00	19.06	C
ATOM	169	CE2	PHE	B	279	15.759	-32.298	-21.052	1.00	17.65	C
ATOM	170	CZ	PHE	B	279	16.515	-32.108	-22.208	1.00	15.61	C
ATOM	171	N	VAL	B	280	17.445	-34.037	-15.461	1.00	23.88	N
ATOM	172	CA	VAL	B	280	17.502	-34.902	-14.281	1.00	25.67	C
ATOM	173	C	VAL	B	280	16.690	-36.136	-14.658	1.00	25.65	C
ATOM	174	O	VAL	B	280	15.509	-36.239	-14.346	1.00	24.57	O
ATOM	175	CB	VAL	B	280	16.883	-34.223	-13.048	1.00	26.89	C
ATOM	176	CG1	VAL	B	280	16.954	-35.159	-11.847	1.00	28.12	C
ATOM	177	CG2	VAL	B	280	17.631	-32.929	-12.742	1.00	27.70	C
ATOM	178	N	PRO	B	281	17.324	-37.080	-15.370	1.00	27.08	N
ATOM	179	CA	PRO	B	281	16.698	-38.320	-15.824	1.00	29.05	C
ATOM	180	C	PRO	B	281	16.092	-39.121	-14.684	1.00	31.51	C
ATOM	181	O	PRO	B	281	16.675	-39.223	-13.603	1.00	32.26	O
ATOM	182	CB	PRO	B	281	17.851	-39.071	-16.492	1.00	29.44	C
ATOM	183	CG	PRO	B	281	18.791	-37.992	-16.895	1.00	29.67	C
ATOM	184	CD	PRO	B	281	18.750	-37.057	-15.726	1.00	27.31	C
ATOM	185	N	PHE	B	282	14.908	-39.668	-14.923	1.00	33.83	N
ATOM	186	CA	PHE	B	282	14.246	-40.496	-13.926	1.00	37.13	C
ATOM	187	C	PHE	B	282	15.078	-41.776	-13.880	1.00	38.09	C
ATOM	188	O	PHE	B	282	15.357	-42.373	-14.921	1.00	38.33	O
ATOM	189	CB	PHE	B	282	12.818	-40.808	-14.372	1.00	38.38	C
ATOM	190	CG	PHE	B	282	12.032	-41.606	-13.377	1.00	40.57	C

ATOM	191	CD1	PHE	B	282	11.720	-41.074	-12.130	1.00	41.80	C
ATOM	192	CD2	PHE	B	282	11.590	-42.886	-13.689	1.00	41.65	C
ATOM	193	CE1	PHE	B	282	10.975	-41.806	-11.209	1.00	42.03	C
ATOM	194	CE2	PHE	B	282	10.843	-43.628	-12.773	1.00	42.49	C
ATOM	195	CZ	PHE	B	282	10.536	-43.085	-11.532	1.00	41.74	C
ATOM	196	N	GLN	B	288	16.212	-45.321	-19.533	1.00	30.94	N
ATOM	197	CA	GLN	B	288	15.622	-44.804	-20.755	1.00	30.77	C
ATOM	198	C	GLN	B	288	15.783	-43.291	-20.885	1.00	29.70	C
ATOM	199	O	GLN	B	288	16.268	-42.801	-21.902	1.00	29.79	O
ATOM	200	CB	GLN	B	288	14.143	-45.158	-20.810	1.00	30.59	C
ATOM	201	CG	GLN	B	288	13.473	-44.772	-22.109	1.00	29.73	C
ATOM	202	CD	GLN	B	288	11.981	-44.971	-22.044	1.00	28.04	C
ATOM	203	OE1	GLN	B	288	11.294	-44.295	-21.279	1.00	29.59	O
ATOM	204	NE2	GLN	B	288	11.468	-45.905	-22.838	1.00	26.98	N
ATOM	205	N	GLN	B	289	15.378	-42.554	-19.857	1.00	29.38	N
ATOM	206	CA	GLN	B	289	15.474	-41.099	-19.904	1.00	29.46	C
ATOM	207	C	GLN	B	289	16.906	-40.613	-20.005	1.00	29.36	C
ATOM	208	O	GLN	B	289	17.173	-39.557	-20.585	1.00	29.12	O
ATOM	209	CB	GLN	B	289	14.772	-40.472	-18.700	1.00	29.25	C
ATOM	210	CG	GLN	B	289	13.265	-40.416	-18.883	1.00	29.32	C
ATOM	211	CD	GLN	B	289	12.575	-39.585	-17.826	1.00	29.84	C
ATOM	212	OE1	GLN	B	289	13.191	-38.728	-17.188	1.00	29.52	O
ATOM	213	NE2	GLN	B	289	11.281	-39.821	-17.647	1.00	28.95	N
ATOM	214	N	TYR	B	290	17.835	-41.374	-19.442	1.00	28.95	N
ATOM	215	CA	TYR	B	290	19.228	-40.984	-19.550	1.00	29.55	C
ATOM	216	C	TYR	B	290	19.593	-41.042	-21.032	1.00	28.80	C
ATOM	217	O	TYR	B	290	20.192	-40.113	-21.567	1.00	29.22	O
ATOM	218	CB	TYR	B	290	20.136	-41.934	-18.768	1.00	31.40	C
ATOM	219	CG	TYR	B	290	21.587	-41.780	-19.148	1.00	33.37	C
ATOM	220	CD1	TYR	B	290	22.332	-40.682	-18.717	1.00	34.57	C
ATOM	221	CD2	TYR	B	290	22.192	-42.684	-20.017	1.00	34.90	C
ATOM	222	CE1	TYR	B	290	23.644	-40.490	-19.148	1.00	35.97	C
ATOM	223	CE2	TYR	B	290	23.497	-42.500	-20.453	1.00	36.03	C
ATOM	224	CZ	TYR	B	290	24.214	-41.402	-20.019	1.00	36.29	C
ATOM	225	OH	TYR	B	290	25.499	-41.215	-20.475	1.00	39.44	O
ATOM	226	N	ASN	B	292	17.658	-40.779	-23.508	1.00	25.52	N
ATOM	227	CA	ASN	B	292	16.902	-39.784	-24.270	1.00	26.06	C
ATOM	228	C	ASN	B	292	17.605	-38.427	-24.258	1.00	25.99	C
ATOM	229	O	ASN	B	292	17.566	-37.687	-25.244	1.00	26.18	O
ATOM	230	CB	ASN	B	292	15.484	-39.599	-23.709	1.00	24.78	C
ATOM	231	CG	ASN	B	292	14.590	-40.811	-23.928	1.00	24.46	C
ATOM	232	OD1	ASN	B	292	14.842	-41.641	-24.798	1.00	25.33	O
ATOM	233	ND2	ASN	B	292	13.523	-40.900	-23.146	1.00	23.83	N
ATOM	234	N	ALA	B	293	18.242	-38.105	-23.139	1.00	25.66	N
ATOM	235	CA	ALA	B	293	18.926	-36.822	-22.979	1.00	25.69	C
ATOM	236	C	ALA	B	293	20.346	-36.800	-23.521	1.00	25.67	C
ATOM	237	O	ALA	B	293	20.855	-35.743	-23.902	1.00	25.52	O
ATOM	238	CB	ALA	B	293	18.940	-36.422	-21.506	1.00	24.17	C
ATOM	239	N	LEU	B	296	21.375	-34.703	-26.688	1.00	25.66	N
ATOM	240	CA	LEU	B	296	21.521	-33.265	-26.481	1.00	25.42	C
ATOM	241	C	LEU	B	296	22.784	-32.935	-25.688	1.00	26.07	C
ATOM	242	O	LEU	B	296	23.435	-31.917	-25.944	1.00	25.26	O
ATOM	243	CB	LEU	B	296	20.283	-32.685	-25.779	1.00	24.45	C
ATOM	244	CG	LEU	B	296	19.066	-32.458	-26.679	1.00	25.59	C
ATOM	245	CD1	LEU	B	296	17.968	-31.718	-25.911	1.00	23.56	C
ATOM	246	CD2	LEU	B	296	19.496	-31.630	-27.893	1.00	25.87	C
ATOM	247	N	ALA	B	302	23.066	-29.504	-23.507	1.00	20.94	N
ATOM	248	CA	ALA	B	302	22.516	-29.770	-22.186	1.00	21.78	C
ATOM	249	C	ALA	B	302	23.503	-30.507	-21.288	1.00	22.69	C
ATOM	250	O	ALA	B	302	24.561	-30.948	-21.739	1.00	22.25	O
ATOM	251	CB	ALA	B	302	21.243	-30.595	-22.327	1.00	20.10	C
ATOM	252	N	LYS	B	303	23.156	-30.613	-20.009	1.00	24.62	N
ATOM	253	CA	LYS	B	303	23.979	-31.340	-19.048	1.00	25.86	C
ATOM	254	C	LYS	B	303	23.083	-32.319	-18.302	1.00	26.41	C
ATOM	255	O	LYS	B	303	22.015	-31.948	-17.802	1.00	25.76	O
ATOM	256	CB	LYS	B	303	24.632	-30.401	-18.036	1.00	27.85	C

ATOM	257	CG	LYS	B	303	25.466	-31.146	-16.986	1.00	29.37	C
ATOM	258	CD	LYS	B	303	26.150	-30.186	-16.025	1.00	32.41	C
ATOM	259	CE	LYS	B	303	27.083	-30.912	-15.056	1.00	33.22	C
ATOM	260	NZ	LYS	B	303	27.827	-29.952	-14.181	1.00	33.62	N
ATOM	261	N	ILE	B	304	23.520	-33.570	-18.234	1.00	25.65	N
ATOM	262	CA	ILE	B	304	22.753	-34.598	-17.550	1.00	27.17	C
ATOM	263	C	ILE	B	304	23.308	-34.855	-16.160	1.00	27.00	C
ATOM	264	O	ILE	B	304	24.511	-35.012	-15.986	1.00	27.46	O
ATOM	265	CB	ILE	B	304	22.786	-35.946	-18.316	1.00	27.06	C
ATOM	266	CG1	ILE	B	304	22.242	-35.769	-19.733	1.00	27.61	C
ATOM	267	CG2	ILE	B	304	21.977	-36.996	-17.555	1.00	28.49	C
ATOM	268	CD1	ILE	B	304	22.380	-37.009	-20.599	1.00	27.05	C
ATOM	269	N	ILE	B	305	22.428	-34.869	-15.168	1.00	27.22	N
ATOM	270	CA	ILE	B	305	22.843	-35.178	-13.813	1.00	29.01	C
ATOM	271	C	ILE	B	305	21.934	-36.302	-13.351	1.00	29.64	C
ATOM	272	O	ILE	B	305	20.806	-36.067	-12.932	1.00	29.25	O
ATOM	273	CB	ILE	B	305	22.713	-33.977	-12.858	1.00	28.91	C
ATOM	274	CG1	ILE	B	305	23.660	-32.855	-13.299	1.00	29.51	C
ATOM	275	CG2	ILE	B	305	23.063	-34.416	-11.432	1.00	30.98	C
ATOM	276	CD1	ILE	B	305	23.674	-31.653	-12.367	1.00	29.43	C

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TABLE 5 ATOMIC COORDINATES OF ACCEPTOR BINDING SITE

REMARK	4	1MUR	COMPLIES WITH FORMAT V. 2.0, 11-MAY-2000									
ATOM	1	N	MET	B	12	-0.734	-48.902	-33.817	1.00	23.68		N
ATOM	2	CA	MET	B	12	-0.523	-49.707	-32.613	1.00	24.54		C
ATOM	3	C	MET	B	12	0.361	-48.840	-31.720	1.00	25.31		C
ATOM	4	O	MET	B	12	1.546	-48.645	-32.006	1.00	23.88		O
ATOM	5	CB	MET	B	12	0.192	-51.019	-32.971	1.00	24.28		C
ATOM	6	CG	MET	B	12	-0.402	-51.726	-34.188	1.00	25.19		C
ATOM	7	SD	MET	B	12	0.399	-53.284	-34.669	1.00	26.54		S
ATOM	8	CE	MET	B	12	1.990	-52.691	-35.289	1.00	22.99		C
ATOM	9	N	ALA	B	13	-0.224	-48.292	-30.657	1.00	27.08		N
ATOM	10	CA	ALA	B	13	0.508	-47.410	-29.752	1.00	29.43		C
ATOM	11	C	ALA	B	13	-0.239	-47.192	-28.436	1.00	31.80		C
ATOM	12	O	ALA	B	13	-1.143	-46.350	-28.352	1.00	32.16		O
ATOM	13	CB	ALA	B	13	0.747	-46.074	-30.429	1.00	28.82		C
ATOM	14	N	GLY	B	14	0.150	-47.934	-27.405	1.00	32.46		N
ATOM	15	CA	GLY	B	14	-0.513	-47.804	-26.120	1.00	33.82		C
ATOM	16	C	GLY	B	14	-0.107	-46.595	-25.299	1.00	34.82		C
ATOM	17	O	GLY	B	14	0.975	-46.040	-25.479	1.00	35.47		O
ATOM	18	N	GLY	B	15	-0.986	-46.188	-24.385	1.00	35.56		N
ATOM	19	CA	GLY	B	15	-0.700	-45.047	-23.536	1.00	36.08		C
ATOM	20	C	GLY	B	15	0.539	-45.254	-22.683	1.00	36.84		C
ATOM	21	O	GLY	B	15	1.293	-44.311	-22.426	1.00	36.03		O
ATOM	22	N	THR	B	16	0.755	-46.488	-22.240	1.00	36.65		N
ATOM	23	CA	THR	B	16	1.920	-46.787	-21.421	1.00	38.51		C
ATOM	24	C	THR	B	16	3.158	-46.497	-22.264	1.00	38.35		C
ATOM	25	O	THR	B	16	3.191	-46.798	-23.460	1.00	39.90		O
ATOM	26	CB	THR	B	16	1.926	-48.258	-20.974	1.00	38.51		C
ATOM	27	OG1	THR	B	16	0.686	-48.558	-20.321	1.00	38.39		O
ATOM	28	CG2	THR	B	16	3.075	-48.518	-20.005	1.00	39.11		C
ATOM	29	N	GLY	B	17	4.168	-45.897	-21.649	1.00	37.68		N
ATOM	30	CA	GLY	B	17	5.367	-45.567	-22.392	1.00	36.57		C
ATOM	31	C	GLY	B	17	5.161	-44.303	-23.211	1.00	35.56		C
ATOM	32	O	GLY	B	17	6.079	-43.843	-23.890	1.00	35.03		O
ATOM	33	N	GLY	B	18	3.949	-43.752	-23.150	1.00	33.83		N
ATOM	34	CA	GLY	B	18	3.631	-42.529	-23.872	1.00	33.48		C
ATOM	35	C	GLY	B	18	3.825	-42.593	-25.378	1.00	33.12		C
ATOM	36	O	GLY	B	18	4.345	-41.650	-25.984	1.00	35.38		O
ATOM	37	N	HIS	B	19	3.416	-43.699	-25.988	1.00	30.26		N
ATOM	38	CA	HIS	B	19	3.548	-43.865	-27.435	1.00	28.22		C
ATOM	39	C	HIS	B	19	2.280	-43.370	-28.144	1.00	27.91		C
ATOM	40	O	HIS	B	19	2.300	-43.049	-29.337	1.00	26.91		O
ATOM	41	CB	HIS	B	19	3.772	-45.349	-27.779	1.00	25.81		C
ATOM	42	CG	HIS	B	19	4.957	-45.966	-27.094	1.00	25.35		C
ATOM	43	ND1	HIS	B	19	4.845	-47.025	-26.217	1.00	24.57		N
ATOM	44	CD2	HIS	B	19	6.281	-45.694	-27.184	1.00	24.18		C
ATOM	45	CE1	HIS	B	19	6.046	-47.380	-25.798	1.00	23.08		C
ATOM	46	NE2	HIS	B	19	6.936	-46.589	-26.369	1.00	25.51		N
ATOM	47	N	VAL	B	20	1.180	-43.310	-27.402	1.00	27.65		N
ATOM	48	CA	VAL	B	20	-0.098	-42.894	-27.965	1.00	27.77		C
ATOM	49	C	VAL	B	20	-0.140	-41.452	-28.470	1.00	27.57		C
ATOM	50	O	VAL	B	20	-0.771	-41.172	-29.486	1.00	27.12		O
ATOM	51	CB	VAL	B	20	-1.248	-43.080	-26.942	1.00	28.57		C
ATOM	52	CG1	VAL	B	20	-1.082	-42.114	-25.787	1.00	30.03		C
ATOM	53	CG2	VAL	B	20	-2.602	-42.873	-27.631	1.00	26.82		C
ATOM	54	N	LEU	B	40	-5.323	-50.004	-32.549	1.00	25.21		N
ATOM	55	CA	LEU	B	40	-5.200	-51.364	-32.026	1.00	24.71		C
ATOM	56	C	LEU	B	40	-4.535	-51.235	-30.655	1.00	23.33		C
ATOM	57	O	LEU	B	40	-3.387	-50.824	-30.563	1.00	23.43		O
ATOM	58	CB	LEU	B	40	-4.326	-52.221	-32.952	1.00	25.21		C
ATOM	59	CG	LEU	B	40	-4.416	-53.754	-32.868	1.00	26.95		C
ATOM	60	CD1	LEU	B	40	-3.037	-54.334	-32.571	1.00	27.63		C
ATOM	61	CD2	LEU	B	40	-5.421	-54.179	-31.817	1.00	26.69		C
ATOM	62	N	GLU	B	47	-4.976	-45.941	-23.678	1.00	32.85		N
ATOM	63	CA	GLU	B	47	-5.458	-45.655	-25.029	1.00	31.79		C

ATOM	64	C	GLU	B	47	-6.938	-46.017	-25.191	1.00	31.81	C
ATOM	65	O	GLU	B	47	-7.626	-45.476	-26.055	1.00	31.31	O
ATOM	66	CB	GLU	B	47	-4.624	-46.402	-26.080	1.00	30.62	C
ATOM	67	CG	GLU	B	47	-4.755	-47.922	-26.051	1.00	29.85	C
ATOM	68	CD	GLU	B	47	-3.793	-48.597	-25.082	1.00	29.78	C
ATOM	69	OE1	GLU	B	47	-3.188	-47.895	-24.247	1.00	28.76	O
ATOM	70	OE2	GLU	B	47	-3.649	-49.840	-25.156	1.00	29.01	O
ATOM	71	N	ILE	B	63	-3.428	-59.342	-24.313	1.00	30.07	N
ATOM	72	CA	ILE	B	63	-2.036	-59.770	-24.231	1.00	31.38	C
ATOM	73	C	ILE	B	63	-1.623	-59.981	-22.775	1.00	33.08	C
ATOM	74	O	ILE	B	63	-0.444	-59.872	-22.430	1.00	33.21	O
ATOM	75	CB	ILE	B	63	-1.081	-58.745	-24.883	1.00	30.06	C
ATOM	76	CG1	ILE	B	63	-1.143	-57.411	-24.137	1.00	29.94	C
ATOM	77	CG2	ILE	B	63	-1.442	-58.567	-26.353	1.00	30.41	C
ATOM	78	CD1	ILE	B	63	-0.128	-56.384	-24.632	1.00	29.62	C
ATOM	79	N	ARG	B	67	2.953	-59.185	-21.440	1.00	31.54	N
ATOM	80	CA	ARG	B	67	3.671	-57.928	-21.277	1.00	30.90	C
ATOM	81	C	ARG	B	67	5.071	-58.142	-20.713	1.00	29.99	C
ATOM	82	O	ARG	B	67	5.294	-59.034	-19.889	1.00	28.67	O
ATOM	83	CB	ARG	B	67	2.888	-56.984	-20.363	1.00	32.28	C
ATOM	84	CG	ARG	B	67	1.540	-56.576	-20.913	1.00	34.65	C
ATOM	85	CD	ARG	B	67	0.926	-55.440	-20.097	1.00	36.69	C
ATOM	86	NE	ARG	B	67	-0.259	-54.889	-20.748	1.00	38.28	N
ATOM	87	CZ	ARG	B	67	-1.425	-55.519	-20.853	1.00	39.05	C
ATOM	88	NH1	ARG	B	67	-1.583	-56.734	-20.341	1.00	39.61	N
ATOM	89	NH2	ARG	B	67	-2.434	-54.935	-21.487	1.00	39.52	N
ATOM	90	N	GLY	B	68	6.014	-57.321	-21.165	1.00	27.75	N
ATOM	91	CA	GLY	B	68	7.380	-57.427	-20.685	1.00	26.79	C
ATOM	92	C	GLY	B	68	8.166	-58.579	-21.280	1.00	25.41	C
ATOM	93	O	GLY	B	68	9.326	-58.779	-20.943	1.00	26.04	O
ATOM	94	N	GLY	B	102	3.556	-48.986	-35.936	1.00	20.96	N
ATOM	95	CA	GLY	B	102	3.796	-49.357	-34.549	1.00	19.23	C
ATOM	96	C	GLY	B	102	4.655	-48.282	-33.918	1.00	18.45	C
ATOM	97	O	GLY	B	102	5.765	-48.016	-34.381	1.00	18.70	O
ATOM	98	N	MET	B	103	4.155	-47.660	-32.857	1.00	18.01	N
ATOM	99	CA	MET	B	103	4.892	-46.597	-32.191	1.00	18.93	C
ATOM	100	C	MET	B	103	5.612	-47.128	-30.957	1.00	18.98	C
ATOM	101	O	MET	B	103	6.134	-46.357	-30.158	1.00	17.96	O
ATOM	102	CB	MET	B	103	3.928	-45.477	-31.781	1.00	20.02	C
ATOM	103	CG	MET	B	103	3.121	-44.888	-32.944	1.00	21.61	C
ATOM	104	SD	MET	B	103	4.212	-44.135	-34.157	1.00	23.45	S
ATOM	105	CE	MET	B	103	4.718	-42.680	-33.271	1.00	21.40	C
ATOM	106	N	GLY	B	104	5.640	-48.450	-30.827	1.00	21.56	N
ATOM	107	CA	GLY	B	104	6.275	-49.080	-29.686	1.00	21.89	C
ATOM	108	C	GLY	B	104	5.192	-49.614	-28.764	1.00	23.28	C
ATOM	109	O	GLY	B	104	4.009	-49.353	-28.980	1.00	22.50	O
ATOM	110	N	GLY	B	105	5.583	-50.364	-27.741	1.00	23.01	N
ATOM	111	CA	GLY	B	105	4.593	-50.905	-26.827	1.00	23.54	C
ATOM	112	C	GLY	B	105	4.358	-52.380	-27.078	1.00	23.17	C
ATOM	113	O	GLY	B	105	4.449	-52.844	-28.214	1.00	22.69	O
ATOM	114	N	TYR	B	106	4.018	-53.118	-26.026	1.00	22.87	N
ATOM	115	CA	TYR	B	106	3.818	-54.554	-26.159	1.00	22.37	C
ATOM	116	C	TYR	B	106	2.719	-55.018	-27.100	1.00	20.52	C
ATOM	117	O	TYR	B	106	2.867	-56.052	-27.746	1.00	20.50	O
ATOM	118	CB	TYR	B	106	3.632	-55.181	-24.774	1.00	25.08	C
ATOM	119	CG	TYR	B	106	4.864	-55.008	-23.929	1.00	28.19	C
ATOM	120	CD1	TYR	B	106	4.869	-54.153	-22.830	1.00	31.96	C
ATOM	121	CD2	TYR	B	106	6.058	-55.631	-24.282	1.00	31.27	C
ATOM	122	CE1	TYR	B	106	6.043	-53.915	-22.108	1.00	33.13	C
ATOM	123	CE2	TYR	B	106	7.234	-55.400	-23.569	1.00	32.27	C
ATOM	124	CZ	TYR	B	106	7.219	-54.541	-22.487	1.00	33.19	C
ATOM	125	OH	TYR	B	106	8.388	-54.291	-21.802	1.00	35.95	O
ATOM	126	N	VAL	B	107	1.628	-54.270	-27.205	1.00	19.06	N
ATOM	127	CA	VAL	B	107	0.557	-54.694	-28.099	1.00	18.06	C
ATOM	128	C	VAL	B	107	1.015	-54.743	-29.559	1.00	17.45	C
ATOM	129	O	VAL	B	107	0.502	-55.536	-30.346	1.00	16.99	O

ATOM	130	CB	VAL	B	107	-0.690	-53.774	-27.978	1.00	20.95	C
ATOM	131	CG1	VAL	B	107	-0.407	-52.407	-28.589	1.00	21.39	C
ATOM	132	CG2	VAL	B	107	-1.879	-54.433	-28.658	1.00	21.30	C
ATOM	133	N	SER	B	108	1.991	-53.916	-29.918	1.00	17.96	N
ATOM	134	CA	SER	B	108	2.488	-53.892	-31.290	1.00	19.67	C
ATOM	135	C	SER	B	108	3.197	-55.187	-31.694	1.00	20.38	C
ATOM	136	O	SER	B	108	3.385	-55.449	-32.884	1.00	21.25	O
ATOM	137	CB	SER	B	108	3.424	-52.691	-31.508	1.00	19.56	C
ATOM	138	OG	SER	B	108	4.666	-52.824	-30.837	1.00	19.63	O
ATOM	139	N	GLY	B	109	3.595	-55.995	-30.710	1.00	19.59	N
ATOM	140	CA	GLY	B	109	4.251	-57.256	-31.023	1.00	20.03	C
ATOM	141	C	GLY	B	109	3.311	-58.170	-31.792	1.00	19.61	C
ATOM	142	O	GLY	B	109	3.579	-58.517	-32.940	1.00	19.24	O
ATOM	143	N	PRO	B	110	2.206	-58.606	-31.173	1.00	19.20	N
ATOM	144	CA	PRO	B	110	1.251	-59.478	-31.855	1.00	18.99	C
ATOM	145	C	PRO	B	110	0.651	-58.761	-33.075	1.00	19.22	C
ATOM	146	O	PRO	B	110	0.406	-59.371	-34.116	1.00	17.13	O
ATOM	147	CB	PRO	B	110	0.198	-59.737	-30.778	1.00	20.41	C
ATOM	148	CG	PRO	B	110	0.998	-59.720	-29.515	1.00	19.81	C
ATOM	149	CD	PRO	B	110	1.914	-58.528	-29.729	1.00	19.94	C
ATOM	150	N	HIS	B	125	8.182	-46.638	-35.447	1.00	21.40	N
ATOM	151	CA	HIS	B	125	8.814	-45.413	-34.981	1.00	21.42	C
ATOM	152	C	HIS	B	125	9.196	-45.642	-33.519	1.00	21.70	C
ATOM	153	O	HIS	B	125	8.378	-46.117	-32.725	1.00	19.81	O
ATOM	154	CB	HIS	B	125	7.858	-44.218	-35.067	1.00	21.57	C
ATOM	155	CG	HIS	B	125	8.432	-42.948	-34.511	1.00	23.73	C
ATOM	156	ND1	HIS	B	125	9.274	-42.127	-35.236	1.00	26.23	N
ATOM	157	CD2	HIS	B	125	8.300	-42.368	-33.295	1.00	22.15	C
ATOM	158	CE1	HIS	B	125	9.631	-41.095	-34.490	1.00	24.20	C
ATOM	159	NE2	HIS	B	125	9.054	-41.218	-33.307	1.00	26.07	N
ATOM	160	N	GLU	B	126	10.444	-45.332	-33.186	1.00	21.20	N
ATOM	161	CA	GLU	B	126	10.947	-45.452	-31.817	1.00	22.15	C
ATOM	162	C	GLU	B	126	11.205	-44.027	-31.326	1.00	21.93	C
ATOM	163	O	GLU	B	126	12.016	-43.300	-31.908	1.00	21.33	O
ATOM	164	CB	GLU	B	126	12.252	-46.246	-31.790	1.00	21.99	C
ATOM	165	CG	GLU	B	126	12.958	-46.206	-30.439	1.00	22.04	C
ATOM	166	CD	GLU	B	126	12.119	-46.824	-29.338	1.00	21.43	C
ATOM	167	OE1	GLU	B	126	11.767	-48.014	-29.471	1.00	21.92	O
ATOM	168	OE2	GLU	B	126	11.807	-46.124	-28.349	1.00	21.08	O
ATOM	169	N	GLN	B	127	10.520	-43.624	-30.259	1.00	22.62	N
ATOM	170	CA	GLN	B	127	10.682	-42.270	-29.735	1.00	22.81	C
ATOM	171	C	GLN	B	127	11.874	-42.087	-28.809	1.00	22.39	C
ATOM	172	O	GLN	B	127	12.399	-40.976	-28.682	1.00	22.43	O
ATOM	173	CB	GLN	B	127	9.414	-41.814	-28.989	1.00	23.56	C
ATOM	174	CG	GLN	B	127	8.147	-41.783	-29.830	1.00	24.46	C
ATOM	175	CD	GLN	B	127	7.312	-43.041	-29.687	1.00	25.85	C
ATOM	176	OE1	GLN	B	127	6.842	-43.366	-28.591	1.00	23.78	O
ATOM	177	NE2	GLN	B	127	7.119	-43.758	-30.797	1.00	24.91	N
ATOM	178	N	ASN	B	128	12.314	-43.173	-28.177	1.00	22.35	N
ATOM	179	CA	ASN	B	128	13.406	-43.097	-27.216	1.00	22.96	C
ATOM	180	C	ASN	B	128	14.824	-43.314	-27.742	1.00	23.87	C
ATOM	181	O	ASN	B	128	15.026	-43.856	-28.830	1.00	24.05	O
ATOM	182	CB	ASN	B	128	13.136	-44.080	-26.064	1.00	22.85	C
ATOM	183	CG	ASN	B	128	11.742	-43.919	-25.474	1.00	23.25	C
ATOM	184	OD1	ASN	B	128	10.804	-44.632	-25.848	1.00	26.04	O
ATOM	185	ND2	ASN	B	128	11.597	-42.975	-24.556	1.00	22.68	N
ATOM	186	N	GLY	B	132	12.851	-49.814	-27.506	1.00	24.52	N
ATOM	187	CA	GLY	B	132	12.007	-50.532	-26.568	1.00	24.05	C
ATOM	188	C	GLY	B	132	12.150	-52.019	-26.831	1.00	23.35	C
ATOM	189	O	GLY	B	132	12.582	-52.419	-27.904	1.00	22.89	O
ATOM	190	N	LEU	B	133	11.788	-52.846	-25.860	1.00	23.38	N
ATOM	191	CA	LEU	B	133	11.903	-54.293	-26.020	1.00	24.54	C
ATOM	192	C	LEU	B	133	11.209	-54.833	-27.276	1.00	22.84	C
ATOM	193	O	LEU	B	133	11.784	-55.619	-28.027	1.00	21.86	O
ATOM	194	CB	LEU	B	133	11.328	-54.996	-24.786	1.00	25.48	C
ATOM	195	CG	LEU	B	133	11.388	-56.527	-24.780	1.00	27.50	C

ATOM	196	CD1	LEU	B	133	12.840	-56.984	-24.866	1.00	28.69	C
ATOM	197	CD2	LEU	B	133	10.735	-57.059	-23.509	1.00	28.04	C
ATOM	198	N	THR	B	134	9.975	-54.401	-27.499	1.00	21.72	N
ATOM	199	CA	THR	B	134	9.202	-54.860	-28.639	1.00	21.22	C
ATOM	200	C	THR	B	134	9.693	-54.326	-29.986	1.00	20.62	C
ATOM	201	O	THR	B	134	9.843	-55.091	-30.932	1.00	20.33	O
ATOM	202	CB	THR	B	134	7.716	-54.509	-28.449	1.00	20.99	C
ATOM	203	OG1	THR	B	134	7.257	-55.075	-27.210	1.00	20.94	O
ATOM	204	CG2	THR	B	134	6.872	-55.073	-29.600	1.00	20.64	C
ATOM	205	N	ASN	B	135	9.932	-53.021	-30.075	1.00	21.24	N
ATOM	206	CA	ASN	B	135	10.407	-52.419	-31.324	1.00	20.50	C
ATOM	207	C	ASN	B	135	11.724	-53.064	-31.767	1.00	20.78	C
ATOM	208	O	ASN	B	135	11.945	-53.290	-32.953	1.00	20.41	O
ATOM	209	CB	ASN	B	135	10.637	-50.911	-31.142	1.00	19.58	C
ATOM	210	CG	ASN	B	135	9.457	-50.058	-31.597	1.00	19.93	C
ATOM	211	OD1	ASN	B	135	9.454	-48.837	-31.390	1.00	21.78	O
ATOM	212	ND2	ASN	B	135	8.467	-50.677	-32.219	1.00	17.21	N
ATOM	213	N	LEU	B	138	10.741	-56.381	-33.386	1.00	21.61	N
ATOM	214	CA	LEU	B	138	9.744	-56.188	-34.431	1.00	23.15	C
ATOM	215	C	LEU	B	138	10.384	-55.558	-35.676	1.00	23.07	C
ATOM	216	O	LEU	B	138	9.958	-55.801	-36.809	1.00	22.68	O
ATOM	217	CB	LEU	B	138	8.618	-55.305	-33.886	1.00	23.87	C
ATOM	218	CG	LEU	B	138	7.312	-55.155	-34.664	1.00	26.48	C
ATOM	219	CD1	LEU	B	138	6.672	-56.508	-34.915	1.00	25.34	C
ATOM	220	CD2	LEU	B	138	6.383	-54.267	-33.851	1.00	25.90	C

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TABLE 6 ATOMIC COORDINATES OF MEMBRANE ASSOCIATION SITE

REMARK	4	1MUR	COMPLIES WITH FORMAT V. 2.0, 11-MAY-2000								
ATOM	1	N	MET	B	12	-0.734	-48.902	-33.817	1.00	23.68	N
ATOM	2	CA	MET	B	12	-0.523	-49.707	-32.613	1.00	24.54	C
ATOM	3	C	MET	B	12	0.361	-48.840	-31.720	1.00	25.31	C
ATOM	4	O	MET	B	12	1.546	-48.645	-32.006	1.00	23.88	O
ATOM	5	CB	MET	B	12	0.192	-51.019	-32.971	1.00	24.28	C
ATOM	6	CG	MET	B	12	-0.402	-51.726	-34.188	1.00	25.19	C
ATOM	7	SD	MET	B	12	0.399	-53.284	-34.669	1.00	26.54	S
ATOM	8	CE	MET	B	12	1.990	-52.691	-35.289	1.00	22.99	C
ATOM	9	N	LEU	B	40	-5.323	-50.004	-32.549	1.00	25.21	N
ATOM	10	CA	LEU	B	40	-5.200	-51.364	-32.026	1.00	24.71	C
ATOM	11	C	LEU	B	40	-4.535	-51.235	-30.655	1.00	23.33	C
ATOM	12	O	LEU	B	40	-3.387	-50.824	-30.563	1.00	23.43	O
ATOM	13	CB	LEU	B	40	-4.326	-52.221	-32.952	1.00	25.21	C
ATOM	14	CG	LEU	B	40	-4.416	-53.754	-32.868	1.00	26.95	C
ATOM	15	CD1	LEU	B	40	-3.037	-54.334	-32.571	1.00	27.63	C
ATOM	16	CD2	LEU	B	40	-5.421	-54.179	-31.817	1.00	26.69	C
ATOM	17	N	ILE	B	61	-7.271	-56.229	-28.295	1.00	29.38	N
ATOM	18	CA	ILE	B	61	-6.832	-57.616	-28.269	1.00	28.55	C
ATOM	19	C	ILE	B	61	-6.344	-57.855	-26.848	1.00	29.13	C
ATOM	20	O	ILE	B	61	-6.124	-56.906	-26.091	1.00	28.80	O
ATOM	21	CB	ILE	B	61	-5.674	-57.923	-29.258	1.00	28.48	C
ATOM	22	CG1	ILE	B	61	-4.422	-57.126	-28.892	1.00	26.70	C
ATOM	23	CG2	ILE	B	61	-6.123	-57.650	-30.694	1.00	27.65	C
ATOM	24	CD1	ILE	B	61	-3.177	-57.615	-29.638	1.00	27.03	C
ATOM	25	N	ARG	B	62	-6.186	-59.116	-26.473	1.00	29.38	N
ATOM	26	CA	ARG	B	62	-5.709	-59.416	-25.133	1.00	30.76	C
ATOM	27	C	ARG	B	62	-4.274	-59.923	-25.156	1.00	29.32	C
ATOM	28	O	ARG	B	62	-3.933	-60.809	-25.934	1.00	28.65	O
ATOM	29	CB	ARG	B	62	-6.630	-60.447	-24.461	1.00	32.36	C
ATOM	30	CG	ARG	B	62	-6.130	-60.955	-23.114	1.00	35.99	C
ATOM	31	CD	ARG	B	62	-5.438	-59.859	-22.311	1.00	37.86	C
ATOM	32	NE	ARG	B	62	-6.297	-58.718	-22.004	1.00	40.01	N
ATOM	33	CZ	ARG	B	62	-5.840	-57.504	-21.711	1.00	39.09	C
ATOM	34	NH1	ARG	B	62	-4.536	-57.275	-21.690	1.00	39.24	N
ATOM	35	NH2	ARG	B	62	-6.686	-56.518	-21.439	1.00	40.03	N
ATOM	36	N	ILE	B	63	-3.428	-59.342	-24.313	1.00	30.07	N
ATOM	37	CA	ILE	B	63	-2.036	-59.770	-24.231	1.00	31.38	C
ATOM	38	C	ILE	B	63	-1.623	-59.981	-22.775	1.00	33.08	C
ATOM	39	O	ILE	B	63	-0.444	-59.872	-22.430	1.00	33.21	O
ATOM	40	CB	ILE	B	63	-1.081	-58.745	-24.883	1.00	30.06	C
ATOM	41	CG1	ILE	B	63	-1.143	-57.411	-24.137	1.00	29.94	C
ATOM	42	CG2	ILE	B	63	-1.442	-58.567	-26.353	1.00	30.41	C
ATOM	43	CD1	ILE	B	63	-0.128	-56.384	-24.632	1.00	29.62	C
ATOM	44	N	SER	B	64	-2.603	-60.284	-21.927	1.00	35.38	N
ATOM	45	CA	SER	B	64	-2.356	-60.520	-20.505	1.00	37.51	C
ATOM	46	C	SER	B	64	-1.326	-61.622	-20.311	1.00	37.32	C
ATOM	47	O	SER	B	64	-1.411	-62.682	-20.933	1.00	37.86	O
ATOM	48	CB	SER	B	64	-3.652	-60.912	-19.792	1.00	38.82	C
ATOM	49	OG	SER	B	64	-4.558	-59.823	-19.750	1.00	42.88	O
ATOM	50	N	GLY	B	65	-0.356	-61.370	-19.441	1.00	37.81	N
ATOM	51	CA	GLY	B	65	0.679	-62.355	-19.199	1.00	37.13	C
ATOM	52	C	GLY	B	65	1.798	-62.283	-20.226	1.00	36.76	C
ATOM	53	O	GLY	B	65	2.858	-62.889	-20.038	1.00	37.57	O
ATOM	54	N	LEU	B	66	1.577	-61.539	-21.307	1.00	34.63	N
ATOM	55	CA	LEU	B	66	2.591	-61.413	-22.355	1.00	33.17	C
ATOM	56	C	LEU	B	66	3.414	-60.133	-22.246	1.00	32.72	C
ATOM	57	O	LEU	B	66	4.451	-60.002	-22.893	1.00	33.13	O
ATOM	58	CB	LEU	B	66	1.936	-61.470	-23.735	1.00	32.08	C
ATOM	59	CG	LEU	B	66	1.162	-62.747	-24.061	1.00	32.52	C
ATOM	60	CD1	LEU	B	66	0.563	-62.626	-25.445	1.00	31.38	C

ATOM	61	CD2	LEU	B	66	2.093	-63.957	-23.984	1.00	31.67	C
ATOM	62	N	ARG	B	67	2.953	-59.185	-21.440	1.00	31.54	N
ATOM	63	CA	ARG	B	67	3.671	-57.928	-21.277	1.00	30.90	C
ATOM	64	C	ARG	B	67	5.071	-58.142	-20.713	1.00	29.99	C
ATOM	65	O	ARG	B	67	5.294	-59.034	-19.889	1.00	28.67	O
ATOM	66	CB	ARG	B	67	2.888	-56.984	-20.363	1.00	32.28	C
ATOM	67	CG	ARG	B	67	1.540	-56.576	-20.913	1.00	34.65	C
ATOM	68	CD	ARG	B	67	0.926	-55.440	-20.097	1.00	36.69	C
ATOM	69	NE	ARG	B	67	-0.259	-54.889	-20.748	1.00	38.28	N
ATOM	70	CZ	ARG	B	67	-1.425	-55.519	-20.853	1.00	39.05	C
ATOM	71	NH1	ARG	B	67	-1.583	-56.734	-20.341	1.00	39.61	N
ATOM	72	NH2	ARG	B	67	-2.434	-54.935	-21.487	1.00	39.52	N
ATOM	73	N	GLY	B	68	6.014	-57.321	-21.165	1.00	27.75	N
ATOM	74	CA	GLY	B	68	7.380	-57.427	-20.685	1.00	26.79	C
ATOM	75	C	GLY	B	68	8.166	-58.579	-21.280	1.00	25.41	C
ATOM	76	O	GLY	B	68	9.326	-58.779	-20.943	1.00	26.04	O
ATOM	77	N	LYS	B	69	7.546	-59.342	-22.170	1.00	24.55	N
ATOM	78	CA	LYS	B	69	8.238	-60.463	-22.796	1.00	23.93	C
ATOM	79	C	LYS	B	69	8.825	-60.062	-24.142	1.00	23.32	C
ATOM	80	O	LYS	B	69	8.151	-59.404	-24.944	1.00	21.96	O
ATOM	81	CB	LYS	B	69	7.284	-61.641	-23.033	1.00	24.12	C
ATOM	82	CG	LYS	B	69	6.757	-62.360	-21.794	1.00	25.08	C
ATOM	83	CD	LYS	B	69	5.887	-63.553	-22.224	1.00	25.44	C
ATOM	84	CE	LYS	B	69	5.357	-64.358	-21.035	1.00	28.31	C
ATOM	85	NZ	LYS	B	69	6.468	-64.877	-20.175	1.00	29.71	N
ATOM	86	N	GLY	B	70	10.075	-60.470	-24.374	1.00	22.48	N
ATOM	87	CA	GLY	B	70	10.755	-60.229	-25.636	1.00	22.26	C
ATOM	88	C	GLY	B	70	10.308	-61.337	-26.588	1.00	22.17	C
ATOM	89	O	GLY	B	70	9.512	-62.183	-26.195	1.00	21.62	O
ATOM	90	N	ILE	B	71	10.819	-61.373	-27.814	1.00	21.85	N
ATOM	91	CA	ILE	B	71	10.357	-62.386	-28.762	1.00	23.55	C
ATOM	92	C	ILE	B	71	10.616	-63.840	-28.359	1.00	23.88	C
ATOM	93	O	ILE	B	71	9.775	-64.707	-28.592	1.00	21.66	O
ATOM	94	CB	ILE	B	71	10.926	-62.142	-30.181	1.00	23.52	C
ATOM	95	CG1	ILE	B	71	10.264	-63.096	-31.182	1.00	24.18	C
ATOM	96	CG2	ILE	B	71	12.435	-62.375	-30.192	1.00	25.96	C
ATOM	97	CD1	ILE	B	71	8.745	-62.981	-31.263	1.00	25.73	C
ATOM	98	N	LYS	B	72	11.764	-64.119	-27.751	1.00	23.82	N
ATOM	99	CA	LYS	B	72	12.038	-65.491	-27.343	1.00	24.92	C
ATOM	100	C	LYS	B	72	11.068	-65.925	-26.245	1.00	23.73	C
ATOM	101	O	LYS	B	72	10.592	-67.062	-26.245	1.00	24.08	O
ATOM	102	CB	LYS	B	72	13.491	-65.634	-26.875	1.00	26.86	C
ATOM	103	CG	LYS	B	72	14.496	-65.590	-28.019	1.00	31.29	C
ATOM	104	CD	LYS	B	72	15.925	-65.791	-27.518	1.00	36.00	C
ATOM	105	CE	LYS	B	72	16.926	-65.816	-28.671	1.00	38.82	C
ATOM	106	NZ	LYS	B	72	18.342	-65.957	-28.192	1.00	41.21	N
ATOM	107	N	ALA	B	73	10.765	-65.016	-25.322	1.00	21.62	N
ATOM	108	CA	ALA	B	73	9.839	-65.306	-24.233	1.00	21.18	C
ATOM	109	C	ALA	B	73	8.412	-65.454	-24.771	1.00	20.36	C
ATOM	110	O	ALA	B	73	7.619	-66.250	-24.267	1.00	18.97	O
ATOM	111	CB	ALA	B	73	9.895	-64.196	-23.187	1.00	22.25	C
ATOM	112	N	LEU	B	74	8.076	-64.673	-25.791	1.00	20.23	N
ATOM	113	CA	LEU	B	74	6.745	-64.762	-26.387	1.00	19.36	C
ATOM	114	C	LEU	B	74	6.549	-66.110	-27.069	1.00	19.37	C
ATOM	115	O	LEU	B	74	5.539	-66.779	-26.863	1.00	20.01	O
ATOM	116	CB	LEU	B	74	6.540	-63.643	-27.417	1.00	18.42	C
ATOM	117	CG	LEU	B	74	6.422	-62.208	-26.884	1.00	18.80	C
ATOM	118	CD1	LEU	B	74	6.473	-61.197	-28.039	1.00	19.86	C
ATOM	119	CD2	LEU	B	74	5.109	-62.071	-26.104	1.00	19.45	C
ATOM	120	N	ILE	B	75	7.520	-66.507	-27.883	1.00	20.59	N
ATOM	121	CA	ILE	B	75	7.434	-67.768	-28.601	1.00	21.18	C
ATOM	122	C	ILE	B	75	7.488	-68.942	-27.624	1.00	21.20	C
ATOM	123	O	ILE	B	75	7.125	-70.063	-27.979	1.00	21.59	O
ATOM	124	CB	ILE	B	75	8.571	-67.896	-29.641	1.00	22.95	C
ATOM	125	CG1	ILE	B	75	8.598	-66.657	-30.540	1.00	26.82	C
ATOM	126	CG2	ILE	B	75	8.334	-69.108	-30.527	1.00	25.38	C

ATOM	127	CD1	ILE	B	75	7.304	-66.442	-31.327	1.00	28.48	C
ATOM	128	N	ALA	B	76	7.940	-68.680	-26.399	1.00	20.49	C
ATOM	129	CA	ALA	B	76	7.996	-69.726	-25.374	1.00	21.72	N
ATOM	130	C	ALA	B	76	6.624	-69.904	-24.732	1.00	21.54	C
ATOM	131	O	ALA	B	76	6.441	-70.778	-23.875	1.00	20.75	C
ATOM	132	CB	ALA	B	76	9.026	-69.372	-24.305	1.00	21.92	O
ATOM	133	N	ALA	B	77	5.668	-69.066	-25.145	1.00	20.61	C
ATOM	134	CA	ALA	B	77	4.289	-69.121	-24.655	1.00	21.07	N
ATOM	135	C	ALA	B	77	3.383	-69.298	-25.881	1.00	21.69	C
ATOM	136	O	ALA	B	77	2.567	-68.430	-26.199	1.00	21.93	C
ATOM	137	CB	ALA	B	77	3.937	-67.830	-23.924	1.00	20.10	O
ATOM	138	N	PRO	B	78	3.507	-70.446	-26.564	1.00	22.38	C
ATOM	139	CA	PRO	B	78	2.772	-70.846	-27.771	1.00	20.95	N
ATOM	140	C	PRO	B	78	1.278	-70.535	-27.813	1.00	21.19	C
ATOM	141	O	PRO	B	78	0.789	-69.939	-28.776	1.00	19.68	C
ATOM	142	CB	PRO	B	78	3.027	-72.350	-27.861	1.00	22.21	O
ATOM	143	CG	PRO	B	78	4.288	-72.547	-27.117	1.00	24.07	C
ATOM	144	CD	PRO	B	78	4.211	-71.603	-25.976	1.00	21.89	C
ATOM	145	N	LEU	B	79	0.544	-70.961	-26.790	1.00	21.21	N
ATOM	146	CA	LEU	B	79	-0.896	-70.728	-26.783	1.00	21.32	C
ATOM	147	C	LEU	B	79	-1.275	-69.263	-26.707	1.00	21.17	C
ATOM	148	O	LEU	B	79	-2.125	-68.800	-27.481	1.00	20.44	C
ATOM	149	CB	LEU	B	79	-1.569	-71.476	-25.630	1.00	20.99	O
ATOM	150	CG	LEU	B	79	-1.397	-72.988	-25.617	1.00	22.40	C
ATOM	151	CD1	LEU	B	79	-2.504	-73.619	-24.772	1.00	22.01	C
ATOM	152	CD2	LEU	B	79	-1.438	-73.521	-27.021	1.00	23.82	C
ATOM	153	N	ARG	B	80	-0.656	-68.529	-25.788	1.00	20.91	N
ATOM	154	CA	ARG	B	80	-0.980	-67.115	-25.637	1.00	21.30	C
ATOM	155	C	ARG	B	80	-0.526	-66.233	-26.790	1.00	21.29	C
ATOM	156	O	ARG	B	80	-1.278	-65.355	-27.223	1.00	21.47	O
ATOM	157	CB	ARG	B	80	-0.444	-66.583	-24.312	1.00	22.12	C
ATOM	158	CG	ARG	B	80	-1.286	-67.051	-23.118	1.00	24.03	C
ATOM	159	CD	ARG	B	80	-0.610	-66.738	-21.807	1.00	23.42	C
ATOM	160	NE	ARG	B	80	0.581	-67.556	-21.610	1.00	24.59	N
ATOM	161	CZ	ARG	B	80	1.466	-67.351	-20.642	1.00	26.08	C
ATOM	162	NH1	ARG	B	80	1.290	-66.349	-19.787	1.00	26.92	N
ATOM	163	NH2	ARG	B	80	2.514	-68.152	-20.519	1.00	27.22	N
ATOM	164	N	ILE	B	81	0.683	-66.448	-27.303	1.00	19.29	N
ATOM	165	CA	ILE	B	81	1.113	-65.621	-28.421	1.00	19.47	C
ATOM	166	C	ILE	B	81	0.256	-65.937	-29.654	1.00	18.99	C
ATOM	167	O	ILE	B	81	-0.149	-65.028	-30.378	1.00	19.38	O
ATOM	168	CB	ILE	B	81	2.639	-65.793	-28.730	1.00	17.92	C
ATOM	169	CG1	ILE	B	81	3.067	-64.753	-29.769	1.00	18.63	C
ATOM	170	CG2	ILE	B	81	2.949	-67.200	-29.206	1.00	17.33	C
ATOM	171	CD1	ILE	B	81	2.746	-63.318	-29.346	1.00	17.46	C
ATOM	172	N	PHE	B	82	-0.056	-67.211	-29.880	1.00	19.39	N
ATOM	173	CA	PHE	B	82	-0.875	-67.582	-31.038	1.00	19.15	C
ATOM	174	C	PHE	B	82	-2.250	-66.931	-30.959	1.00	19.94	C
ATOM	175	O	PHE	B	82	-2.777	-66.444	-31.970	1.00	19.64	O
ATOM	176	CB	PHE	B	82	-1.057	-69.103	-31.136	1.00	19.27	C
ATOM	177	CG	PHE	B	82	-1.811	-69.548	-32.368	1.00	19.87	C
ATOM	178	CD1	PHE	B	82	-1.180	-69.602	-33.603	1.00	20.87	C
ATOM	179	CD2	PHE	B	82	-3.154	-69.898	-32.289	1.00	21.11	C
ATOM	180	CE1	PHE	B	82	-1.872	-70.002	-34.753	1.00	21.20	C
ATOM	181	CE2	PHE	B	82	-3.857	-70.297	-33.429	1.00	22.26	C
ATOM	182	CZ	PHE	B	82	-3.212	-70.349	-34.663	1.00	22.14	C
ATOM	183	N	ASN	B	83	-2.832	-66.923	-29.764	1.00	19.29	N
ATOM	184	CA	ASN	B	83	-4.150	-66.332	-29.577	1.00	20.90	C
ATOM	185	C	ASN	B	83	-4.178	-64.821	-29.812	1.00	20.83	C
ATOM	186	O	ASN	B	83	-5.036	-64.316	-30.472	1.00	21.92	O
ATOM	187	CB	ASN	B	83	-4.693	-66.641	-29.178	1.00	20.55	C
ATOM	188	CG	ASN	B	83	-6.158	-66.244	-28.028	1.00	22.79	C
ATOM	189	OD1	ASN	B	83	-6.505	-65.374	-27.229	1.00	25.14	O
ATOM	190	ND2	ASN	B	83	-7.018	-66.877	-28.807	1.00	20.47	N
ATOM	191	N	ALA	B	84	-3.203	-64.092	-29.275	1.00	19.74	N
ATOM	192	CA	ALA	B	84	-3.177	-62.647	-29.484	1.00	19.30	C

ATOM	193	C	ALA	B	84	-2.967	-62.380	-30.981	1.00	19.94	C
ATOM	194	O	ALA	B	84	-3.561	-61.459	-31.552	1.00	19.69	O
ATOM	195	CB	ALA	B	84	-2.060	-62.008	-28.662	1.00	18.59	C
ATOM	196	N	TRP	B	85	-2.118	-63.197	-31.603	1.00	19.77	N
ATOM	197	CA	TRP	B	85	-1.820	-63.111	-33.032	1.00	20.56	C
ATOM	198	C	TRP	B	85	-3.090	-63.354	-33.865	1.00	21.76	C
ATOM	199	O	TRP	B	85	-3.339	-62.658	-34.859	1.00	20.40	O
ATOM	200	CB	TRP	B	85	-0.754	-64.148	-33.396	1.00	21.46	C
ATOM	201	CG	TRP	B	85	-0.365	-64.167	-34.856	1.00	23.00	C
ATOM	202	CD1	TRP	B	85	0.301	-63.189	-35.548	1.00	23.17	C
ATOM	203	CD2	TRP	B	85	-0.588	-65.232	-35.785	1.00	23.69	C
ATOM	204	NE1	TRP	B	85	0.509	-63.585	-36.848	1.00	24.28	N
ATOM	205	CE2	TRP	B	85	-0.024	-64.835	-37.022	1.00	24.14	C
ATOM	206	CE3	TRP	B	85	-1.206	-66.486	-35.693	1.00	24.79	C
ATOM	207	CZ2	TRP	B	85	-0.060	-65.650	-38.160	1.00	24.90	C
ATOM	208	CZ3	TRP	B	85	-1.243	-67.299	-36.827	1.00	25.45	C
ATOM	209	CH2	TRP	B	85	-0.671	-66.875	-38.045	1.00	25.15	C
ATOM	210	N	ARG	B	86	-3.885	-64.346	-33.467	1.00	22.03	N
ATOM	211	CA	ARG	B	86	-5.140	-64.660	-34.166	1.00	23.28	C
ATOM	212	C	ARG	B	86	-6.151	-63.517	-34.007	1.00	22.98	C
ATOM	213	O	ARG	B	86	-6.890	-63.195	-34.942	1.00	21.37	O
ATOM	214	CB	ARG	B	86	-5.754	-65.965	-33.623	1.00	24.72	C
ATOM	215	CG	ARG	B	86	-4.999	-67.236	-34.021	1.00	27.21	C
ATOM	216	CD	ARG	B	86	-5.368	-67.725	-35.418	1.00	29.60	C
ATOM	217	NE	ARG	B	86	-6.626	-68.477	-35.422	1.00	31.45	N
ATOM	218	CZ	ARG	B	86	-7.185	-69.004	-36.508	1.00	31.37	C
ATOM	219	NH1	ARG	B	86	-6.607	-68.862	-37.696	1.00	32.19	N
ATOM	220	NH2	ARG	B	86	-8.314	-69.694	-36.405	1.00	31.39	N
ATOM	221	N	GLN	B	87	-6.190	-62.916	-32.821	1.00	22.90	N
ATOM	222	CA	GLN	B	87	-7.101	-61.802	-32.567	1.00	24.07	C
ATOM	223	C	GLN	B	87	-6.738	-60.618	-33.457	1.00	23.85	C
ATOM	224	O	GLN	B	87	-7.613	-60.012	-34.077	1.00	24.02	O
ATOM	225	CB	GLN	B	87	-7.046	-61.382	-31.097	1.00	24.33	C
ATOM	226	CG	GLN	B	87	-7.873	-62.280	-30.187	1.00	27.24	C
ATOM	227	CD	GLN	B	87	-7.720	-61.943	-28.723	1.00	28.81	C
ATOM	228	OE1	GLN	B	87	-8.567	-62.296	-27.908	1.00	33.25	O
ATOM	229	NE2	GLN	B	87	-6.632	-61.275	-28.375	1.00	29.95	N
ATOM	230	N	ALA	B	88	-5.449	-60.293	-33.521	1.00	23.39	N
ATOM	231	CA	ALA	B	88	-4.996	-59.183	-34.355	1.00	23.78	C
ATOM	232	C	ALA	B	88	-5.257	-59.485	-35.831	1.00	24.73	C
ATOM	233	O	ALA	B	88	-5.655	-58.595	-36.592	1.00	24.72	O
ATOM	234	CB	ALA	B	88	-3.508	-58.909	-34.116	1.00	23.33	C
ATOM	235	N	ARG	B	89	-5.038	-60.735	-36.244	1.00	24.26	N
ATOM	236	CA	ARG	B	89	-5.285	-61.111	-37.636	1.00	24.94	C
ATOM	237	C	ARG	B	89	-6.752	-60.909	-38.013	1.00	25.29	C
ATOM	238	O	ARG	B	89	-7.056	-60.420	-39.104	1.00	24.27	O
ATOM	239	CB	ARG	B	89	-4.904	-62.575	-37.893	1.00	25.14	C
ATOM	240	CG	ARG	B	89	-3.461	-62.774	-38.353	1.00	24.54	C
ATOM	241	CD	ARG	B	89	-3.142	-64.253	-38.510	1.00	25.50	C
ATOM	242	NE	ARG	B	89	-3.809	-64.901	-39.641	1.00	24.93	N
ATOM	243	CZ	ARG	B	89	-3.329	-64.930	-40.882	1.00	25.90	C
ATOM	244	NH1	ARG	B	89	-2.178	-64.336	-41.170	1.00	25.98	N
ATOM	245	NH2	ARG	B	89	-3.979	-65.596	-41.831	1.00	26.36	N
ATOM	246	N	GLY	B	105	5.583	-50.364	-27.741	1.00	23.01	N
ATOM	247	CA	GLY	B	105	4.593	-50.905	-26.827	1.00	23.54	C
ATOM	248	C	GLY	B	105	4.358	-52.380	-27.078	1.00	23.17	C
ATOM	249	O	GLY	B	105	4.449	-52.844	-28.214	1.00	22.69	O
ATOM	250	N	TYR	B	106	4.018	-53.118	-26.026	1.00	22.87	N
ATOM	251	CA	TYR	B	106	3.818	-54.554	-26.159	1.00	22.37	C
ATOM	252	C	TYR	B	106	2.719	-55.018	-27.100	1.00	20.52	C
ATOM	253	O	TYR	B	106	2.867	-56.052	-27.746	1.00	20.50	O
ATOM	254	CB	TYR	B	106	3.632	-55.181	-24.774	1.00	25.08	C
ATOM	255	CG	TYR	B	106	4.864	-55.008	-23.929	1.00	28.19	C
ATOM	256	CD1	TYR	B	106	4.869	-54.153	-22.830	1.00	31.96	C
ATOM	257	CD2	TYR	B	106	6.058	-55.631	-24.282	1.00	31.27	C
ATOM	258	CE1	TYR	B	106	6.043	-53.915	-22.108	1.00	33.13	C

ATOM	259	CE2	TYR	B	106	7.234	-55.400	-23.569	1.00	32.27	C
ATOM	260	CZ	TYR	B	106	7.219	-54.541	-22.487	1.00	33.19	C
ATOM	261	OH	TYR	B	106	8.388	-54.291	-21.802	1.00	35.95	C
ATOM	262	N	VAL	B	107	1.628	-54.270	-27.205	1.00	19.06	O
ATOM	263	CA	VAL	B	107	0.557	-54.694	-28.099	1.00	18.06	N
ATOM	264	C	VAL	B	107	1.015	-54.743	-29.559	1.00	17.45	C
ATOM	265	O	VAL	B	107	0.502	-55.536	-30.346	1.00	16.99	C
ATOM	266	CB	VAL	B	107	-0.690	-53.774	-27.978	1.00	20.95	O
ATOM	267	CG1	VAL	B	107	-0.407	-52.407	-28.589	1.00	21.39	C
ATOM	268	CG2	VAL	B	107	-1.879	-54.433	-28.658	1.00	21.30	C
ATOM	269	N	SER	B	108	1.991	-53.916	-29.918	1.00	17.96	N
ATOM	270	CA	SER	B	108	2.488	-53.892	-31.290	1.00	19.67	C
ATOM	271	C	SER	B	108	3.197	-55.187	-31.694	1.00	20.38	C
ATOM	272	O	SER	B	108	3.385	-55.449	-32.884	1.00	21.25	O
ATOM	273	CB	SER	B	108	3.424	-52.691	-31.508	1.00	19.56	C
ATOM	274	OG	SER	B	108	4.666	-52.824	-30.837	1.00	19.63	O
ATOM	275	N	GLY	B	109	3.595	-55.995	-30.710	1.00	19.59	N
ATOM	276	CA	GLY	B	109	4.251	-57.256	-31.023	1.00	20.03	C
ATOM	277	C	GLY	B	109	3.311	-58.170	-31.792	1.00	19.61	C
ATOM	278	O	GLY	B	109	3.579	-58.517	-32.940	1.00	19.24	O
ATOM	279	N	PRO	B	110	2.206	-58.606	-31.173	1.00	19.20	N
ATOM	280	CA	PRO	B	110	1.251	-59.478	-31.855	1.00	18.99	C
ATOM	281	C	PRO	B	110	0.651	-58.761	-33.075	1.00	19.22	C
ATOM	282	O	PRO	B	110	0.406	-59.371	-34.116	1.00	17.13	O
ATOM	283	CB	PRO	B	110	0.198	-59.737	-30.778	1.00	20.41	C
ATOM	284	CG	PRO	B	110	0.998	-59.720	-29.515	1.00	19.81	C
ATOM	285	CD	PRO	B	110	1.914	-58.528	-29.729	1.00	19.94	C
ATOM	286	N	GLY	B	111	0.407	-57.462	-32.927	1.00	19.03	N
ATOM	287	CA	GLY	B	111	-0.160	-56.702	-34.025	1.00	19.60	C
ATOM	288	C	GLY	B	111	0.764	-56.714	-35.226	1.00	19.59	C
ATOM	289	O	GLY	B	111	0.330	-56.979	-36.339	1.00	21.10	O
ATOM	290	N	GLY	B	112	2.043	-56.429	-34.995	1.00	19.78	N
ATOM	291	CA	GLY	B	112	3.014	-56.417	-36.074	1.00	19.97	C
ATOM	292	C	GLY	B	112	3.147	-57.783	-36.724	1.00	20.43	C
ATOM	293	O	GLY	B	112	3.233	-57.896	-37.949	1.00	19.94	O
ATOM	294	N	LEU	B	113	3.167	-58.828	-35.903	1.00	19.26	N
ATOM	295	CA	LEU	B	113	3.265	-60.184	-36.429	1.00	19.49	C
ATOM	296	C	LEU	B	113	2.040	-60.521	-37.274	1.00	18.73	C
ATOM	297	O	LEU	B	113	2.143	-61.252	-38.255	1.00	18.44	O
ATOM	298	CB	LEU	B	113	3.405	-61.198	-35.289	1.00	18.38	C
ATOM	299	CG	LEU	B	113	4.777	-61.270	-34.605	1.00	20.59	C
ATOM	300	CD1	LEU	B	113	4.656	-62.059	-33.311	1.00	20.01	C
ATOM	301	CD2	LEU	B	113	5.794	-61.914	-35.538	1.00	20.23	C
ATOM	302	N	ALA	B	114	0.875	-60.010	-36.892	1.00	18.96	N
ATOM	303	CA	ALA	B	114	-0.334	-60.292	-37.661	1.00	18.70	C
ATOM	304	C	ALA	B	114	-0.288	-59.578	-39.019	1.00	19.30	C
ATOM	305	O	ALA	B	114	-0.602	-60.167	-40.052	1.00	20.62	O
ATOM	306	CB	ALA	B	114	-1.562	-59.855	-36.889	1.00	16.45	C
ATOM	307	N	ALA	B	115	0.082	-58.303	-39.000	1.00	20.57	N
ATOM	308	CA	ALA	B	115	0.167	-57.516	-40.229	1.00	21.84	C
ATOM	309	C	ALA	B	115	1.140	-58.192	-41.189	1.00	21.58	C
ATOM	310	O	ALA	B	115	0.815	-58.464	-42.345	1.00	22.14	O
ATOM	311	CB	ALA	B	115	0.636	-56.108	-39.911	1.00	19.85	C
ATOM	312	N	TRP	B	116	2.334	-58.476	-40.688	1.00	22.12	N
ATOM	313	CA	TRP	B	116	3.365	-59.126	-41.478	1.00	23.22	C
ATOM	314	C	TRP	B	116	2.871	-60.434	-42.123	1.00	23.55	C
ATOM	315	O	TRP	B	116	3.048	-60.643	-43.329	1.00	22.19	O
ATOM	316	CB	TRP	B	116	4.584	-59.367	-40.579	1.00	26.08	C
ATOM	317	CG	TRP	B	116	5.699	-60.136	-41.204	1.00	27.40	C
ATOM	318	CD1	TRP	B	116	6.473	-59.761	-42.271	1.00	28.30	C
ATOM	319	CD2	TRP	B	116	6.168	-61.418	-40.793	1.00	28.77	C
ATOM	320	NE1	TRP	B	116	7.401	-60.742	-42.547	1.00	29.04	N
ATOM	321	CE2	TRP	B	116	7.234	-61.771	-41.655	1.00	30.37	C
ATOM	322	CE3	TRP	B	116	5.794	-62.308	-39.778	1.00	30.49	C
ATOM	323	CZ2	TRP	B	116	7.929	-62.981	-41.529	1.00	31.08	C
ATOM	324	CZ3	TRP	B	116	6.485	-63.510	-39.653	1.00	31.85	C

ATOM	325	CH2	TRP	B	116	7.541	-63.834	-40.527	1.00	32.27	C
ATOM	326	N	SER	B	117	2.231	-61.304	-41.338	1.00	21.35	N
ATOM	327	CA	SER	B	117	1.735	-62.573	-41.873	1.00	22.61	C
ATOM	328	C	SER	B	117	0.665	-62.383	-42.940	1.00	23.56	C
ATOM	329	O	SER	B	117	0.463	-63.262	-43.780	1.00	23.11	O
ATOM	330	CB	SER	B	117	1.167	-63.462	-40.756	1.00	20.72	C
ATOM	331	OG	SER	B	117	0.010	-62.889	-40.169	1.00	22.72	O
ATOM	332	N	LEU	B	133	11.788	-52.846	-25.860	1.00	23.38	N
ATOM	333	CA	LEU	B	133	11.903	-54.293	-26.020	1.00	24.54	C
ATOM	334	C	LEU	B	133	11.209	-54.833	-27.276	1.00	22.84	C
ATOM	335	O	LEU	B	133	11.784	-55.619	-28.027	1.00	21.86	O
ATOM	336	CB	LEU	B	133	11.328	-54.996	-24.786	1.00	25.48	C
ATOM	337	CG	LEU	B	133	11.388	-56.527	-24.780	1.00	27.50	C
ATOM	338	CD1	LEU	B	133	12.840	-56.984	-24.866	1.00	28.69	C
ATOM	339	CD2	LEU	B	133	10.735	-57.059	-23.509	1.00	28.04	C
ATOM	340	N	THR	B	134	9.975	-54.401	-27.499	1.00	21.72	N
ATOM	341	CA	THR	B	134	9.202	-54.860	-28.639	1.00	21.22	C
ATOM	342	C	THR	B	134	9.693	-54.326	-29.986	1.00	20.62	C
ATOM	343	O	THR	B	134	9.843	-55.091	-30.932	1.00	20.33	O
ATOM	344	CB	THR	B	134	7.716	-54.509	-28.449	1.00	20.99	C
ATOM	345	OG1	THR	B	134	7.257	-55.075	-27.210	1.00	20.94	O
ATOM	346	CG2	THR	B	134	6.872	-55.073	-29.600	1.00	20.64	C
ATOM	3608	N	LYS	B	136	12.595	-53.366	-30.809	1.00	21.46	N
ATOM	3609	CA	LYS	B	136	13.886	-53.949	-31.144	1.00	22.79	C
ATOM	3610	CB	LYS	B	136	14.713	-54.196	-29.879	1.00	24.70	C
ATOM	3611	CG	LYS	B	136	16.183	-54.424	-30.178	1.00	27.75	C
ATOM	3612	CD	LYS	B	136	16.998	-54.494	-28.902	1.00	30.17	C
ATOM	3613	CE	LYS	B	136	18.479	-54.671	-29.203	1.00	32.33	C
ATOM	3614	NZ	LYS	B	136	19.278	-54.641	-27.944	1.00	33.37	N
ATOM	3615	C	LYS	B	136	13.793	-55.229	-31.966	1.00	23.46	C
ATOM	3616	O	LYS	B	136	14.561	-55.407	-32.912	1.00	23.71	O
ATOM	347	N	TRP	B	137	12.868	-56.127	-31.633	1.00	21.78	N
ATOM	348	CA	TRP	B	137	12.753	-57.345	-32.424	1.00	22.06	C
ATOM	349	C	TRP	B	137	11.768	-57.202	-33.574	1.00	21.75	C
ATOM	350	O	TRP	B	137	11.936	-57.822	-34.623	1.00	21.76	O
ATOM	351	CB	TRP	B	137	12.361	-58.552	-31.553	1.00	21.20	C
ATOM	352	CG	TRP	B	137	10.990	-58.525	-30.922	1.00	20.23	C
ATOM	353	CD1	TRP	B	137	10.696	-58.231	-29.618	1.00	19.62	C
ATOM	354	CD2	TRP	B	137	9.748	-58.877	-31.544	1.00	18.68	C
ATOM	355	NE1	TRP	B	137	9.349	-58.385	-29.390	1.00	19.31	N
ATOM	356	CE2	TRP	B	137	8.743	-58.780	-30.555	1.00	18.97	C
ATOM	357	CE3	TRP	B	137	9.383	-59.270	-32.840	1.00	19.75	C
ATOM	358	CZ2	TRP	B	137	7.401	-59.058	-30.821	1.00	18.18	C
ATOM	359	CZ3	TRP	B	137	8.046	-59.549	-33.107	1.00	18.87	C
ATOM	360	CH2	TRP	B	137	7.072	-59.440	-32.099	1.00	18.94	C
ATOM	361	N	LEU	B	138	10.741	-56.381	-33.386	1.00	21.61	N
ATOM	362	CA	LEU	B	138	9.744	-56.188	-34.431	1.00	23.15	C
ATOM	363	C	LEU	B	138	10.384	-55.558	-35.676	1.00	23.07	C
ATOM	364	O	LEU	B	138	9.958	-55.801	-36.809	1.00	22.68	O
ATOM	365	CB	LEU	B	138	8.618	-55.305	-33.886	1.00	23.87	C
ATOM	366	CG	LEU	B	138	7.312	-55.155	-34.664	1.00	26.48	C
ATOM	367	CD1	LEU	B	138	6.672	-56.508	-34.915	1.00	25.34	C
ATOM	368	CD2	LEU	B	138	6.383	-54.267	-33.851	1.00	25.90	C
ATOM	3644	N	LYS	B	140	12.801	-56.332	-37.241	1.00	27.38	N
ATOM	3645	CA	LYS	B	140	13.279	-57.337	-38.182	1.00	28.05	C
ATOM	3646	CB	LYS	B	140	13.893	-58.501	-37.401	1.00	29.91	C
ATOM	3647	CG	LYS	B	140	15.134	-58.057	-36.635	1.00	31.62	C
ATOM	3648	CD	LYS	B	140	15.719	-59.149	-35.757	1.00	33.53	C
ATOM	3649	CE	LYS	B	140	16.974	-58.634	-35.055	1.00	34.46	C
ATOM	3650	NZ	LYS	B	140	17.692	-59.713	-34.320	1.00	36.17	N
ATOM	3651	C	LYS	B	140	12.254	-57.833	-39.212	1.00	27.83	C
ATOM	3652	O	LYS	B	140	12.602	-58.562	-40.142	1.00	27.80	O
ATOM	369	N	ILE	B	141	10.992	-57.445	-39.052	1.00	26.40	N
ATOM	370	CA	ILE	B	141	9.963	-57.818	-40.016	1.00	26.09	C
ATOM	371	C	ILE	B	141	9.316	-56.542	-40.530	1.00	25.81	C
ATOM	372	O	ILE	B	141	8.353	-56.586	-41.305	1.00	26.10	O

ATOM	373	CB	ILE	B	141	8.854	-58.721	-39.405	1.00	26.39	C
ATOM	374	CG1	ILE	B	141	8.298	-58.092	-38.127	1.00	26.45	C
ATOM	375	CG2	ILE	B	141	9.401	-60.118	-39.145	1.00	28.33	C
ATOM	376	CD1	ILE	B	141	7.136	-58.845	-37.549	1.00	26.95	C
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The following examples are presented for purposes of illustration only and are not intended to limit the scope of the invention in any way.

EXAMPLE 1

This example describes the crystallization of the *E. coli* MurG protein and the determination of the coordinates of the three-dimensional crystal structure. This example also describes the identification of the donor nucleotide binding site, the acceptor binding site and the membrane association site of the MurG protein.

Abstract

The 1.9 Å X-ray structure of a membrane-associated glycosyltransferase involved in peptidoglycan biosynthesis is reported. This enzyme, MurG, contains two α open sheet domains separated by a deep cleft. The C-terminal domain contains the UDP-GlcNAc binding site while the N-terminal domain contains the acceptor binding site and likely membrane association site. Combined with sequence data from other MurG homologs, this structure provides insight into the residues that are important in substrate binding and catalysis. We have also noted that a conserved region found in many UDP-sugar transferases maps to a α supersecondary structural motif in the donor binding region of MurG, an observation that is helpful in glycosyltransferase structure prediction.

Methods

Crystallization

E. coli MurG containing a C-terminal LEHHHHHH sequence was purified as described (Ha *et al.*, 1999) and concentrated to 10 mg ml⁻¹ in 20 mM Tris-HCl, pH 7.9/ 150 mM NaCl/ 50 mM EDTA. The protein concentrate was mixed with UDP-GlcNAc

in a 1:3 molar ratio. Crystals were grown at room temperature using the hanging-drop vapor-diffusion method by mixing equal volumes of protein with reservoir solution (0.1 M NaMES, pH 6.5/ 0.96 M $(\text{NH}_4)_2\text{SO}_4$ / 0.4% Triton X-100/ 10 mM DTT). Triclinic crystals with a typical size of 0.2 mm X 0.1 mm X 0.1 mm grew within a week. The crystals belong to the P1 space group, with two molecules per asymmetric unit. The cell dimensions are $a=60.613 \text{ \AA}$, $b=66.356 \text{ \AA}$, $c=67.902 \text{ \AA}$, $\alpha=64.294^\circ$, $\beta=83.520^\circ$, $\gamma=90.000^\circ$.

Data collection and processing

All data sets were collected at 100 K on previously flash frozen crystals. Crystals were equilibrated in a cryoprotectant buffer with 0.1 M NaMES, pH 6.5, 1.44 M $(\text{NH}_4)_2\text{SO}_4$, 0.4% Triton X-100, and 20% glycerol. Heavy-atom soaks were carried out in the same buffer containing one of the following heavy-atom solutions: 2 mM HgCl_2 , 1 mM $(\text{NH}_4)_2\text{WS}_4$, 1 mM $(\text{NH}_4)_2\text{OsBr}_6$. Crystals were flash-frozen in liquid nitrogen. HgCl_2 (form A derivative) and $(\text{NH}_4)_2\text{OsBr}_6$ derivative data were collected at an R-AXISIIIC imaging plate detector mounted on a Rigaku 200HB generator. Native, HgCl_2 (form B derivative), and $(\text{NH}_4)_2\text{WS}_4$ derivative diffraction data were collected at beam-line BioCARS-14B at the Advanced Photon Source, at wavelengths 1.0092 \AA , 0.9900 \AA and 1.2147 \AA respectively. Collection of data on the HgCl_2 derivative was initially designed for MAD phasing; however, the mercury derivative proved to be unstable to X-rays, and after a two-hour exposure to synchrotron radiation the form A derivative metamorphosed into a different mercury derivative (form B) that was suitable for MIR phasing. All the data were reduced using DENZO and SCALEPACK (Otwinowski & Minor, 1997), and processed with CCP4 programs (CCP4, 1994).

Structure determination and refinement

The structure was solved by multiple isomorphous replacement combined with anomalous scattering of mercuric derivatives (Table 1). Initial MIR phases calculated with program MLPHARE had a mean figure of merit of 0.44 to 2.5 \AA , and were improved by solvent flattening and histogram matching using DM. An MIR map was generated which had continuous electron density for most regions of the protein. A model was built with the program O (Jones *et al.*, 1991), and the structure was refined against 1.9 \AA data using energy minimization, simulated annealing and B-factor

refinement with the program CNS (Brunger *et al.*, 1998). The N-terminal six residues and the C-terminal His-tag had no electron density and were not included in this model. There was no electron density for UDP-GlcNAc.

Results and discussion

Overall fold

The crystal structure of *E. coli* MurG was solved by a combination of multiple isomorphous replacement and anomalous scattering, and refined to 1.9 Å resolution (Table 1).

Table 1. Summary of crystallographic and refinement data

Data set	Native	HgCl ₂ (form A derivative)	HgCl ₂ (form B derivative)	(NH ₄) ₂ WS ₄	(NH ₄) ₂ OsBi
Resolution (Å)	1.9	2.0	1.9	2.4	2.3
Observations	288,150	101,913	245,320	44,366	106,606
Unique reflections	65,567	53,391	65,581	27,950	36,443
R _{sym} ¹ (last shell)	0.032 (0.187)	0.043 (0.200)	0.042 (0.296)	0.031 (0.080)	0.056 (0.30)
I/σ (last shell)	41.9 (7.0)	20.4 (2.9)	29.0 (3.7)	24.6 (8.2)	19.6 (2.5)
Completeness (last shell)	97.7% (96.4%)	91.4% (66.6%)	97.4% (94.0%)	83.8% (62.0%)	94.3% (78.6%)
MIR analysis (40.0 - 2.5 Å)					
Mean isomorphous difference ²		0.163	0.130	0.068	0.134
Phasing power ³ (last shell)		1.09 (0.73)	0.57 (0.50)	0.61 (0.24)	0.61 (0.58)
R _{cullis} ⁴ (last shell)		0.81 (0.91)	0.94 (0.96)	0.92 (0.99)	0.94 (0.95)
Anomalous R _{cullis} ⁴ (last shell)		0.96 (1.00)	0.95 (1.00)		
Refinement statistics					
Resolution	40.0 - 1.9 Å		R. m. s. d. ⁷		
Reflections (F > 2σ)	61,989		Bonds (Å)		0.006
Protein atoms (a. u.)	5,280		Angles (°)		1.29
Water Atoms	298		Ramachandran plot ⁸		
Sulfate groups	1		Residues in most favored region		94.6%
R-factor ⁵	22.0%		Residues in additional allowed region		5.4%
R-free ⁶	24.7%				

¹R_{sym} = $\sum_i |I_i - \langle I \rangle| / \sum_i I_i$, where I_i is the intensity of a reflection, and $\langle I \rangle$ is the average intensity of that reflection.

²Mean isomorphous difference = $\sum |F_{PH} - F_P| / \sum F_{PH}$, where F_{PH} and F_P are the derivative and native structure factors respectively.

³Phasing power is the ratio of the mean calculated derivative structure factor to the mean lack of closure error.

⁴R_{cullis} is the mean residual lack of closure error divided by the dispersive or anomalous difference.

⁵R-factor = $\sum |F_{obs}| - |F_{calc}| / \sum |F_{obs}|$

⁶R-free is the R-factor calculated using 10% of the reflection data chosen randomly and omitted from the start of refinement.

⁷R. m. s. d., root-mean-square deviations from ideal bond lengths and bond angles.

⁸Calculated with program PROCHECK.

The structure consists of two domains separated by a deep cleft (Fig. 2a). Both domains exhibit an α/β open-sheet structure and have high structural homology despite minimal sequence homology (RMSD = 2.02 over 85 aligned C α atoms). The N-domain includes residues 7-163 and 341-357, and contains seven parallel β -strands and six α -helices, the last of which originates in the C-domain (Fig. 2b). The C-domain comprises residues 164-340 and contains six parallel β -strands and eight α -helices, including one irregular bipartite helix (α -link) that connects the N-domain to the first β -strand of the C-domain. The β -strands in both domains are ordered as for a typical Rossman fold. The N- and C-domains are joined by a short linker between the seventh β -strand of the N-domain and the α -link of the C-domain. This inter-domain linker and the peptide segment that joins the last helix of the C-domain to the last helix of the N-domain define the floor of the cleft between the two domains. The cleft itself is about 20 Å deep and 18 Å across at its widest point. Contacts < 4 Å across the cleft are limited primarily to interactions between residues from C-25 to the loop connecting N-25 to N-25.

The α/β open-sheet motif (Rossman fold) adopted by both the N- and C-domains of MurG is characteristic of domains that bind nucleotides (Branden & Tooze, 1998). Classical Rossman domains typically contain at least one conserved glycine rich motif, with the consensus sequence GXGXXG, located at a turn between the carboxyl end of one β -strand and the amino terminus of the adjacent α -helix (Baker *et al.*, 1992). This motif is involved in binding the negatively charged phosphates (Carugo & Argos, 1997). There are three glycine rich loops (G loops) in *E. coli* MurG (Fig. 3a) that may be variants on the phosphate binding loops found in other dinucleotide binding proteins (see below).

Sequence homology

Amino acid sequences for eighteen MurG homologs are now available. The sequence similarity between *E. coli* MurG and homologs from other bacterial strains ranges from less than 30% to more than 90% depending on the evolutionary relationship between the organisms. In all MurG homologs, however, there are several invariant residues. Fig. 3a shows a sequence alignment for a subset of MurG homologs with the invariant and

highly conserved residues indicated. These residues, which include the three G loops, have been highlighted in the *E. coli* MurG structure (Fig. 3b). Almost all of the invariant residues are located at or near the cleft between the two domains. Two of the G loops are found in the N domain (between N-21/N-21 and N-24/N-24) and one is found in the C-domain (between C-21/C-21). The strict conservation of the highlighted residues among different bacterial strains, and their location as determined from the *E. coli* MurG structure, implicates them in substrate binding and catalytic activity.

Structural homology reveals the donor binding site

The three-dimensional backbone structure of *E. coli* MurG was compared to known protein structures, including the three other NDP-glycosyltransferase structures that have been reported (Charnok & Davies, 1999; Gastinel *et al.*, 1999; Vrielink *et al.*, 1994). The C-terminal domain was found to have significant structural homology (RMSD= 2.218 Å for 89 aligned C α atoms) to the C-terminal domain of phage T4 β -glucosyltransferase (BGT), an enzyme that catalyzes the glucosylation of hydroxymethyl-cytosines in duplex DNA. A co-crystal structure of BGT with UDP bound in the C-terminal domain reveals the topology of the UDP binding pocket and also shows important contacts to the nucleotide (Moréra *et al.*, 1999; Vrielink *et al.*, 1994). These contacts include: a) hydrogen bonds from the backbone amide of I238 to the N3 and O4 positions of the base; b) hydrogen bonds between the carboxyl side chain of E272 and the O2' and O3' hydroxyls of the ribose ring; and c) contacts from a GGS motif in the loop following the first β -strand of the C domain to the alpha phosphate of UDP. The structurally homologous C-domain of MurG contains a topologically similar pocket (Fig. 4a). Furthermore, even though the two domains share only 11% sequence identity overall, there are identical residues in the same spatial location in *E. coli* MurG and in BGT. Based on this comparison, we have concluded that the C-domain of *E. coli* MurG is the UDP-GlcNAc binding site.

We have docked UDP-GlcNAc into the C-domain of *E. coli* MurG using the information on how UDP binds to BGT as a guide. As shown in Figure 4b, the uracil is held in place by contacts from the N3 and O4 atoms to the backbone amide of I245. The O2' and O3' hydroxyls on the ribose sugar are within hydrogen bonding distance of the invariant glutamate residue (E269) in the middle of helix C-24. The conserved GGS

motif in G loop 3 is positioned to contact the alpha phosphate. When these contacts are made, the UDP-GlcNAc substrate fits nicely into a pocket in the C-domain, where it is surrounded by many of the invariant residues identified through sequence analysis of other MurG homologs. It is possible to propose roles for some of these invariant residues from the model. For example, the side chain of R261 can be rotated to contact the second phosphate; this contact may help explain why UDP binds significantly better to MurG than UMP. We propose that R261 plays an important role in catalysis by stabilizing the UDP leaving group via electrostatic interactions. The side chain of Q289 is within hydrogen bonding distance of the C4 hydroxyl of the GlcNAc sugar. This contact may explain why MurG can discriminate between UDP-GlcNAc and its C4 axial isomer, UDP-GalNAc (Ha *et al.*, 1999).

The acceptor binding site

Structural considerations suggest that the primary acceptor binding site is located in the N-terminal domain of MurG. This domain contains three highly conserved regions, two of which are glycine-rich loops that face the cleft (Fig 3a and 4c). These G loops are reminiscent of the phosphate binding loops found in other nucleotide binding proteins, and are most likely involved in binding to the diphosphate on Lipid I. The N-termini of the helices following each G loop form opposite walls of a small pocket between the G loops. The helix dipoles create a positively charged electrostatic field in the pocket that can stabilize the negative charged diphosphates. When the diphosphate of the acceptor is anchored in the pocket created by the G-loops, the MurNAc sugar emerges into the cleft between domains and the C4 hydroxyl can be directed towards the anomeric carbon of the GlcNAc for attack on the face opposite the UDP leaving group. The third conserved region in the N domain spans the loop from the end of N-75 to the middle of N-75. Kinetic analysis of mutants is required to evaluate the roles of these residues (Ha *et al.*, 1999; Men *et al.*, 1998).

Proposed membrane association site

MurG associates with the cytoplasmic surface of bacterial membranes where it couples a soluble donor sugar to the membrane anchored acceptor sugar, Lipid I. Analysis of the *E. coli* MurG structure shows that there is a hydrophobic patch consisting of residues

I75, L79, F82, W85 and W116 in the N-domain, which is surrounded by basic residues (K72, K140, K69, R80, R86, R89). We propose that this is the membrane association site and that association involves both hydrophobic and electrostatic interactions with the negatively charged bacterial membrane. The location of this patch in MurG is also consistent with the proposed acceptor binding site: membrane association at this patch would bring the two N-terminal G loops close to the membrane surface where the diphosphate portion of the acceptor is located (Fig. 4c). Moreover, the cleft between the two domains would remain accessible, consistent with the biochemical requirement that the soluble UDP-GlcNAc donor be able to find its binding site from the cytoplasm.

Implications for other glycosyltransferases

Glycosyltransferases that utilize an activated nucleotide sugar as a donor comprise a large family of enzymes in both prokaryotes and eukaryotes, and they play central roles in many important biological processes (Dennis *et al.*, 1999; Koya *et al.*, 1999; Verbert & Cacan, 1999). Glycosyltransferases are typically classified according to the nucleotide sugar they utilize, and it has frequently been noted that there is no significant sequence homology even among glycosyltransferases in the same family. This has made it difficult to identify common structural features and residues important in binding and catalysis. There are only three other glycosyltransferase structures available, and although none of them shows any sequence homology to MurG, a structural comparison indicates that one of them, BGT, contains a related donor binding site.

In addition to this structural homology, we have identified a strikingly similar sequence motif in the MurG family and certain other UDP-glycosyltransferase families. This sequence motif spans about a thirty amino acid stretch in the C-domain of MurG and includes most of the invariant residues found in that domain. As shown in Figure 3a, a similar motif is found in the UDP-glucuronosyltransferases (Mackenzie, 1990). Certain residues are identical, including a number of prolines and glycines, and the spacing between them is invariant. This suggests that the UDP-glucuronosyltransferases contain a region of ??? supersecondary structure that is involved in a similar function as the corresponding region in MurG (Fig. 3c). This region binds the donor sugar. By analyzing the similarities and differences between the conserved residues in this subdomain in the MurG family and other UDP-glycosyltransferase families, it may be

possible to identify – and perhaps alter - residues that are involved in determining donor selectivity. We note that it would be useful to be able to manipulate donor specificity because it would extend the utility of glycosyltransferases as reagents for glycosylation of complex molecules. Altered glycosyltransferases could also be useful for remodeling cell surfaces and for probing the biological roles of particular carbohydrate structures.

Conclusion

This first structure of a member of the MurG family of glycosyltransferases lays the groundwork for further mechanistic and structural investigations, which may lead to the design of inhibitors and perhaps even new antibiotics. The work also shows that there can be conserved subdomains even in very different glycosyltransferase families. Information on conserved subdomains will be useful for structure prediction and may help guide experiments directed towards changing substrate specificity.

EXAMPLE 2

This example describes a method of isolating the C-terminal domain of the *E. coli* MurG protein, expressing the domain in *E. coli* cells and utilizing nuclear magnetic resonance (NMR) to determine the ability of compounds to bind.

MurG can also be used to determine the ability of a chemical compound to bind to the C domain by a) determining the start of c domain based on the MurG crystal structure; b) independently expressing the C domain; and c) using NMR methods to identify binding site and/or bound conformation of ligand. The same procedure is used for the acceptor binding domains.

NMR methods are used to identify the protein binding sites and screen for ligands that bind. The MurG C-terminal domain region of the protein has been expressed independently. The C domain has a much lower molecular weight than the full-length protein. Therefore, the expression of the C domain results in much sharper NMR peaks which will facilitate the NMR interpretation. Also the protein chemical shifts are very sensitive to their environment. Binding of a compound will introduce local environment changes, thus changing the proton chemical shifts. In this way, residues involved in the binding can be differentiated easily from other amino acid residues not involved in

binding a ligand. This method has also been used to identify ligands that bind to low molecular weight drug targets (i.e., small proteins).

Relevant references to NMR techniques are: Discovering high-affinity ligands for proteins: SAR by NMR, S. Shuker, P. Hajduk, R. Meadows, and S. Fesik, Science 274, 1531 (1996); Lin Y, Nageswara Rao BD. Structural characterization of adenine nucleotides bound to Escherichia coli adenylate kinase. 1. Adenosine conformations by proton two-dimensional transferred nuclear Overhauser effect spectroscopy. Biochemistry. 2000 Apr 4;39(13):3636-46; and Fejzo J, et al., Chem Biol 1999 Oct;6(10):755-69 (incorporated herein by reference).

The SHAPES strategy is also useful for NMR identification of binding residues, ligands and drug discover which is an NMR-based approach for lead generation in drug discovery. Recently, it has been shown that nuclear magnetic resonance (NMR) may be used to identify ligands that bind to low molecular weight protein drug targets. Recognizing the utility of NMR as a very sensitive method for detecting binding, we have focused on developing alternative approaches that are applicable to larger molecular weight drug targets and do not require isotopic labeling. A new method for lead generation (SHAPES) uses NMR to detect the binding of a limited but diverse library of small molecules to a potential drug target. The compound scaffolds are derived from shapes most commonly found in known therapeutic agents. NMR detection of low (microM-mM) affinity binding is achieved using either differential line broadening or transferred NOE (nuclear Overhauser effect) NMR techniques. The SHAPES method for lead generation by NMR is useful for identifying potential lead classes of drugs early in a drug design program, and is easily integrated with other discovery tools such as virtual screening, high-throughput screening and combinatorial chemistry.

EXAMPLE 3

This example describes the method of using the three-dimensional structure of *E. coli* MurG to determine the crystal structures of its mutant, enzyme-ligand complex, and MurG homologs, which share the same folding motif.

First, a crystalline form of the new protein or the protein complex should be obtained. The *E. coli* MurG mutants should be crystallized in a condition very similar to

what we have showed in the method section. The protein-ligand complex can be obtained by soaking the protein crystals in a ligand-containing buffer. Other MurG homologs can be expressed in a His-tagged fashion and purified using affinity column. Presumably they can be crystallized in a similar way using a detergent as the additive. Next, the diffraction data should be collected and processed. After the data collection, the molecular replacement method is used to determine the unknown structure. Either the whole *E. coli* MurG protein or one single domain can serve as a search model. This search model can be rotated and translated until the correct orientation is located in the unit cell of this unknown structure. The search model may only represent part of the contents of the asymmetric unit. However, the location of the first model is now already available. While the first location of the search model is fixed, the second round of translation search can be carried out to search more molecules or domains in the asymmetric unit cell. The phases from the final model generated by molecular replacement can be used to calculate the electron density map. Finally, a model is built based on the electron density map, and the model needs to be refined using program CNS or XPLOR.

EXAMPLE 4

This example describes the method of using the three-dimensional coordinate structure of *E. coli* MurG to produce a protein fragment that can be used in an NMR-based lead discovery program. The crystal structure reveals the boundaries of the C domain and permits us to design a gene containing only the C domain from the gene containing both domains. The C domain starting at residue 164 and ending at residue 340 was cloned into an expression vector to generate a C-terminal His tag fusion. It was over-expressed in *E. coli* cells and purified by affinity column. The protein was shown to be monomeric by size exclusion chromatography and to be soluble at least up to 0.15 mM, a concentration more than adequate for NMR analysis. C domains from other Murg homologues can be similarly expressed and used.

EXAMPLE 5

This example describes the co-crystallization of a MurG protein with a ligand. A MurG-ligand complex is formed by either co-crystallizing MurG protein with appropriate ligand or soaking the MurG crystals in buffers containing appropriate ligand. Co-crystallization is done by pre-mixing the protein sample with a certain amount of substrate or substrate analogs. Then the hanging drop method is used to produce crystals as described infra.

Alternatively, ligands are incorporated into the crystals by soaking the protein crystals in the ligand containing buffer for a period of time to allow for infiltration into the crystal. The time ranges from a couple of hours to a couple of days. The concentration of ligand in the buffer ranges from several milimolar to several hundred mili molar.

DEPOSIT OF COORDINATES

The crystal structure three-dimensional coordinates of the *E. coli* MurG as set forth in Table 1 were deposited with the Protein Data Bank and have been assigned the indicated ID Code (Accession No.) 1F0K.

Although the invention is described in detail with reference to specific embodiments thereof, it will be understood that variations which are functionally equivalent are within the scope of this invention. Indeed, various modifications of the invention in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and accompanying drawings. Such modifications are intended to fall within the scope of the appended claims.

Various publications are cited herein, the disclosures of which are incorporated by reference in their entireties.

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WHAT IS CLAIMED IS:

1. A composition comprising the *E. coli* MurG protein in crystalline form.
2. A composition comprising a MurG protein in crystalline form.
3. A three dimensional structure of the crystalline form of an *E. coli* MurG protein, wherein the three dimensional structure substantially conforms to the atomic coordinates represented in Table 1.
4. A three dimensional structure of the crystalline form of a MurG protein, wherein the three dimensional structure substantially conforms to the atomic coordinates represented in Table 1.
5. A three dimensional structure of the α -carbon backbone of the crystalline form of an *E. coli* MurG protein, wherein the three dimensional structure substantially conforms to the atomic coordinates represented in Table 2.
6. A three dimensional structure of the α -carbon backbone and conserved amino acid residues of an *E. coli* MurG protein, wherein the three dimensional structure substantially conforms to the atomic coordinates represented in Table 3.
7. A three dimensional structure of a donor nucleotide binding site of a MurG protein wherein the three dimensional structure of the donor nucleotide binding site substantially conforms to the atomic coordinates in Table 4.
8. The three dimensional structure of claim 7, wherein the donor nucleotide is UDP-GlcNAc.
9. A three dimensional structure of an acceptor binding site of a MurG protein substantially conforming to the atomic coordinates in Table 5.
10. A three dimensional structure of a membrane association site of a MurG protein substantially conforming to the atomic coordinates in Table 6.
11. A three-dimensional computer image of the three-dimensional structure of a MurG protein.
12. The image of claim 11, wherein the structure substantially conforms with the three-dimensional coordinates listed in Table 1.
13. The image of claim 11, wherein the computer image is that is generated when a set of three-dimensional coordinates comprising the three-dimensional coordinates represented in Table 1 are analyzed on a computer using a graphical display software

program to create an electronic file of the image and visualizing the electronic file on a computer capable of representing the electronic file as a three-dimensional image.

14. The image of claim 11, wherein the three-dimensional computer image is represented by a two dimensional image selected from the group consisting of Fig. 2a, 3a, or 4c.

15. The image of claim 11, wherein the three-dimensional computer image is used to design a compound.

16. A three dimensional computer image of the three dimensional structure of the α -carbon backbone of a MurG protein.

17. The image of claim 16, wherein the structure substantially conforms with the three-dimensional coordinates listed in Table 2.

18. The image of claim 16, wherein the computer image is that is generated when a set of three-dimensional coordinates comprising the three-dimensional coordinates represented in Table 2 are analyzed on a computer using a graphical display software program to create an electronic file of the image and visualizing the electronic file on a computer capable of representing the electronic file as a three-dimensional image.

19. The image of claim 16, wherein the three-dimensional computer image is used to design a compound.

20. A three dimensional image of the three dimensional image of an α -carbon backbone and conserved amino acid residues of a MurG protein.

21. The image of claim 20, wherein the structure substantially conforms with the three-dimensional coordinates in Table 3.

22. The image of claim 21, wherein the computer image is that is generated when a set of three-dimensional coordinates comprising the three-dimensional coordinates represented in Table 3 are analyzed on a computer using a graphical display software program to create an electronic file of the image and visualizing the electronic file on a computer capable of representing the electronic file as a three-dimensional image.

23. The image of claim 21, wherein the three-dimensional computer image is used to design a compound.

24. A three-dimensional computer image of the three-dimensional structure of a donor nucleotide binding site of a MurG protein.

25. The image of claim 24, wherein the structure substantially conforms with the three-dimensional coordinates in Table 4.
26. The image of claim 24, wherein the computer image is that is generated when a set of three-dimensional coordinates comprising the three-dimensional coordinates represented in Table 4 are analyzed on a computer using a graphical display software program to create an electronic file of the image and visualizing the electronic file on a computer capable of representing the electronic file as a three-dimensional image.
27. The image of claim 24, wherein the three-dimensional computer image is represented by a two dimensional image selected from the group consisting of Fig. 3c, 4a or 4b.
28. The image of claim 24, wherein the three-dimensional computer image is used to design a compound.
29. A three-dimensional computer image of the three-dimensional structure of an acceptor binding site of a MurG protein.
30. The image of claim 29, wherein the structure substantially conforms with the three-dimensional coordinates Table 5.
31. The image of claim 29, wherein the computer image is that is generated when a set of three-dimensional coordinates comprising the three-dimensional coordinates represented in Table 5 are analyzed on a computer using a graphical display software program to create an electronic file of the image and visualizing the electronic file on a computer capable of representing the electronic file as a three-dimensional image.
32. The image of claim 29, wherein the three-dimensional computer image is represented by the two dimensional image of Fig. 4a.
33. The image of claim 29, wherein the three-dimensional computer image is used to design a compound.
34. A three-dimensional computer image of the three-dimensional structure of a membrane association site of a MurG protein.
35. The image of claim 34, wherein the structure substantially conforms with the three-dimensional coordinates Table 6.
36. The image of claim 34, wherein the computer image is that is generated when a set of three-dimensional coordinates comprising the three-dimensional coordinates represented in Table 6 are analyzed on a computer using a graphical display software

program to create an electronic file of the image and visualizing the electronic file on a computer capable of representing the electronic file as a three-dimensional image.

37. The image of claim 34, wherein the three-dimensional computer image is represented by the two dimensional image of Fig. 4a.

38. The image of claim 34, wherein the three-dimensional computer image is used to design a compound.

39. A computer readable medium encoded with a set of three-dimensional coordinates of a MurG protein having a three-dimensional structure that substantially conforms to the atomic coordinates of Table 1, wherein using a graphical display software program, the three-dimensional coordinates create an electronic file that can be visualized on a computer capable of representing said electronic file as a three dimensional image.

40. A computer readable medium encoded with a set of three-dimensional coordinates of an α -carbon backbone of a MurG protein having a three-dimensional structure that substantially conforms to the atomic coordinates of Table 2, wherein using a graphical display software program, the three-dimensional coordinates create an electronic file that can be visualized on a computer capable of representing said electronic file as a three dimensional image.

41. A computer readable medium encoded with a set of three-dimensional coordinates of an α -carbon backbone and conserved amino acid residues of a MurG protein having a three-dimensional structure that substantially conforms to the atomic coordinates of Table 3, wherein using a graphical display software program, the three-dimensional coordinates create an electronic file that can be visualized on a computer capable of representing said electronic file as a three dimensional image.

42. A computer readable medium encoded with a set of three-dimensional coordinates of a donor nucleotide binding site of a MurG protein having a three-dimensional structure that substantially conforms to the atomic coordinates of Table 4, wherein using a graphical display software program, the three-dimensional coordinates create an electronic file that can be visualized on a computer capable of representing said electronic file as a three dimensional image.

43. A computer readable medium encoded with a set of three-dimensional coordinates of an acceptor binding site of a MurG protein having a three-dimensional structure that substantially conforms to the atomic coordinates of Table 5, wherein using

a graphical display software program, the three-dimensional coordinates create an electronic file that can be visualized on a computer capable of representing said electronic file as a three dimensional image..

44. A computer readable medium encoded with a set of three-dimensional coordinates of a membrane association site of a MurG protein having a three-dimensional structure that substantially conforms to the atomic coordinates of Table 5, wherein using a graphical display software program, the three-dimensional coordinates create an electronic file that can be visualized on a computer capable of representing said electronic file as a three dimensional image.

45. A method for identifying a potential inhibitor of a UDP-glycosyltransferase enzyme, the method comprising the steps of:

a. using a three-dimensional structure of UDP-glycosyltransferase enzyme as defined by atomic coordinates of UDP-glycosyltransferase enzyme according to FIG. 5;

b. employing said three-dimensional structure to design or select said potential inhibitor;

c. synthesizing said potential inhibitor; and

d. contacting said potential inhibitor with said UDP-glycosyltransferase enzyme in the presence of a substrate to test the ability of said potential inhibitor to inhibit said UDP-glycosyltransferase enzyme.

46. The method according to claim 45, wherein said potential inhibitor is selected from a database.

47. The method according to claim 45, wherein said potential inhibitor is designed de novo.

48. The method according to claim 45, wherein said potential inhibitor is designed from a known inhibitor.

49. The method according to claim 45, wherein said step of employing said three-dimensional structure to design or select said potential inhibitor comprises the steps of:

a. identifying chemical entities or fragments capable of associating with UDP-glycosyltransferase enzyme; and

b. assembling the identified chemical entities or fragments into a single molecule to provide the structure of said potential inhibitor.

50. The method according to claim 45, wherein the potential inhibitor is a competitive inhibitor of mutant UDP-glycosyltransferase enzyme.

51. The method according to claim 45, wherein said potential inhibitor is a non-competitive or uncompetitive inhibitor of mutant UDP-glycosyltransferase enzyme.

52. A model of a UDP-glycosyltransferase, wherein the model represents a three-dimensional structure that substantially conforms to the atomic coordinates of Table 1.

53. The model of claim 52, wherein the structure substantially conforms to the atomic coordinates and B-values represented by Table 1.

54. The model of claim 52, wherein the structure is monomeric.

55. The model of claim 52, wherein at least about 50% of the structure has an average root-mean-square deviation (RMSD) of less than about 2.5 Å for backbone atoms in secondary structure elements in each domain of the structure.

56. The model of claim 52, wherein the MurG protein comprises an amino acid sequence that is at least about 25% identical to the amino acid sequence of the *E. coli* MurG protein.

57. The model of claim 52, wherein the MurG protein comprises an amino acid sequence that is at least about 40% identical to the amino acid sequence of the *E. coli* MurG protein.

58. The model of claim 52, wherein the MurG protein comprises an amino acid sequence that is at least about 60% identical to the amino acid sequence of the *E. coli* MurG protein.

59. The model of claim 52, wherein the MurG protein comprises an amino acid sequence selected from the group consisting of the amino acid sequence of a MurG protein from *Escherichia coli*, *Bacillus subtilis*, *Aquifex aeolicus*, *Borrelia burgdorferi*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Enterococcus faecalis*, *Enterococcus hirae*, *Haemophilus influenzae*, *Helicobacter pylori* J99, *Helicobacter pylori*, *Mycobacterium tuberculosis*, *Porphyromonas gingivalis*, *Rickettsia prowazekii*, *Streptomyces coelicolor*, *Streptomyces collinus*, *Streptococcus pneumoniae*, *Synechocystis* sp. (strain PCC6803), *Thermotoga maritime*, and *Treponema pallidum*, a mutant of any of the amino acid sequences, and a variants of any of the amino acid sequences.

60. The model of claim 52, wherein the MurG protein comprises an amino acid sequence selected from the group consisting of the amino acid sequences of MurG proteins as deposited in the NCBI database and identified with Accession Nos. CAB51993, A71316, E70579, C71699, F70195, A43727, JC1275, BVECMG, CEECAM, O83535, Q9ZK59, CAB85280, AAF39020, BAA18775, AAD26629, CAB73295, P37585, Q9ZHA9, Q9ZHDC0, Q9ZBA5, Q9X4H4, Q9WY74, P74657, O06224, Q9Z702, O84766, O69552, J67238, O51708, O25770, O07670, O07109, P45065, CAB66324, AAC68356, AAF06830, P18579, P17443, P17952, P16457, P07862, AAE23178, AAD53936, CAA18668, CAA38869, CAA38868, CAA38867, CAA38866, AAD08196, BAA01453, BAA01455, BAA01454, AAD19042, CAA45558, CAA74235, AAD10537, AAD06652, AAC95450, CAA14869, AAC73201, AAC65509, AAC67113, AAC45636, CAB08640, AAC22793, AAC07193, BAA24357, CAB13395, BAA01355, AAB35538, 1904153C, 1808265B, 1808265A, CAA36866, CAA36869, CAA36868, CAA36867, CAA36776, and AAA99436.

61. The model of claim 52, wherein the MurG protein comprises an amino acid sequence obtained from an organism selected from the group consisting of bacteria, small pathogenic organisms, cyano bacteria, higher-order bacteria, spirochetes and thermal stable bacteria.

62. The model of claim 52, wherein the MurG protein comprises an amino acid sequence obtained from an organism selected from the group consisting of *Escherichia coli*, *Bacillus subtilis*, *Aquefex aeolicus*, *Borrelia burgdorferi*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Enterococcus faecalis*, *Enterococcus hirae*, *Haemophilus influenzae*, *Helicobacter pylori* J99, *Helicobacter pylori*, *Mycobacterium tuberculosis*, *Porphyromonas gingivalis*, *Rickettsia prowazekii*, *Streptomyces coelicolor*, *Streptomyces collinus*, *Streptococcus pneumoniae*, *Synechocystis* sp. (strain PCC6803), *Thermotoga maritima*, and *Treponema pallidum*.

63. The model of claim 52, wherein the MurG protein is a structural homologue of the *E. coli* MurG protein.

64. The model of claim 52, wherein the structure comprises an n-terminal and C-terminal domain connected by a covalent peptide linker, and wherein each domain has an alpha/beta fold.

65. The model of claim 52, wherein the RMSD is less than 2.5 Å over at least 80 aligned C-alpha atoms in each domain.

66. The model of claim 52, wherein the N-terminal domain comprises two glycine rich loops.
67. The model of claim 66, wherein the amino acid sequence of the two glycine rich loops comprises GGTGGH and G-GGYVSG.
68. The model of claim 52, wherein the C-terminal domain comprises one glycine rich loop.
69. The model of claim 68, wherein the glycine rich loop comprises the amino acid sequence GGSQGAR or GGS-GAR.
70. The model of claim 52, wherein the atomic coordinates are generated by the method comprising the steps of:
- providing a MurG protein in crystalline form;
 - generating an electron-density map of the crystalline MurG protein; and
 - analyzing the electron-density map to produce the atomic coordinates.
71. The model of claim 70, wherein the crystalline MurG protein is produced by a method comprising the steps of:
- combining MurG protein with UDP-GlcNAc, and
 - inducing crystal formation to produce said crystalline MurG protein.
72. The model of claim 70, wherein the crystalline MurG protein is produced by the hanging drop method in which MurG in buffer is at a concentration of at least 5 ug/ml and is combined with a reservoir solution and crystallizes.
73. The model of claim 72, wherein the buffer has a pH range from about 6.5 to about 9.0, and a buffer concentration range from about 10 mM to about 200 mM.
74. The model of 73, wherein the buffer is a Tris or a Hepes buffer, having a pH from about 7.0 to about 8.5.
75. The model of 74, wherein the buffer has a pH of about 7.9.
76. The model of claim 73, wherein the buffer further comprises at least one salt, chelating agent, or reducing agent.
77. The model of claim 72, wherein the reservoir solution has a pH range from about 5.0 to about 9.0 and the buffer concentration ranges from about 10 mM to about 1M.
78. The model of claim 77, wherein the reservoir solution further comprises at least one suitable precipitant, a detergent, and a reducing agent.
79. The model of claim 78, wherein the reservoir solution comprises a NaMES or sodium citrate buffer having a pH from about 6.0 to about 7.0.

80. The model of claim 79, wherein the buffer has a pH of about 6.5.
81. The model of claim 78, wherein the precipitant is selected from the group consisting of ammonium sulfate and sodium potassium tartrate.
82. The model of 78, wherein the detergent is TritonX-100.
83. The model of 78, wherein the reducing agent is DTT, DTE or beta-mercaptoethanol.
84. The model of claim 71, wherein the MurG protein and the UDP-GlcNAc are in a 1:3 molar ratio.
85. The model of claim 71, wherein the buffer comprises 0.1 M NaMES, pH6.5, 0.9M (NH₄)₂SO₄, 0.4% TRITON X-100®, and 10 mM dithiothreitol (DTT).
86. The model of claim 71, wherein the step of generating an electron-density map comprises analyzing the crystalline MurG protein by X-ray diffraction.
87. The model of claim 70, wherein the model is a computer image generated by a computer-readable medium encoded with a set of three-dimensional coordinates of the three-dimensional structure, wherein, using a graphical display software program, the three-dimensional coordinates create an electronic file that can be visualized on a computer capable of representing the electronic file as a three-dimensional image.
88. A model of a donor nucleotide binding site of a UDP-glycosyltransferase (MurG) protein, wherein the model represents a three-dimensional structure that substantially conforms to the atomic coordinates of Table 4.
89. The model of claim 88, wherein the donor nucleotide binding site is located within the MurG C-terminal domain.
90. The model of claim 88, wherein the structure substantially conforms to the atomic coordinates and B-values of Table 4.
91. The model of claim 88, wherein at least about 50% of the structure has an average root-mean-square (RMSD) of less than about 2.5Å for the conserved amino acid residues for the donor nucleotide binding site of the E. coli MurG.
92. The model of claim 88, wherein the donor nucleotide binding site comprises an amino acid sequence that is at least about 70% identical to the conserved amino acid residues of the donor nucleotide binding site of E. coli MurG.
93. The model of claim 88, wherein the donor nucleotide binding site comprises an amino acid sequence that is at least about 80% identical to the conserved amino acid residues of the donor nucleotide binding site of the E. coli MurG.

94. The model of claim 88, wherein the donor nucleotide binding site comprises an amino acid sequence that is at least about 90% identical to the conserved amino acid residues of the donor nucleotide binding site of the E. coli MurG.

95. The model of claim 88, wherein the donor nucleotide binding site comprises an amino acid sequence that is at least about 95% identical to the conserved amino acid residues of the donor nucleotide binding site of the E. coli MurG.

96. The model of claim 88, wherein the atomic coordinates are generated by a method comprising the steps of:

- a) providing a Murg protein in a crystalline form;
- b) generating an electron-density map of said crystalline MurG protein; and
- c) analyzing the electron-density map to produce the atomic coordinates.

97. The model of claim 88, wherein the model is a computer image generated by a computer-readable medium encoded with a set of three-dimensional coordinates of the three-dimensional structure, wherein, using a graphical display software program, the three-dimensional coordinates create an electronic file that can be visualized on a computer capable of representing the electronic file as a three-dimensional image.

98. A model of an acceptor binding site of a UDP-glycosyltransferase (MurG) protein, wherein the model represents a three-dimensional structure that substantially conforms to the atomic coordinates of Table 5.

99. The model of claim 98, wherein the structure substantially conforms to the atomic coordinates and B-values of Table 5.

100. The model of claim 98, wherein at least about 50% of the structure has an average root-mean-square (RMSD) of less than about 1.5 Å for the conserved amino acid residues in the acceptor binding site.

101. The model of claim 98, wherein the acceptor binding site comprises an amino acid sequence that is at least about 70% identical to the conserved amino acid residues of the acceptor binding site of E. coli MurG.

102. The model of claim 98, wherein the acceptor binding site comprises an amino acid sequence that is at least about 80% identical to the conserved amino acid residues of the acceptor binding site of E. coli MurG.

103. The model of claim 98, wherein the acceptor binding site comprises an amino acid sequence that is at least about 90% identical to the conserved amino acid residues of the E. coli MurG.

104. The model of claim 98, wherein the acceptor binding site comprises an amino acid sequence that is at least about 95% identical to the conserved amino acid residues of the acceptor binding site of the *E. coli* MurG.

105. The model of claim 98, wherein the acceptor binding site comprises an amino acid sequence that is at least about 70% identical to the amino acid sequence selected from the group consisting of *Escherichia coli*, *Bacillus subtilis*, *Aquifex aeolicus*, *Borrelia burgdorferi*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Enterococcus faecalis*, *Enterococcus hirae*, *Haemophilus influenzae*, *Helicobacter pylori* J99, *Helicobacter pylori*, *Mycobacterium tuberculosis*, *Porphyromonas gingivalis*, *Rickettsia prowazekii*, *Streptomyces coelicolor*, *Streptomyces collinus*, *Streptococcus pneumoniae*, *Synechocystis* sp. (strain PCC6803), *Thermotoga maritime*, and *Treponema pallidum*.

106. The model of claim 98, wherein the atomic coordinates are generated by the method comprising the steps of:

- a) providing a MurG protein in a crystalline form;
- b) generating an electron-density map of said crystalline MurG protein; and
- c) analyzing the electron-density map to produce the atomic coordinates.

107. The model of claim 98, wherein the model is a computer image generated by a computer-readable medium encoded with a set of three-dimensional coordinates of the three-dimensional structure, wherein, using a graphical display software program, the three-dimensional coordinates create an electronic file that can be visualized on a computer capable of representing the electronic file as a three-dimensional image.

108. A model of a membrane association site of a UDP-glycosyltransferase (MurG) protein, wherein the model represents a three-dimensional structure that substantially conforms to the atomic coordinates of Table 6.

109. The model of claim 108, wherein the structure substantially conforms to the atomic coordinates and B-values of Table 4.

110. The model of claim 108, wherein at least about 50% of the structure has an average root-mean-square (RMSD) of less than about 1.5 Å for conserved amino acid residues in the *E. coli* membrane association site.

111. The model of claim 108, wherein the membrane association site comprises an amino acid sequence that is at least about 70% identical to the conserved amino acid residues of the membrane association site of *E. coli* MurG.

112. The model of claim 108, wherein the membrane association site comprises an amino acid sequence that is at least about 80% identical to the conserved amino acid residues of the membrane association site of the *E. coli* MurG.

113. The model of claim 108, wherein the membrane association site comprises an amino acid sequence that is at least about 90% identical to the conserved amino acid residues of the membrane association site of the *E. coli* MurG.

114. The model of claim 108, wherein the membrane association site comprises an amino acid sequence that is at least about 95% identical to the conserved amino acid residues of a membrane association site of the *E. coli* MurG.

115. The model of claim 108, wherein the membrane association site comprises an amino acid sequence that is at least about 70% identical to the amino acid sequence from organisms selected from the group consisting of *Escherichia coli*, *Bacillus subtilis*, *Aquifex aeolicus*, *Borrelia burgdorferi*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Enterococcus faecalis*, *Enterococcus hirae*, *Haemophilus influenzae*, *Helicobacter pylori* J99, *Helicobacter pylori*, *Mycobacterium tuberculosis*, *Porphyromonas gingivalis*, *Rickettsia prowazekii*, *Streptomyces coelicolor*, *Streptomyces collinus*, *Streptococcus pneumoniae*, *Synechocystis* sp. (strain PCC6803), *Thermotoga maritime*, and *Treponema pallidum*.

116. The model of claim 108, wherein the model is a computer image generated by a computer-readable medium encoded with a set of three-dimensional coordinates of the three-dimensional structure, wherein, using a graphical display software program, the three-dimensional coordinates create an electronic file that can be visualized on a computer capable of representing the electronic file as a three-dimensional image.

117. A computer-assisted method of structure based drug design of bioactive compounds, comprising the steps of:

(a) providing a model of a UDP-glycosyltransferase (MurG) protein or a donor nucleotide binding site, acceptor binding site or membrane association site; and

(b) designing a chemical compound using said model.

118. The method of claim 117, further comprising the step of synthesizing the chemical compound.

119. The method of claim 118, further comprising the step of evaluating the bioactivity of the synthesized chemical compound.

120. The method of claim 118, wherein the model of the UDP-glycosyltransferase (MurG) protein represents a three-dimensional structure comprising the atomic coordinates listed in Table 1.
121. The method of claim 118, wherein the model of the donor nucleotide binding site represents a three-dimensional structure comprising the atomic coordinates Table 4.
122. The method of claim 118, wherein the model of the acceptor binding site represents a three-dimensional structure comprising the atomic coordinates in Table 5.
123. The method of claim 118, wherein the model of the membrane association site represent a three-dimensional structure comprising the atomic coordinates in Table 6.
124. The method of claim 118, wherein the model comprises a computer image generated when the atomic coordinates listed in Table 1 are analyzed on a computer using a graphical display software program to create an electronic file of the image and visualizing the electronic file on a computer capable of representing the electronic file as a three-dimensional image.
125. The method of claim 118, wherein the step of designing comprises computational screening of one or more databases of chemical compounds in which the three dimensional structure of said compounds are known.
126. The method of claim 125, further comprising interacting a compound identified by the screening step with the model by computer.
127. The method of claim 118, wherein the step of designing comprises directed drug design.
128. The method of claim 118, wherein the step of designing comprises random drug design.
129. The method of claim 118, wherein the step of designing comprises grid-based drug design.
130. The method of claim 118, wherein the step of designing comprises selecting compounds which are predicted to mimic the three-dimensional structure of the three-dimensional structure of the MurG protein.
131. The method of claim 118, wherein the step of designing comprises selecting compounds which are predicted to bind to the three-dimensional structure of the MurG protein.
132. The method of claim 118, wherein the bioactivity is selected from the group consisting of inhibiting binding of a nucleotide donor compound to the MurG protein,

inhibiting binding of an acceptor compound to the MurG protein, or inhibiting association of the MurG Protein to a membrane.

133. A model of the three dimensional structure of a MurG protein, wherein the model is produced by the following method comprising the steps of:

- (a) providing an amino acid sequence of a MurG protein and the amino acid sequence of the *Escherichia coli* MurG protein;
- (b) identifying structurally conserved regions shared between the the MurG protein and the E. coli MurG protein; and
- (c) determining atomic coordinates for the MurG protein by assigning the structurally conserved regions of the MurG protein to a three dimensional structure using a three dimensional structure of the MurG protein which substantially conforms to the atomic coordinates represented in Table 1, to derive a model of the three dimensional structure of the MurG protein amino acid sequence.

134. The model of claim 133, wherein the MurG protein amino acid sequence comprises the sequence of an amino acid sequence selected from the group consisting of the amino acid sequences of MurG proteins as deposited in the NCBI database and identified with Accession Nos. CAB51993, A71316, E70579, C71699, F70195, A43727, JC1275, BVECMG, CEECAM, O83535, Q9ZK59, CAB85280, AAF39020, BAA18775, AAD26629, CAB73295, P37585, Q9ZHA9, Q9ZHDC0, Q9ZBA5, Q9X4H4, Q9WY74, P74657, O06224, Q9Z702, O84766, O69552, J67238, O51708, O25770, O07670, O07109, P45065, CAB66324, AAC68356, AAF06830, P18579, P17443, P17952, P16457, P07862, AAE23178, AAD53936, CAA18668, CAA38869, CAA38868, CAA38867, CAA38866, AAD08196, BAA01453, BAA01455, BAA01454, AAD19042, CAA45558, CAA74235, AAD10537, AAD06652, AAC95450, CAA14869, AAC73201, AAC65509, AAC67113, AAC45636, CAB08640, AAC22793, AAC07193, BAA24357, CAB13395, BAA01355, AAB35538, 1904153C, 1808265B, 1808265A, CAA36866, CAA36869, CAA36868, CAA36867, CAA36776, and AAA99436.

135. A composition for inhibiting the activity of a glycosyltransferase comprising a compound that inhibits the activity of a glycosyltransferase, wherein the compound is identified by the method comprising the steps of:

- (a) providing a three-dimensional structure of a MurG protein;

- (b) using the three-dimensional structure of the MurG protein to design a chemical compound that inhibits activity of a glycosyltransferase;
 - (c) synthesizing the chemical compound; and
 - (d) evaluating the ability of the chemical compound to inhibit the activity of a glycosyltransferase.
136. e composition of claim 135, wherein the glycosyltransferase is a MurG protein.
137. The composition of claim 135, wherein the three-dimensional structure of the MurG protein substantially conforms to atomic coordinates represented by Table 1.
138. The composition of claim 135, wherein the compound is selected from the group consisting of an inorganic and an organic compound.
139. The composition of claim 135, wherein the compound is a substituted pyrimidine analogs
140. The composition of claim 135, wherein the compound is selected from the group consisting of an analog of a MurG protein, a substrate analog of a MurG protein, a donor molecule analog of a MurG protein, and a membrane analog of a MurG protein.
141. The composition of claim 135, further comprising a component selected from the group consisting of an excipient an adjuvant, and a carrier.
142. A composition for stimulating the activity of a glycosyltransferase comprising a compound that stimulates the activity of a glycosyltransferase, wherein the compound is identified by the method comprising the steps of:
- (a) providing a three-dimensional structure of a MurG protein;
 - (b) using the three-dimensional structure of the MurG protein to design a chemical compound that inhibits activity of a glycosyltransferase;
 - (c) synthesizing the chemical compound; and
 - (d) evaluating the ability of the chemical compound to stimulate the activity of a glycosyltransferase.
143. A method to determine a three-dimensional structure of a MurG protein comprising the steps of:
- (a) providing an amino acid sequence of a MurG protein, wherein the three-dimensional structure of the MurG protein is not known;
 - (b) analyzing the pattern of folding of the amino acid sequence in a three-dimensional conformation by fold recognition; and

(c) comparing the pattern of folding of the MurG protein amino acid sequence with the three dimensional structure of the E. coli MurG protein, wherein the three-dimensional structure of the E. coli MurG protein substantially conforms to the atomic coordinates represented in Table 1.

144. A method to derive a model of the three-dimensional structure of a MurG protein comprising the steps of:

- (a) providing an amino acid sequence of a MurG protein;
- (b) identifying structurally conserved regions shared between the MurG protein and the E. coli MurG protein;

(c) determining atomic coordinates for the MurG protein structure by assigning the structurally conserved regions of the MurG protein to a three-dimensional structure using a three dimensional structure of the E. coli MurG protein based on atomic coordinates represented in Table 1 to derive a model of the three dimensional structure of the MurG protein amino acid sequence.

145. The method of claim 144, further comprising assigning atomic coordinates for side chains of said MurG protein by determining sterically allowable positions using a library of rotamers.

146. A method to derive a three dimensional structure of a crystallized MurG protein comprising the steps of:

- (a) comparing the Patterson function of a crystallized MurG protein with the Patterson function of crystalline E. coli MurG protein to produce an electron-density map of the crystallized MurG protein; and

(b) analyzing the electron-density map to produce the three dimensional structure of the crystallized MurG protein.

147. The method of claim 146, further comprising the step of rotating the Patterson function of the crystallized MurG protein on the Patterson function of the crystalline E. coli MurG protein to determine the correct orientation of the crystallized MurG protein in a crystal of said crystallized MurG protein to identify the initial phases of the crystallized MurG protein.

148. The method of claim 146, further comprising the step of electronically stimulating the three dimensional structure of the crystallized MurG protein to derive a computer image of the three dimensional structure of the crystallized MurG protein.

Fig. 1

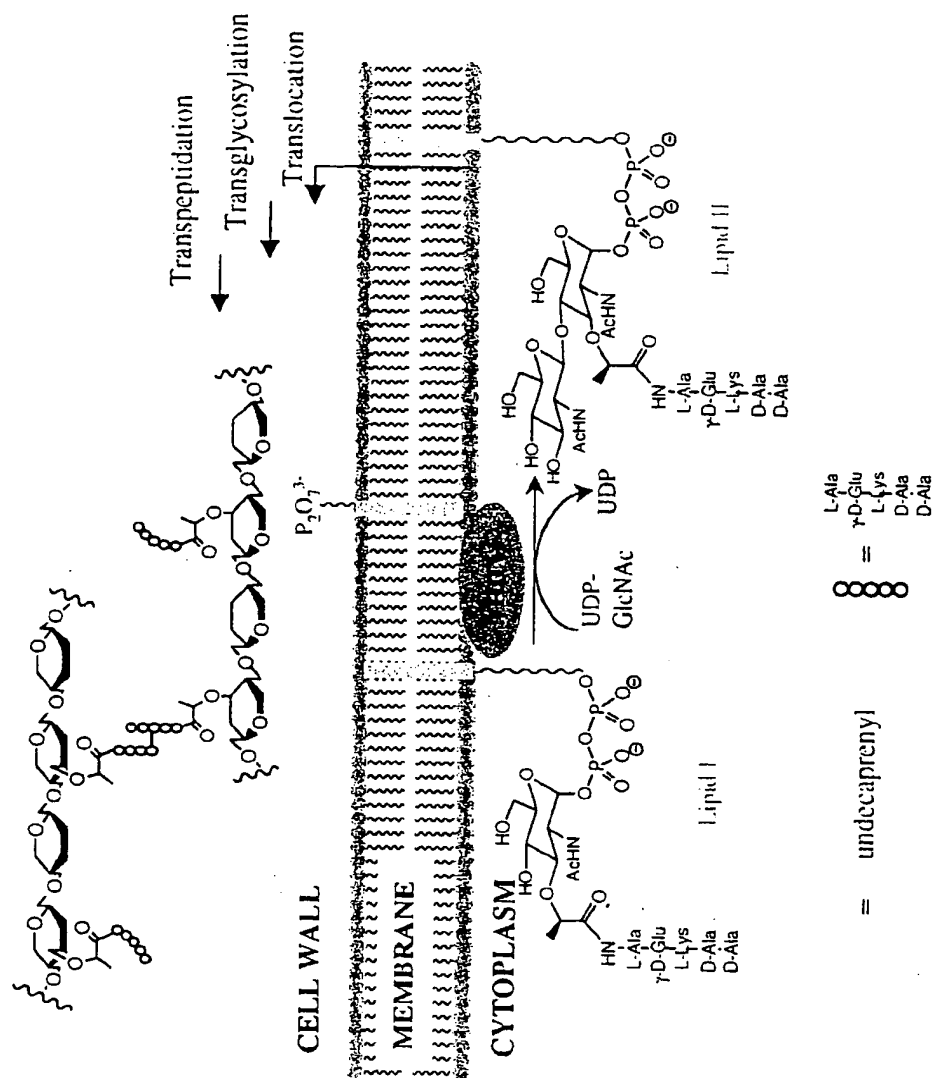


Fig. 2a

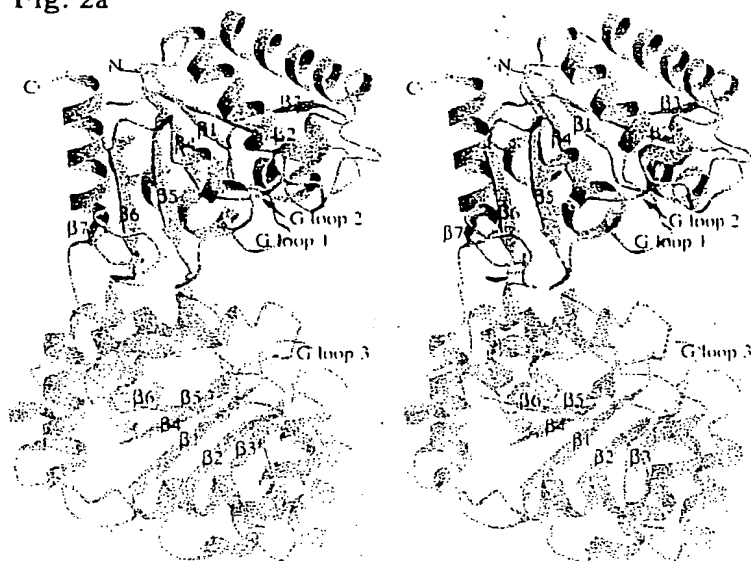
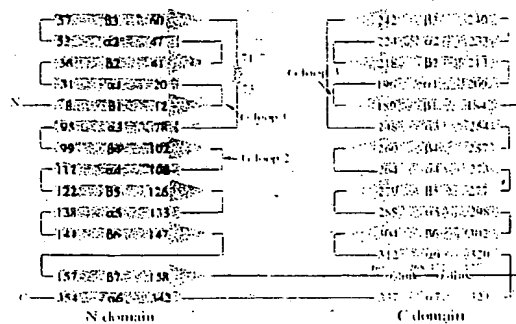


Fig. 2b



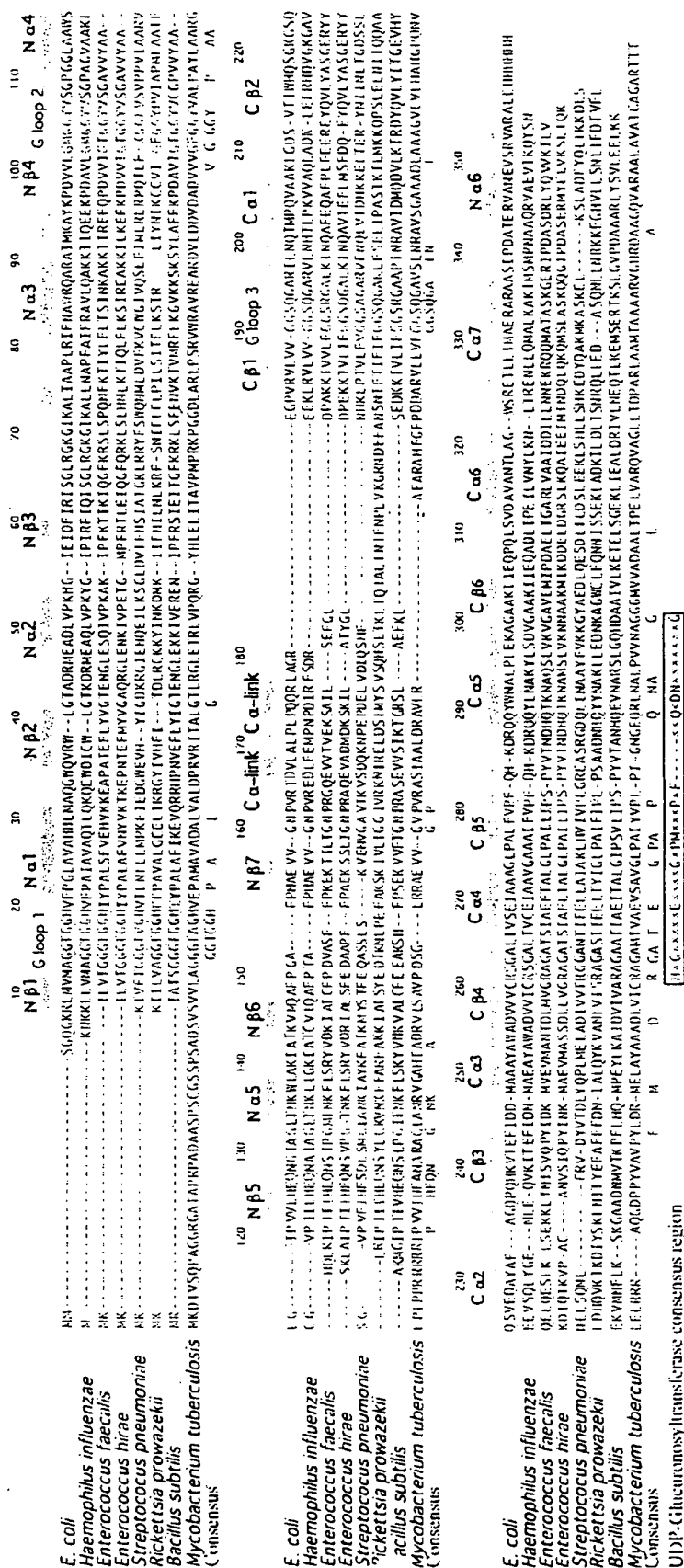


Fig. 3b

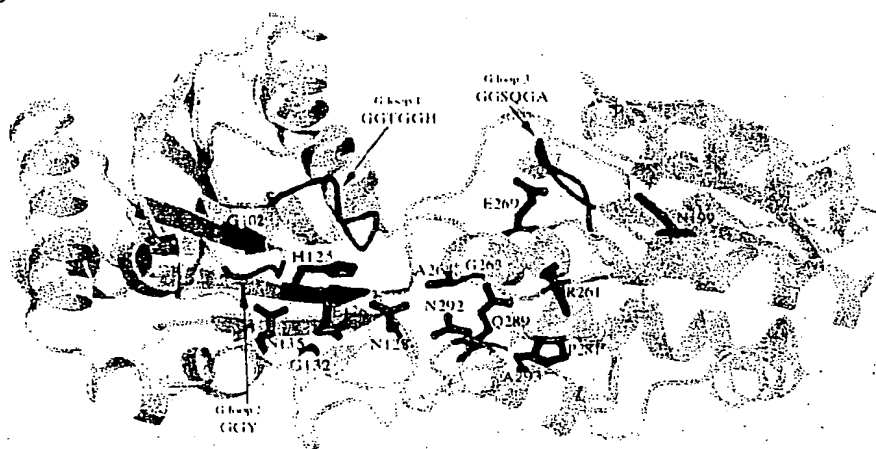
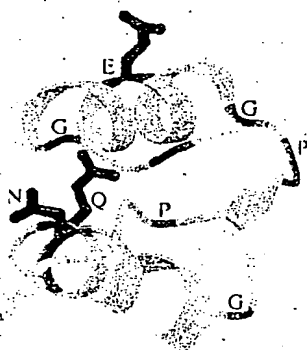
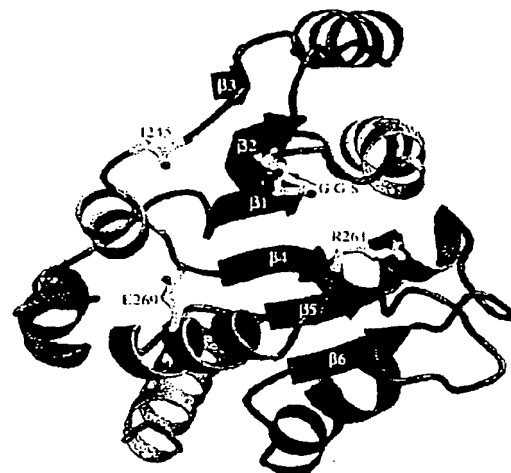
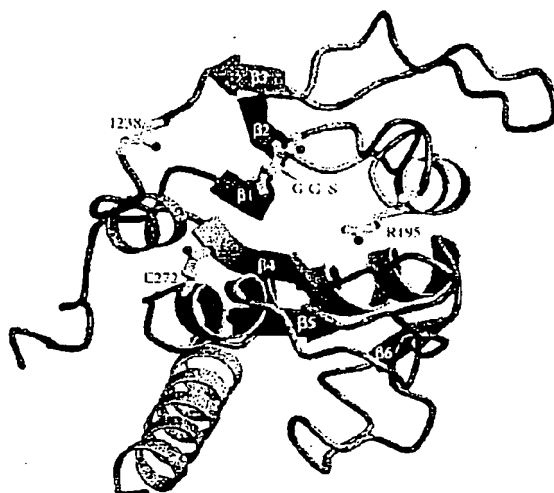


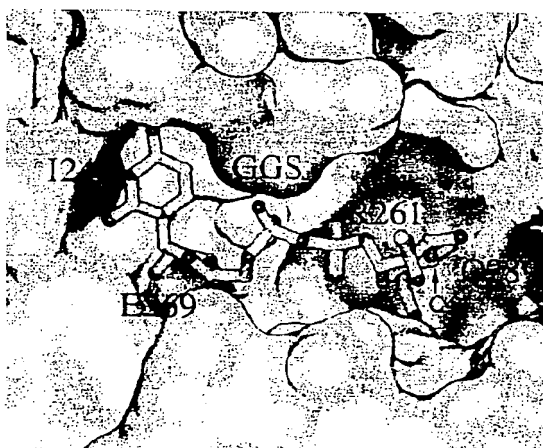
Fig. 3c



A



B



C

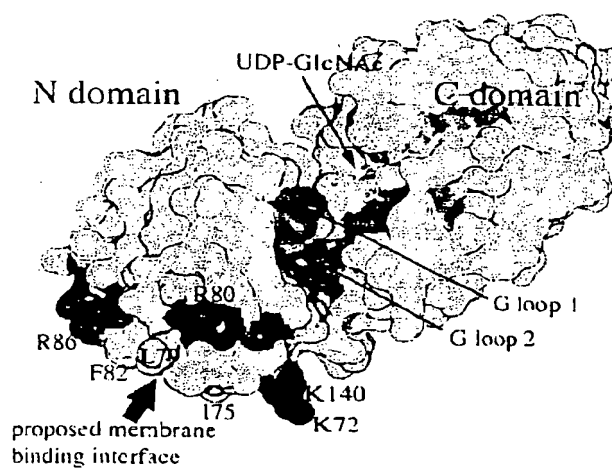


Fig. 4

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ance Notes on Codes and Abbreviations" appearing at the begin-
ning of each regular issue of the PCT Gazette.

(54) Title: CRYSTALLIZING MURG PROTEIN, METHODS OF MAKING AND USING MODELS THEREOF FOR INHIBI-
TION AND STIMULATION VIA COMPOUNDS

(57) Abstract: The present invention relates to crystals of the Escherichia coli MurG, a membrane-associated UDP-glycosyltrans-
ferase involved in peptidoglycan biosynthesis. The present invention also relates to three-dimensional atomic coordinates of the
MurG protein, three-dimensional structures of the protein, and images thereof. The present invention also relates to the atomic co-
ordinates and three-dimensional structures of the α -carbon backbone and the α -carbon backbone and conserved amino acid residue
sidechains of the MurG protein and images thereof. The present invention further relates to three-dimensional atomic coordinates of
the donor nucleotide binding site, the acceptor binding site, and the membrane association site of the MurG protein, three-dimensional
structures of the binding domains, and images thereof. The present invention also relates to computer readable media encoded with
sets of the three dimensional coordinates described herein. The present invention relates to methods of crystallizing MurG proteins.
The present invention relates to models of three dimensional structures of UDP-glycosyltransferases and, in particular, MurG pro-
teins, based on the three dimensional structure of crystals of the Escherichia coli MurG. The present invention
also relates to models of the three dimensional structures of the α -carbon backbone and the α -carbon backbone and conserved amino
acid residue sidechains of UDP-glycosyltransferases and MurG proteins and of the binding sites thereof. The present invention also
relates to methods of drug design using models of this invention, the compounds identified using models of the present invention that
bind, inhibit or stimulate UDP-glycosyltransferases or MurG proteins, and compositions comprising compounds identified using the
models of this invention for therapeutic or diagnostic uses. Also, the present invention relates to methods of making models of the
present invention.

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INTERNATIONAL SEARCH REPORT

International application No.
PCT/US01/11500

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : C12N 9/00

US CL : +35/183

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : +35/183

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

STN: West

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 99/38958 A1 (PRINCETON UNIVERSITY) 05 August 1999, see entire document.	1-2
X	US 5,068,191 A (CLAUSEN et al.) 26 November 1991, see entire document.	45-51



Further documents are listed in the continuation of Box C.



See patent family annex.

* Special categories of cited documents:	"T"	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"A" document defining the general state of the art which is not considered to be of particular relevance	"X"	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"E" earlier document published on or after the international filing date	"Y"	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"Z"	document member of the same patent family
"O" document referring to an oral disclosure, use, exhibition or other means		
"P" document published prior to the international filing date but later than the priority date claimed		

Date of the actual completion of the international search

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INTERNATIONAL SEARCH REPORT

International application No.
PCT/US01/11500

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

Please See Extra Sheet.

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☒ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
1-2; +5-51
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
☐ No protest accompanied the payment of additional search fees.

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION WAS LACKING

This ISA found multiple inventions as follows:

- Group I, Claims 1-2, drawn to the crystalline form of the MurG protein
Group II, Claims 3-6, drawn to the 3-D structure of the crystalline form of the MurG protein.
Group III, Claims 7-8, drawn to the 3-D structure of the donor nucleotide binding site of the MurG protein.
Group IV, Claim 9, drawn to the 3-D structure of the acceptor binding site of the MurG protein.
Group V, Claim 10, drawn to the 3-D structure of the membrane association site of the MurG protein.
Group VI, Claims 11-19, drawn to the computer image of the 3-D MurG protein.
Group VII, Claims 20-23, drawn to the 3-D image of the 3-D image of an alpha-carbon backbone.
Group VIII, Claims 24-26, drawn to the 3-D computer image of the 3-D structure of a donor nucleotide of a donor nucleotide binding site of the MurG protein.
Group IX, Claims 29-33, drawn to the 3-D computer image of a 3-D structure of an acceptor binding site of the MurG protein.
Group X, Claims 34-38, drawn to the 3-D computer image of the 3-D structure of a membrane association site of the MurG protein.
Group XI, Claims 39-41, drawn to the computer readable medium encoded with a set of 3-D coordinates of a MurG protein.
Group XII, Claim 42, drawn to the computer readable medium encoded with a set of 3-D coordinates of a donor nucleotide binding site of a MurG protein.
Group XIII, Claim 43, drawn to the computer readable medium with a set of 3-D coordinates of an acceptor binding site of the MurG protein.
Group XIV, Claim 44, drawn to a computer readable medium encoded with 3-D coordinates of a membrane association site of the MurG protein.
Group XV, Claims 45-51, drawn to a method for identifying a potential inhibitor of a UDP-glycotransferase enzyme.
Group XVI, Claims 52-57, drawn to a model of UDP-glycotransferase where the model represents a 3-D structure.
Group XVII, Claims 58-67, drawn to a model a donor nucleotide binding site of a UDP-glycosyltransferase protein.
Group XVIII, Claims 68-107, drawn to a model of an acceptor binding site of a UDP-glycotransferase protein.
Group XIX, Claims 108-116, drawn to a model of a membrane association site of a UDP-glycotransferase protein.
Group XX, Claims 117-132, drawn to a computer-assisted method of structure based drug design of bioreactive compounds.
Group XXI, Claims 133-134, drawn to a model of a 3-D structure of a MurG protein.
Group XXII, Claims 135-141, drawn to a composition for inhibiting the activity of a glycotransferase.
Group XXIII, Claim 142, drawn to a composition for stimulating the activity of glycotransferase.
Group XXIV, Claims 143-148, drawn to a method to determine the 3-D structure of a MurG protein.

This International Searching Authority considers the international application does not comply with the requirements of unity of invention (Rules 13.1, 13.2 and 13.3) for the reasons indicated below: The inventions listed in Groups 1-24 do not relate a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: the special technical feature for Group I is that the MurG is being claimed in its crystalline form. In Group II the special technical feature is that the 3-D structure of the crystalline form of the MurG protein is being claimed. Group III's special technical feature is that the Group is claiming the 3-D structure of the binding site of MurG. In Group IV the special technical feature emerges as the 3-D structure of the acceptor binding site of the MurG protein. Group V embraces the special technical feature of the 3-D structure of a membrane association site. In Group VI the special technical feature is that of the 3-D computer image of the 3-D structure of the MurG protein. Group VII has the special technical feature of a 3-D structure of a 3-D structure of an alpha-carbon backbone of the MurG protein. Group VIII deals with the special technical feature of the 3-D computer image of the 3-D structure of a donor nucleotide binding site of the instant protein. Group IX involves the special technical feature of the 3-D computer image of the 3-D structure of an acceptor binding site. Group X develops the special technical feature of the 3-D computer image of the 3-D structure of a membrane association site of the MurG protein. In Group XI the subject of the special technical feature of a computer readable medium encoded within a set of 3-D coordinates of the MurG protein are described. Group XII addresses the technical feature of a computer readable medium that is encoded with a set of 3-D coordinates of a donor nucleotide binding site of the MurG protein. In Group XIII is drawn to the special technical feature of a computer readable medium with a 3-D set of coordinates to accommodate the acceptor binding site of a MurG protein. Group XIV involves the special technical feature of a computer readable medium that is encoded with a set of 3-D coordinates that is used for the membrane association site of the MurG protein. Group V is involved with the special technical feature of a method for identifying a potential inhibitor a UDP-glycotransferase enzyme. The special technical feature of Group XVI is that of a 3-D model of UDP-glycotransferase. Group XVII addresses the special technical feature of a model of a donor nucleotide binding site of UDP-glycotransferase. Group XVIII addresses the special technical feature of the model of an acceptor binding site of a UDP glycotransferase. Group XIX consists of the special technical feature of a model of the membrane association site of a UDP-glycotransferase. In Group XX we see that the special

technical feature is that of a computer-assisted method of structure based drug design. In Group XXI the special technical feature that emerges is that of a model of a 3-D structure of a MurG protein. Group XXII deals with the special technical feature of a composition for inhibiting the activity of a glycotransferase. Group XXIII addresses the special technical feature of a composition for the stimulation of activity of a glycotransferase. Finally Group XXIV speaks to the special technical feature of a method to determine the 3-D structure of the MurG protein.

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